



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 106579**

**TO: James Schultz**  
**Location: cm1/12e18/11e12**  
**Art Unit: 1635**  
**Wednesday, October 29, 2003**  
  
**Case Serial Number: 09331204**

**From: Toby Port**  
**Location: Biotech-Chem Library**  
**CM1-6A04**  
**Phone: 308-3534**  
  
**toby.port@uspto.gov**

### **Search Notes**

Dear Examiner Schultz,

Here are the results of your search.  
Please feel free to contact me if you have any questions.

Toby Port



# STIC SEARCH RESULTS FEEDBACK FORM

## Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher* or contact:

Mary Hale, Information Branch Supervisor  
308-4258, CM1-1E01

## Voluntary Results Feedback Form

➤ I am an examiner in Workgroup:  Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature  
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library CM1 – Circ. Desk



106579

STIC-Biotech/ChemLib

---

**From:** Schultz, James  
**Sent:** Thursday, October 23, 2003 9:39 AM  
**To:** STIC-Biotech/ChemLib  
**Subject:** Seq Search request 09/331,204

Hello,

Could you please perform a length limited nucleotide sequence search against SEQ ID NOS: 4-8 and 13 in the above entitled application, where the maximum size of the returned hit is no longer than 22 nucleotides? SEQ ID NOS: 4, 5, 7, and 8 are 18mers, SEQ ID NO: 6 is a 21mer, and SEQ ID NO: 13 is a 12mer. This application recited multiple sequences as originally filed, before we started restricting to one sequence. Also, I need the interference databases searched.

Thanks,  
Doug Schultz

J. Douglas Schultz, Ph.D.  
AU 1635 (Biotechnology)  
Patent Examiner  
United States Patent and Trademark Office  
(703) 308-9355  
(703) 746-3973 (fax)  
Office: CM1 12E18  
Mail: CM1 11E12

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 11:09:34 ; Search time 307.029 Seconds  
(without alignments)  
97.777 Million cell updates/sec

Title: US-09-331-204A-4  
Perfect score: 18  
Sequence: 1 ttggaggggtgtgtggg 18

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2231628 seqs, 833900706 residues

Total number of hits satisfying chosen parameters: 264402

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents NA New.\*

- 1: /cgn2\_6/ptodata/1/pna/PCT\_NEW\_COMB.seq.\*
- 2: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq.\*
- 7: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	14.4	80.0	18	1	PCT-US02-38216-41647 Sequence 41647, A
2	14.4	80.0	19	1	PCT-US02-38216-38943 Sequence 38943, A
3	14.4	80.0	19	1	PCT-US02-38216-46976 Sequence 46976, A
C	14.4	80.0	22	1	PCT-US02-38216-26689 Sequence 26689, A
	14.4	80.0	22	1	PCT-US02-38216-42141 Sequence 42141, A
	14	77.8	18	1	PCT-US02-38216-27376 Sequence 27376, A
6	14	77.8	18	1	PCT-US02-38216-27360 Sequence 27360, A
7	13.8	76.7	19	1	PCT-US02-38216-18278 Sequence 18278, A
8	13.8	76.7	19	1	PCT-US02-38216-47426 Sequence 47426, A
9	13.8	76.7	19	1	PCT-US02-38216-61865 Sequence 61865, A
C	13.8	76.7	20	1	PCT-US02-38216-18418 Sequence 18418, A
	13.8	76.7	20	1	PCT-US02-38216-39237 Sequence 39237, A
	13.8	76.7	21	1	PCT-US02-38216-51847 Sequence 51847, A
12	13.8	76.7	21	1	PCT-US02-38216-75562 Sequence 75562, A
13	13.8	76.7	21	1	PCT-US02-38216-75562 Sequence 75562, A
14	13.8	76.7	21	1	PCT-US02-38216-39240 Sequence 39240, A
15	13.8	76.7	21	1	PCT-US02-38216-38927 Sequence 38927, A
16	13.4	74.4	18	1	PCT-US02-38216-38943 Sequence 38943, A
C	17	13.4	19	1	PCT-US02-38216-53577 Sequence 53577, A
	18	13.4	19	1	PCT-US02-38216-78687 Sequence 78687, A
	19	13.4	20	1	PCT-US02-38216-41804 Sequence 41804, A
19	13.4	74.4	20	1	PCT-US02-38216-41804 Sequence 41804, A
20	13.4	74.4	20	5	US-09-978-333B-2 Sequence 2, Appli
21	13.4	74.4	20	5	US-09-978-333B-2 Sequence 2, Appli
22	13.4	74.4	21	1	PCT-US02-38216-41967 Sequence 41967, A
23	13.4	74.4	21	1	PCT-US02-38216-55622 Sequence 55622, A
24	13.4	74.4	21	1	PCT-US02-38216-57364 Sequence 57364, A
25	13.4	74.4	21	1	PCT-US02-38216-78761 Sequence 78761, A
26	13.4	74.4	22	1	PCT-US02-38216-39492 Sequence 39492, A

27	13.2	73.3	18	1	PCT-US02-38216-51896 Sequence 51896, A
28	13.2	73.3	18	1	PCT-US02-38216-86378 Sequence 86378, A
29	13.2	73.3	19	1	PCT-US02-38216-68852 Sequence 68852, A
30	13.2	73.3	22	1	PCT-US02-38216-57248 Sequence 57248, A
C	31	13	17	6	US-10-669-841-4725 Sequence 4725, Ap
	32	13	17	6	US-10-669-841-4725 Sequence 4725, Ap
C	33	13	17	6	US-10-669-841-5015 Sequence 5015, Ap
	34	13	17	6	US-10-669-841-5015 Sequence 5015, Ap
35	13	72.2	18	1	PCT-US02-38216-9770 Sequence 9770, Ap
36	13	72.2	18	1	PCT-US02-38216-70363 Sequence 70363, A
37	13	72.2	20	1	PCT-US02-38216-76556 Sequence 76556, A
38	12.8	71.1	16	1	PCT-US02-38216-86854 Sequence 86854, A
39	12.8	71.1	18	1	PCT-US02-38216-9675 Sequence 9675, Ap
40	12.8	71.1	18	1	PCT-US02-38216-9731 Sequence 9731, Ap
41	12.8	71.1	18	1	PCT-US02-38216-29535 Sequence 29535, A
42	12.8	71.1	18	1	PCT-US02-38216-36098 Sequence 36098, A
43	12.8	71.1	18	1	PCT-US02-38216-41599 Sequence 41599, A
44	12.8	71.1	18	1	PCT-US02-38216-51842 Sequence 51842, A
45	12.8	71.1	18	1	PCT-US02-38216-60928 Sequence 60928, A

ALIGNMENTS

RESULT 1  
PCT-US02-38216-41647  
; Sequence 41647, Application PC/TUS0238216  
; GENERAL INFORMATION:  
; APPLICANT: Rosetta Genomics LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
; TITLE OF INVENTION: GENES AND USES THEREOF  
; FILE REFERENCE: 55002  
; CURRENT APPLICATION NUMBER: PCT/US02/38216  
; CURRENT FILING DATE: 2002-11-12  
; NUMBER OF SEQ ID NOS: 86841  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 41647  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US02-38216-41647

Query Match 80.0%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 1e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGGGTGGTGGG 18  
|||  
Db 1 GGAGGGGTGGAGGG 16

RESULT 2  
PCT-US02-38216-38943  
; Sequence 38943, Application PC/TUS0238216  
; GENERAL INFORMATION:  
; APPLICANT: Rosetta Genomics LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
; TITLE OF INVENTION: GENES AND USES THEREOF  
; FILE REFERENCE: 55002  
; CURRENT APPLICATION NUMBER: PCT/US02/38216  
; CURRENT FILING DATE: 2002-11-12  
; NUMBER OF SEQ ID NOS: 86841  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 38943  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US02-38216-38943

Query Match 80.0%; Score 14.4; DB 1; Length 19;  
Best Local Similarity 93.8%; Pred. No. 1e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



```
QY      3 GGAGGGGGTGGTGGG 18
      |||||
Db      4 GGAGGGGGTGGCGGG 19

RESULT 3
PCT-US02-38216-46976
; Sequence 46976, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46976
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-46976

Query Match      80.0%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 GGAGGGGGTGGTGGG 18
      |||||
Db      4 GGTGGGGGTGGTGGG 19

RESULT 4
PCT-US02-38216-26689/c
; Sequence 26689, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26689
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-26689

Query Match      80.0%; Score 14.4; DB 1; Length 22;
Best Local Similarity 93.8%; Pred. No. 9.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 TTGAGGGGGTGGTGG 16
      |||||
Db      16 TTGAGGAGGTGGTGG 1

RESULT 5
PCT-US02-38216-42141
; Sequence 42141, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 42141
; LENGTH: 22

QY      3 GGAGGGGGTGGTGGG 18
      |||||
Db      2 GGTGGGGGTGGTGGG 17

Query Match      80.0%; Score 14.4; DB 1; Length 22;
Best Local Similarity 93.8%; Pred. No. 9.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 GGAGGGGGTGGTGGG 18
      |||||
Db      2 GGTGGGGGTGGTGGG 17

RESULT 6
PCT-US02-38216-27376
; Sequence 27376, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27376
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-27376

Query Match      77.8%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TGGAGGGGGTGGTG 15
      |||||
Db      3 TGGAGGGGGTGGTG 16

RESULT 7
PCT-US02-38216-27360
; Sequence 27360, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27360
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-27360

Query Match      77.8%; Score 14; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GGAGGGGGTGGTGG 16
      |||||
Db      5 GGAGGGGGTGGTGG 18

RESULT 8
PCT-US02-38216-18278
; Sequence 18278, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
```

```

; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18278
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-18278

Query Match          76.7%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.7e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGTGGTGGG 17
   |||||
Db 1 TGGAGGGGGTGGAGGG 17

RESULT 9
PCT-US02-38216-47426
; Sequence 47426, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47426
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-47426

Query Match          76.7%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.7e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGAGGGGGTGGTGGG 18
   |||||
Db 3 TGGAGGGGGAGGAGGG 19

RESULT 10
PCT-US02-38216-61865/c
; Sequence 61865, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61865
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-61865

Query Match          76.7%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.7e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGAGGGGGTGGTGGG 18
   |||||
Db 17 TGGAGGGGGTGGTGGT 1

TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: PatentIn version 3.2
SEQ ID NO 18278
LENGTH: 19
TYPE: DNA
ORGANISM: Homo sapiens
PCT-US02-38216-18278

Query Match          76.7%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.7e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGTGGTGGG 17
   |||||
Db 1 TGGAGGGGGTGGAGGG 17

TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: PatentIn version 3.2
SEQ ID NO 18278
LENGTH: 19
TYPE: DNA
ORGANISM: Homo sapiens
PCT-US02-38216-18278

Query Match          76.7%; Score 13.8; DB 1; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.7e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGAGGGGGTGGTGGG 18
   |||||
Db 1 TGGAGGGGGTGGGAGG 17

TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: PatentIn version 3.2
SEQ ID NO 39237
LENGTH: 20
TYPE: DNA
ORGANISM: Homo sapiens
PCT-US02-38216-39237

Query Match          76.7%; Score 13.8; DB 1; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.7e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGAGGGGGTGGTGGG 18
   |||||
Db 4 TGGAGGAGTAGTGGTGGG 20

TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: PatentIn version 3.2
SEQ ID NO 51847
LENGTH: 21
TYPE: DNA
ORGANISM: Homo sapiens
PCT-US02-38216-51847
```

```

RESULT 11
PCT-US02-38216-18418
; Sequence 18418, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18418
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-18418

Query Match          76.7%; Score 13.8; DB 1; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.7e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGAGGGGGTGGTGGG 18
   |||||
Db 1 TGGAGGGGGTGGGAGG 17

RESULT 12
PCT-US02-38216-39237
; Sequence 39237, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39237
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-39237

Query Match          76.7%; Score 13.8; DB 1; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.7e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGAGGGGGTGGTGGG 18
   |||||
Db 4 TGGAGGAGTAGTGGTGGG 20

RESULT 13
PCT-US02-38216-51847
; Sequence 51847, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51847
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-51847
```

Query Match 76.7%; Score 13.8; DB 1; Length 21;  
Best Local Similarity 88.2%; Pred. No. 1.6e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGAGGGGGTGGTGGG 18  
Db 4 TGGTGGGGGGGTGGG 20

RESULT 14  
PCT-US02-38216-75562  
; Sequence 75562, Application PC/TUS0238216  
; GENERAL INFORMATION:  
; APPLICANT: Rosetta Genomics LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
; FILE REFERENCE: 55002  
; CURRENT APPLICATION NUMBER: PCT/US02/38216  
; CURRENT FILING DATE: 2002-11-12  
; NUMBER OF SEQ ID NOS: 86841  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 75562  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US02-38216-75562

Query Match 76.7%; Score 13.8; DB 1; Length 21;  
Best Local Similarity 88.2%; Pred. No. 1.6e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGAGGGGGTGGTGGG 18  
Db 1 TGCAGGGGGTGGTGGAG 17

RESULT 15  
PCT-US02-38216-63940  
; Sequence 63940, Application PC/TUS0238216  
; GENERAL INFORMATION:  
; APPLICANT: Rosetta Genomics LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
; FILE REFERENCE: 55002  
; CURRENT APPLICATION NUMBER: PCT/US02/38216  
; CURRENT FILING DATE: 2002-11-12  
; NUMBER OF SEQ ID NOS: 86841  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 63940  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US02-38216-63940

Query Match 76.7%; Score 13.8; DB 1; Length 22;  
Best Local Similarity 88.2%; Pred. No. 1.6e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGAGGGGGTGGTGGG 18  
Db 3 TGGGGGGGGTGGGGGG 19

Search completed: October 27, 2003, 18:22:55  
Job time : 308.029 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.  
OM nucleic - nucleic search, using sw model  
Run on: October 27, 2003, 10:32:35 ; Search time 2356.29 Seconds  
(without alignments)  
253.343 Million cell updates/sec

Title: US-09-331-204A-4  
Perfect score: 18  
Sequence: 1 ttggaggggtgtgtgggg 18

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 33363688 seqs, 16581889874 residues

Total number of hits satisfying chosen parameters: 2938060

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents\_NA Main:  
1: /cgn2\_6/ptodata/1/pna/PCTUS COMB.seq:  
2: /cgn2\_6/ptodata/1/pna/PCTUS COMB.seq.old:  
3: /cgn2\_6/ptodata/1/pna/US06 COMB.seq:  
4: /cgn2\_6/ptodata/1/pna/US07 COMB.seq:  
5: /cgn2\_6/ptodata/1/pna/US08 COMB.seq:  
6: /cgn2\_6/ptodata/1/pna/US081 COMB.seq:  
7: /cgn2\_6/ptodata/1/pna/US082 COMB.seq:  
8: /cgn2\_6/ptodata/1/pna/US083 COMB.seq:  
9: /cgn2\_6/ptodata/1/pna/US084 COMB.seq:  
10: /cgn2\_6/ptodata/1/pna/US085 COMB.seq:  
11: /cgn2\_6/ptodata/1/pna/US086 COMB.seq:  
12: /cgn2\_6/ptodata/1/pna/US087 COMB.seq:  
13: /cgn2\_6/ptodata/1/pna/US088 COMB.seq:  
14: /cgn2\_6/ptodata/1/pna/US089 COMB.seq:  
15: /cgn2\_6/ptodata/1/pna/US090 COMB.seq:  
16: /cgn2\_6/ptodata/1/pna/US091 COMB.seq:  
17: /cgn2\_6/ptodata/1/pna/US092A COMB.seq:  
18: /cgn2\_6/ptodata/1/pna/US092B COMB.seq:  
19: /cgn2\_6/ptodata/1/pna/US093A COMB.seq:  
20: /cgn2\_6/ptodata/1/pna/US093B COMB.seq:  
21: /cgn2\_6/ptodata/1/pna/US094 COMB.seq:  
22: /cgn2\_6/ptodata/1/pna/US095A COMB.seq:  
23: /cgn2\_6/ptodata/1/pna/US095B COMB.seq:  
24: /cgn2\_6/ptodata/1/pna/US095C COMB.seq:  
25: /cgn2\_6/ptodata/1/pna/US095D COMB.seq:  
26: /cgn2\_6/ptodata/1/pna/US096A COMB.seq:  
27: /cgn2\_6/ptodata/1/pna/US096B COMB.seq:  
28: /cgn2\_6/ptodata/1/pna/US096C COMB.seq:  
29: /cgn2\_6/ptodata/1/pna/US096D COMB.seq:  
30: /cgn2\_6/ptodata/1/pna/US096E COMB.seq:  
31: /cgn2\_6/ptodata/1/pna/US097A COMB.seq:  
32: /cgn2\_6/ptodata/1/pna/US097B COMB.seq:  
33: /cgn2\_6/ptodata/1/pna/US097C COMB.seq:  
34: /cgn2\_6/ptodata/1/pna/US098A COMB.seq:  
35: /cgn2\_6/ptodata/1/pna/US098B COMB.seq:  
36: /cgn2\_6/ptodata/1/pna/US098C COMB.seq:  
37: /cgn2\_6/ptodata/1/pna/US098D COMB.seq:  
38: /cgn2\_6/ptodata/1/pna/US099A COMB.seq:  
39: /cgn2\_6/ptodata/1/pna/US099B COMB.seq:  
40: /cgn2\_6/ptodata/1/pna/US099C COMB.seq:  
41: /cgn2\_6/ptodata/1/pna/US099D COMB.seq:  
42: /cgn2\_6/ptodata/1/pna/US099E COMB.seq:  
43: /cgn2\_6/ptodata/1/pna/US099F COMB.seq:

44: /cgn2\_6/ptodata/1/pna/US100A COMB.seq:  
45: /cgn2\_6/ptodata/1/pna/US100B COMB.seq:  
46: /cgn2\_6/ptodata/1/pna/US101A COMB.seq:  
47: /cgn2\_6/ptodata/1/pna/US101B COMB.seq:  
48: /cgn2\_6/ptodata/1/pna/US102A COMB.seq:  
49: /cgn2\_6/ptodata/1/pna/US102B COMB.seq:  
50: /cgn2\_6/ptodata/1/pna/US103A COMB.seq:  
51: /cgn2\_6/ptodata/1/pna/US103B COMB.seq:  
52: /cgn2\_6/ptodata/1/pna/US104A COMB.seq:  
53: /cgn2\_6/ptodata/1/pna/US104B COMB.seq:  
54: /cgn2\_6/ptodata/1/pna/US6000 COMB.seq:  
55: /cgn2\_6/ptodata/1/pna/US6001 COMB.seq:  
56: /cgn2\_6/ptodata/1/pna/US6002 COMB.seq:  
57: /cgn2\_6/ptodata/1/pna/US6003 COMB.seq:  
58: /cgn2\_6/ptodata/1/pna/US6004 COMB.seq:  
59: /cgn2\_6/ptodata/1/pna/US6005 COMB.seq:  
60: /cgn2\_6/ptodata/1/pna/US6006 COMB.seq:  
61: /cgn2\_6/ptodata/1/pna/US6007 COMB.seq:  
62: /cgn2\_6/ptodata/1/pna/US6008 COMB.seq:  
63: /cgn2\_6/ptodata/1/pna/US6009 COMB.seq:  
64: /cgn2\_6/ptodata/1/pna/US6010 COMB.seq:  
65: /cgn2\_6/ptodata/1/pna/US6011 COMB.seq:  
66: /cgn2\_6/ptodata/1/pna/US6012 COMB.seq:  
67: /cgn2\_6/ptodata/1/pna/US6013 COMB.seq:  
68: /cgn2\_6/ptodata/1/pna/US6014 COMB.seq:  
69: /cgn2\_6/ptodata/1/pna/US6015 COMB.seq:  
70: /cgn2\_6/ptodata/1/pna/US6016 COMB.seq:  
71: /cgn2\_6/ptodata/1/pna/US6017 COMB.seq:  
72: /cgn2\_6/ptodata/1/pna/US6018 COMB.seq:  
73: /cgn2\_6/ptodata/1/pna/US6019 COMB.seq:  
74: /cgn2\_6/ptodata/1/pna/US6020 COMB.seq:  
75: /cgn2\_6/ptodata/1/pna/US6021 COMB.seq:  
76: /cgn2\_6/ptodata/1/pna/US6022 COMB.seq:  
77: /cgn2\_6/ptodata/1/pna/US6023A COMB.seq:  
78: /cgn2\_6/ptodata/1/pna/US6023B COMB.seq:  
79: /cgn2\_6/ptodata/1/pna/US6024 COMB.seq:  
80: /cgn2\_6/ptodata/1/pna/US6025 COMB.seq:  
81: /cgn2\_6/ptodata/1/pna/US6026 COMB.seq:  
82: /cgn2\_6/ptodata/1/pna/US6027 COMB.seq:  
83: /cgn2\_6/ptodata/1/pna/US6028 COMB.seq:  
84: /cgn2\_6/ptodata/1/pna/US6029 COMB.seq:  
85: /cgn2\_6/ptodata/1/pna/US6030 COMB.seq:  
86: /cgn2\_6/ptodata/1/pna/US6031 COMB.seq:  
87: /cgn2\_6/ptodata/1/pna/US6032 COMB.seq:  
88: /cgn2\_6/ptodata/1/pna/US6033 COMB.seq:  
89: /cgn2\_6/ptodata/1/pna/US6034 COMB.seq:  
90: /cgn2\_6/ptodata/1/pna/US6035 COMB.seq:  
91: /cgn2\_6/ptodata/1/pna/US6036 COMB.seq:  
92: /cgn2\_6/ptodata/1/pna/US6037 COMB.seq:  
93: /cgn2\_6/ptodata/1/pna/US6038 COMB.seq:  
94: /cgn2\_6/ptodata/1/pna/US6039 COMB.seq:  
95: /cgn2\_6/ptodata/1/pna/US6040 COMB.seq:  
96: /cgn2\_6/ptodata/1/pna/US6041 COMB.seq:  
97: /cgn2\_6/ptodata/1/pna/US6042 COMB.seq:  
98: /cgn2\_6/ptodata/1/pna/US6043 COMB.seq:  
99: /cgn2\_6/ptodata/1/pna/US6044 COMB.seq:  
100: /cgn2\_6/ptodata/1/pna/US6045 COMB.seq:  
101: /cgn2\_6/ptodata/1/pna/US6046 COMB.seq:  
102: /cgn2\_6/ptodata/1/pna/US6047 COMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	8	US-08-387-041A-3 Sequence 3, Appli
2	18	100.0	18	19	US-09-331-204-1 Sequence 1, Appli
3	18	100.0	18	19	US-09-331-204A-4 Sequence 4, Appli
4	18	100.0	18	33	US-09-786-436-17 Sequence 17, Appli

C 5 18 100.0 18 33 US-09-786-436-42 Sequence 42, Appl  
6 18 100.0 21 8 US-08-387-041A-4 Sequence 4, Appl  
7 18 100.0 21 19 US-09-331-204-6 Sequence 6, Appl  
8 18 100.0 21 19 US-09-331-204A-6 Sequence 6, Appl  
9 16.4 91.1 18 19 US-09-331-204-5 Sequence 5, Appl  
10 16.4 91.1 18 19 US-09-331-204A-8 Sequence 8, Appl  
11 14.8 82.2 18 19 US-09-331-204A-7 Sequence 7, Appl  
12 14.8 82.2 18 19 US-09-331-204A-9 Sequence 9, Appl  
13 14.8 82.2 19 19 US-09-331-204-4 Sequence 4, Appl  
14 14.4 80.0 18 50 US-10-310-188-41647 Sequence 41647, A  
15 14.4 80.0 19 50 US-10-310-188-38943 Sequence 38943, A  
16 14.4 80.0 19 50 US-10-310-188-46976 Sequence 46976, A  
17 14.4 80.0 22 50 US-10-310-188-26689 Sequence 26689, A  
18 14.4 80.0 22 50 US-10-310-188-42141 Sequence 42141, A  
19 14 77.8 18 50 US-10-310-188-27376 Sequence 27376, A  
20 14 77.8 19 50 US-10-310-188-27360 Sequence 27360, A  
21 13.8 76.7 19 50 US-10-310-188-18278 Sequence 18278, A  
22 13.8 76.7 19 50 US-10-310-188-47426 Sequence 47426, A  
23 13.8 76.7 19 50 US-10-310-188-61865 Sequence 61865, A  
24 13.8 76.7 20 50 US-10-310-188-18418 Sequence 18418, A  
25 13.8 76.7 20 50 US-10-310-188-39237 Sequence 39237, A  
26 13.8 76.7 21 50 US-10-310-188-51847 Sequence 51847, A  
27 13.8 76.7 21 50 US-10-310-188-75562 Sequence 75562, A  
28 13.8 76.7 22 9 US-08-472-801-186 Sequence 186, App  
29 13.8 76.7 22 9 US-08-472-801-2653 Sequence 2653, App  
30 13.8 76.7 22 9 US-08-472-801-2660 Sequence 2660, App  
31 13.8 76.7 22 11 US-08-668-235-186 Sequence 186, App  
32 13.8 76.7 22 11 US-08-668-235-2653 Sequence 2653, App  
33 13.8 76.7 22 11 US-08-668-235-2660 Sequence 2660, App  
34 13.8 76.7 22 47 US-10-160-499-186 Sequence 186, App  
35 13.8 76.7 22 47 US-10-160-499-2653 Sequence 2653, App  
36 13.8 76.7 22 47 US-10-160-499-2660 Sequence 2660, App  
37 13.8 76.7 22 50 US-10-310-188-63940 Sequence 63940, A  
38 13.6 75.6 22 42 US-09-979-666B-79 Sequence 79, Appl  
39 13.4 74.4 15 1 PCT-US01-12255-8 Sequence 8, Appl  
40 13.4 74.4 15 2 PCT-US01-12255-8 Sequence 8, Appl  
41 13.4 74.4 16 50 US-10-303-778-1282 Sequence 1282, App  
42 13.4 74.4 18 50 US-10-310-188-38927 Sequence 38927, A  
43 13.4 74.4 19 49 US-10-293-338-6664 Sequence 6664, App  
44 13.4 74.4 19 50 US-10-310-188-53577 Sequence 53577, A  
45 13.4 74.4 19 50 US-10-310-188-78687 Sequence 78687, A

ALIGNMENTS

RESULT 1  
US-08-387-041A-3  
; Sequence 3, Application US/08387041A  
; GENERAL INFORMATION:  
; APPLICANT: Tam, Robert C.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATION  
; TITLE OF INVENTION: OF CD28 EXPRESSION  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/387,041A  
; FILING DATE: 02-FEB-1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Halluin, Albert P.  
; REGISTRATION NUMBER: 25,227

; REFERENCE/DOCKET NUMBER: 8250-011  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-854-3660  
; TELEFAX: 415-854-3694  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
US-08-387-041A-3  
Query Match 100.0%; Score 18; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGGAGGGGGTGGTGGGG 18  
|||  
Db 1 TTGGAGGGGGTGGTGGGG 18  
|||  
RESULT 2  
US-09-331-204-1  
; Sequence 1, Application US/09331204  
; GENERAL INFORMATION:  
; APPLICANT: Tam, Robert  
; TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN  
; TITLE OF INVENTION: IMMUNE RESPONSE  
; FILE REFERENCE: ICNSequence  
; CURRENT APPLICATION NUMBER: US/09/331,204  
; CURRENT FILING DATE: 1999-08-20  
; PRIOR APPLICATION NUMBER: PCT/US97/23927  
; PRIOR FILING DATE: 1997-12-19  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: An oligomer  
; OTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic  
; OTHER INFORMATION: acid including oligomers consisting of naturally  
; OTHER INFORMATION: occurring bases, sugars and intersugar  
US-09-331-204-1  
Query Match 100.0%; Score 18; DB 19; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGGAGGGGGTGGTGGGG 18  
|||  
Db 1 TTGGAGGGGGTGGTGGGG 18  
|||  
RESULT 3  
US-09-331-204A-4  
; Sequence 4, Application US/09331204A  
; GENERAL INFORMATION:  
; APPLICANT: ICN Pharmaceuticals, Inc.  
; APPLICANT: Tam, Robert  
; TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Res  
; FILE REFERENCE: 216/013-US1  
; CURRENT APPLICATION NUMBER: US/09/331,204A  
; CURRENT FILING DATE: 1999-08-20  
; PRIOR APPLICATION NUMBER: PCT/US97/23927  
; PRIOR FILING DATE: 1997-12-19  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4  
; LENGTH: 18

; TYPE: DNA  
; ORGANISM: synthetic construct  
US-09-331-204A-4

Query Match 100.0%; Score 18; DB 19; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGAGGGGGTGGTGGG 18  
Db 1 TTGGAGGGGGTGGTGGG 18

RESULT 4

US-09-786-436-17  
; Sequence 17, Application US/09786436  
; GENERAL INFORMATION:  
; APPLICANT: Wagner, Hermann  
; APPLICANT: Lipford, Grayson  
; APPLICANT: Heeg, Klaus  
; TITLE OF INVENTION: G-Motif Oligonucleotides and Uses  
; FILE REFERENCE: C1041/7010 (AWS)  
; CURRENT APPLICATION NUMBER: US/09/786,436  
; CURRENT FILING DATE: 2001-03-02  
; PRIOR APPLICATION NUMBER: PCT/EP99/06502  
; PRIOR FILING DATE: 1999-09-03  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 17  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-09-786-436-17

Query Match 100.0%; Score 18; DB 33; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGAGGGGGTGGTGGG 18  
Db 1 TTGGAGGGGGTGGTGGG 18

RESULT 5

US-09-786-436-42/c  
; Sequence 42, Application US/09786436  
; GENERAL INFORMATION:  
; APPLICANT: Wagner, Hermann  
; APPLICANT: Lipford, Grayson  
; APPLICANT: Heeg, Klaus  
; TITLE OF INVENTION: G-Motif Oligonucleotides and Uses  
; FILE REFERENCE: C1041/7010 (AWS)  
; CURRENT APPLICATION NUMBER: US/09/786,436  
; CURRENT FILING DATE: 2001-03-02  
; PRIOR APPLICATION NUMBER: PCT/EP99/06502  
; PRIOR FILING DATE: 1999-09-03  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 42  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-09-786-436-42

Query Match 100.0%; Score 18; DB 33; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGAGGGGGTGGTGGG 18  
Db 18 TTGGAGGGGGTGGTGGG 1

RESULT 6

US-08-387-041A-4  
; Sequence 4, Application US/08387041A  
; GENERAL INFORMATION:  
; APPLICANT: Tam, Robert C.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATION  
; TITLE OF INVENTION: OF CD28 EXPRESSION  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/387,041A  
; FILING DATE: 02-FEB-1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Halluin, Albert P.  
; REGISTRATION NUMBER: 25,227  
; REFERENCE/DOCKET NUMBER: 8250-011  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-854-3660  
; TELEFAX: 415-854-3694  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 21 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
US-08-387-041A-4

Query Match 100.0%; Score 18; DB 8; Length 21;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGAGGGGGTGGTGGG 18  
Db 4 TTGGAGGGGGTGGTGGG 21

RESULT 7

US-09-331-204-6  
; Sequence 6, Application US/09331204  
; GENERAL INFORMATION:  
; APPLICANT: Tam, Robert  
; TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN  
; TITLE OF INVENTION: IMMUNE RESPONSE  
; FILE REFERENCE: ICNsequence  
; CURRENT APPLICATION NUMBER: US/09/331,204  
; CURRENT FILING DATE: 1999-08-20  
; PRIOR APPLICATION NUMBER: PCT/US97/23927  
; PRIOR FILING DATE: 1997-12-19  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 21  
; TYPE: DNA



```
/ CURRENT APPLICATION NUMBER: US/09/331,204A
/ CURRENT FILING DATE: 1999-08-20
/ PRIOR APPLICATION NUMBER: PCT/US97/23927
/ PRIOR FILING DATE: 1997-12-19
/ NUMBER OF SEQ ID NOS: 28
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 9
/ LENGTH: 18
/ TYPE: DNA
/ ORGANISM: synthetic construct
US-09-331-204A-9

Query Match      82.2%; Score 14.8; DB 19; Length 18;
Best Local Similarity 88.9%; Pred. No. 7.8e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TTGAGGGGGTGGTGGG 18
      ||||| ||||| |||||
Db      1 TTGAGGCGGTGGTGGC 18

RESULT 13
US-09-331-204-4
; Sequence 4, Application US/09331204
; GENERAL INFORMATION:
; APPLICANT: Tam, Robert
; TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN
; FILE REFERENCE: ICNSequence
; CURRENT APPLICATION NUMBER: US/09/331,204
; CURRENT FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: PCT/US97/23927
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: An oligomer
; OTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic
; OTHER INFORMATION: acid. This term includes oligomers consisting of
; OTHER INFORMATION: naturally occurring bases, sugars and intersugar (
US-09-331-204-4

Query Match      82.2%; Score 14.8; DB 19; Length 19;
Best Local Similarity 88.9%; Pred. No. 7.8e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TTGAGGGGGTGGTGGG 18
      ||||| ||||| |||||
Db      1 TTGAGGGGGGAGGAGGG 18

RESULT 14
US-10-310-188-41647
; Sequence 41647, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGemonics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41647
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-41647
```

```
Query Match      80.0%; Score 14.4; DB 50; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.1e+05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 GGAGGGGGTGGTGGG 18
      ||||| ||||| |||||
Db      1 GGAGGGGGTGGAGGG 16

RESULT 15
US-10-310-188-38943
; Sequence 38943, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGemonics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38943
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-38943

Query Match      80.0%; Score 14.4; DB 50; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.1e+05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 GGAGGGGGTGGTGGG 18
      ||||| ||||| |||||
Db      4 GGAGGGGGTGGCGGG 19

Search completed: October 27, 2003, 17:52:51
Job time : 2357.29 secs
```



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: October 27, 2003, 11:25:34 ; Search time 387.943 Seconds  
(without alignments)  
124.432 Million cell updates/sec

Title: US-09-331-204A-4  
Perfect score: 18  
Sequence: 1 ttggaggggggtgtgggg 18

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1792395 seqs, 1340900451 residues

Total number of hits satisfying chosen parameters: 408622

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA.\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*
- 16: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*
- 17: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	13.4	74.4	20	10	US-09-874-162A-22
C 2	13	72.2	17	11	US-09-740-332-2132
C 3	13	72.2	17	11	US-09-740-332-2133
C 4	13	72.2	17	11	US-09-740-332-2422
C 5	13	72.2	17	11	US-09-740-332-2423
C 6	13	72.2	17	12	US-09-817-879-2132
C 7	13	72.2	17	12	US-09-817-879-2133
C 8	13	72.2	17	12	US-09-817-879-2422
C 9	13	72.2	17	12	US-09-817-879-2423
C 10	12.8	71.1	17	12	US-10-059-877-26
C 11	12.8	71.1	17	12	US-10-303-109A-30
C 12	12.8	71.1	17	14	US-10-059-888-26
C 13	12.8	71.1	20	14	US-10-181-846-35
C 14	12.8	71.1	22	11	US-09-988-115A-3
C 15	12.8	71.1	22	11	US-09-988-115A-13
C 16	12.8	71.1	22	11	US-09-988-115A-20

C 17	71.1	12.8	22	11	US-09-988-115A-22	Sequence 22, Appl
C 18	68.9	12.4	20	12	US-10-032-585-5333	Sequence 5333, Ap
C 19	67.8	12.2	17	10	US-09-263-959-904	Sequence 904, App
C 20	67.8	12.2	18	14	US-10-196-460-4	Sequence 4, Appli
C 21	67.8	12.2	19	12	US-10-318-628-9	Sequence 9, Appli
C 22	67.8	12.2	20	9	US-09-854-883-174	Sequence 174, App
C 23	67.8	12.2	20	10	US-09-755-004-10	Sequence 10, Appl
C 24	67.8	12.2	20	11	US-09-779-152-56	Sequence 56, Appl
C 25	67.8	12.2	20	12	US-09-767-421-36	Sequence 36, Appl
C 26	67.8	12.2	20	14	US-10-023-610-56	Sequence 56, Appl
C 27	67.8	12.2	21	9	US-09-828-034-11	Sequence 11, Appl
C 28	67.8	12.2	21	9	US-09-828-034-30	Sequence 30, Appl
C 29	67.8	12.2	21	9	US-09-828-034-31	Sequence 31, Appl
C 30	66.7	12	18	12	US-10-204-884-59	Sequence 59, Appl
C 31	65.6	11.8	16	12	US-10-059-877-22	Sequence 22, Appl
C 32	65.6	11.8	16	14	US-10-059-888-22	Sequence 22, Appl
C 33	65.6	11.8	17	10	US-09-263-959-900	Sequence 900, App
C 34	65.6	11.8	17	11	US-09-930-423-522	Sequence 523, App
C 35	65.6	11.8	17	11	US-09-930-423-523	Sequence 523, App
C 36	65.6	11.8	17	12	US-09-745-237A-522	Sequence 523, App
C 37	65.6	11.8	17	12	US-09-745-237A-523	Sequence 523, App
C 38	65.6	11.8	17	12	US-10-061-201-1934	Sequence 1934, Ap
C 39	65.6	11.8	17	12	US-10-061-201-1935	Sequence 1935, Ap
C 40	65.6	11.8	17	12	US-10-061-201-1936	Sequence 1936, Ap
C 41	65.6	11.8	18	10	US-09-263-959-921	Sequence 921, App
C 42	65.6	11.8	18	11	US-09-846-033B-117	Sequence 117, App
C 43	65.6	11.8	18	14	US-10-006-069A-117	Sequence 117, App
C 44	65.6	11.8	19	14	US-10-010-920-67	Sequence 67, Appl
C 45	65.6	11.8	19	14	US-10-008-721-67	Sequence 67, Appl

ALIGNMENTS

RESULT 1

US-09-874-162A-22/c  
; Sequence 22, Application US/09874162A  
; Patent No. US20020155452A1  
; GENERAL INFORMATION:  
; APPLICANT: Koontz, Jason  
; APPLICANT: Sklar, Jeffrey  
; TITLE OF INVENTION: FUSION OF JAZF1 AND JJAZ1 GENES IN  
; TITLE OF INVENTION: ENDOMETRIAL STROMAL TUMORS  
; FILE REFERENCE: 05311-024001  
; CURRENT APPLICATION NUMBER: US/09/874,162A  
; CURRENT FILING DATE: 2001-06-04  
; PRIOR APPLICATION NUMBER: US 60/209,093  
; PRIOR FILING DATE: 2000-06-02  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 22  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: primer for PCR

US-09-874-162A-22

Query Match 74.4%; Score 13.4; DB 10; Length 20;  
Best Local Similarity 93.3%; Pred. No. 1.3e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGGGGTGTGGG 17

|||||

Db 19 GGAGGGGGTGTGGG 5

RESULT 2

US-09-740-332-2132/c  
; Sequence 2132, Application US/09740332  
; Publication No. US20030125270A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals Inc.





; Sequence 30, Application US/10303109A  
; Publication No. US20030194726A1  
; GENERAL INFORMATION:  
; APPLICANT: BOLCHAKOVA, Elena  
; APPLICANT: ROZZELLE, James  
; TITLE OF INVENTION: Thermus Oshimai Nucleic Acid Polymerases  
; FILE REFERENCE: 4777US  
; CURRENT APPLICATION NUMBER: US/10/303,109A  
; CURRENT FILING DATE: 2002-11-22  
; PRIOR APPLICATION NUMBER: US 60/334,798  
; PRIOR FILING DATE: 2001-11-30  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 30:  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Thermus oshimai  
US-10-303-109A-30

Query Match 71.1%; Score 12.8; DB 12; Length 17;  
Best Local Similarity 87.5%; Pred. No. 2.4e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGAGGGGGTGGTGGG 17  
|||||  
Db 16 TGGAGGTGGAGGTGGG 1

RESULT 12  
US-10-059-888-26  
; Sequence 26, Application US/10059888  
; Publication No. US20030025882A1  
; GENERAL INFORMATION:  
; APPLICANT: CHAO, LEE  
; APPLICANT: CHAO, JULIE  
; APPLICANT: SONG, QING  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CORRELATING  
; TITLE OF INVENTION: TISSUE KALLIKREIN GENE PROMOTER POLYMORPHISMS WITH ESSENTIAL  
; TITLE OF INVENTION: HYPERTENSION  
; FILE REFERENCE: 19113.0081U2  
; CURRENT APPLICATION NUMBER: US/10/059,888  
; CURRENT FILING DATE: 2002-01-29  
; PRIOR APPLICATION NUMBER: 09/495,140  
; PRIOR FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: 09/389,566  
; PRIOR FILING DATE: 1999-09-03  
; PRIOR APPLICATION NUMBER: 08/856,141  
; PRIOR FILING DATE: 1997-05-14  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 26  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence./No. US20030025882A1e =  
; OTHER INFORMATION: synthetic construct  
US-10-059-888-26

Query Match 71.1%; Score 12.8; DB 14; Length 17;  
Best Local Similarity 87.5%; Pred. No. 2.4e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGGTGGTGGG 18  
|||||  
Db 1 GGAGGGGGGGGGGGG 16

RESULT 13  
US-10-181-846-35  
; Sequence 35, Application US/10181846  
; Publication No. US20030083297A1  
; GENERAL INFORMATION:

; APPLICANT: Nicholas M. Dean  
; APPLICANT: Lex M. Cowser  
; TITLE OF INVENTION: ANTISENSE MODULATION OF DAXX EXPRESSION  
; FILE REFERENCE: RTSP-0363  
; CURRENT APPLICATION NUMBER: US/10/181,846  
; CURRENT FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: PCT/US01/01416  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: 09/490,692  
; PRIOR FILING DATE: 2000-01-24  
; NUMBER OF SEQ ID NOS: 176  
; SEQ ID NO 35  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-181-846-35

Query Match 71.1%; Score 12.8; DB 14; Length 20;  
Best Local Similarity 87.5%; Pred. No. 2.3e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGTGGTGG 16  
|||||  
Db 3 TTGGAGGTGGTGGCGG 18

RESULT 14  
US-09-988-115A-3/c  
; Sequence 3, Application US/09988115A  
; Publication No. US20030037347A1  
; GENERAL INFORMATION:  
; APPLICANT: Robl, James M.  
; APPLICANT: Goldsby, Richard A.  
; APPLICANT: Ferguson, Stacy E.  
; APPLICANT: Kuroiwa, Yoshima  
; APPLICANT: Tomizuka, Kazuma  
; APPLICANT: Ishida, Isao  
; TITLE OF INVENTION: Expression of Xenogenous (Human)  
; TITLE OF INVENTION: Immunoglobulins in Cloned, Transgenic Ungulates  
; FILE REFERENCE: 50195/008003  
; CURRENT APPLICATION NUMBER: US/09/988,115A  
; CURRENT FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,625  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: US 60/256,458  
; PRIOR FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: US 09/714,185  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: US 60/166,410  
; PRIOR FILING DATE: 1999-11-19  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Primer  
US-09-988-115A-3

Query Match 71.1%; Score 12.8; DB 11; Length 22;  
Best Local Similarity 87.5%; Pred. No. 2.3e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGTGGTGG 16  
|||||  
Db 21 TTGGAGGGTTTGGTGG 6

RESULT 15  
US-09-988-115A-13/c

```
; Sequence 13, Application US/09988115A
; Publication No. US20030037347A1
; GENERAL INFORMATION:
; APPLICANT: Robt, James M.
; APPLICANT: Goldsby, Richard A.
; APPLICANT: Ferguson, Stacy E.
; APPLICANT: Kuroiwa, Yoshima
; APPLICANT: Tomizuka, Kazuma
; APPLICANT: Ishida, Isao
; TITLE OF INVENTION: Expression of Xenogenous (Human)
; FILE OF INVENTION: Immunoglobulins in Cloned, Transgenic Ungulates
; FILE REFERENCE: 50195/008003
; CURRENT APPLICATION NUMBER: US/09/988,115A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,625
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: US 60/256,458
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/714,185
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 60/166,410
; PRIOR FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Primer
US-09-988-115A-13
```

```
Query Match      71.1%; Score 12.8; DB 11; Length 22;
Best Local Similarity 87.5%; Pred. No. 2.3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TTGGAGGGGGTGGTGG 16
Db      21 TTGGAGGGTGGTGG 6
```

Search completed: October 27, 2003, 19:00:52  
Job time : 387.943 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:34 ; Search time 41.3143 Seconds  
(without alignments)  
192.304 Million cell updates/sec

Title: US-09-331-204A-4  
Perfect score: 18  
Sequence: 1 ttggagggggtgtgtggg 18

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 376294

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA.\*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	2	US-08-529-878B-3
2	18	100.0	18	2	US-08-529-878B-44
3	18	100.0	21	2	US-08-529-878B-4
4	18	100.0	21	2	US-08-529-878B-45
5	13.4	74.4	20	2	US-08-476-712-2
6	13.4	74.4	20	4	US-09-411-291-2
7	12.8	71.1	17	4	US-09-495-140-26
8	12.8	71.1	18	3	US-09-017-974-57
9	12.8	71.1	18	4	US-08-682-255A-57
10	12.8	71.1	18	4	US-09-429-130-57
11	12.8	71.1	20	3	US-09-490-692-35
12	12.8	71.1	21	2	US-08-632-575B-19
13	12.8	71.1	21	4	US-09-199-542B-19
14	12.2	67.8	17	4	US-09-809-713-3
15	12.2	67.8	18	1	US-08-013-801-4
16	12.2	67.8	18	1	US-08-072-063-13
17	12.2	67.8	18	1	US-08-212-132-4
18	12.2	67.8	18	1	US-08-064-693-13
19	12.2	67.8	18	1	US-08-430-417-4
20	12.2	67.8	18	1	US-08-470-366-4
21	12.2	67.8	18	1	US-08-466-822-4
22	12.2	67.8	18	2	US-08-704-504-4
23	12.2	67.8	18	3	US-08-885-366-13
24	12.2	67.8	18	3	US-09-223-342-4
25	12.2	67.8	18	4	US-09-425-034A-4
26	12.2	67.8	18	5	PCT-US93-04754-13
27	12.2	67.8	18	5	PCT-US94-01235-4

28	12.2	67.8	18	5	PCT-US95-03125-4	Sequence 4, Appli
C 29	12.2	67.8	19	1	US-08-486-913-2	Sequence 2, Appli
C 30	12.2	67.8	19	2	US-08-486-535-2	Sequence 2, Appli
C 31	12.2	67.8	19	2	US-08-300-484-2	Sequence 2, Appli
C 32	12.2	67.8	19	3	US-08-486-885-2	Sequence 2, Appli
C 33	12.2	67.8	19	3	US-08-486-536-2	Sequence 2, Appli
C 34	12.2	67.8	19	3	PCT-US95-11234-2	Sequence 9, Appli
C 35	12.2	67.8	19	5	US-08-486-913-3	Sequence 2, Appli
C 36	12.2	67.8	20	1	US-08-486-535-3	Sequence 3, Appli
C 37	12.2	67.8	20	2	US-08-300-484-3	Sequence 3, Appli
C 38	12.2	67.8	20	2	US-08-890-980-56	Sequence 56, Appl
C 39	12.2	67.8	20	3	US-08-890-979-56	Sequence 56, Appl
C 40	12.2	67.8	20	3	US-09-032-894-56	Sequence 56, Appl
C 41	12.2	67.8	20	3	US-08-486-885-3	Sequence 3, Appli
C 42	12.2	67.8	20	3	US-09-031-626-56	Sequence 56, Appl
C 43	12.2	67.8	20	3	US-08-486-536-3	Sequence 3, Appli
C 44	12.2	67.8	20	3	US-09-487-368A-174	Sequence 174, App
C 45	12.2	67.8	20	3		

ALIGNMENTS

RESULT 1  
US-08-529-878B-3  
; Sequence 3, Application US/08529878B  
; Patent No. 5932556  
; GENERAL INFORMATION:  
; APPLICANT: Tam, Robert C.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
; TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Crockett & Fish  
; STREET: 3000 S. Augusta Court  
; CITY: La Habra  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 90631  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/529,878B  
; FILING DATE: 13-SEP-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fish, Robert D.  
; REGISTRATION NUMBER: 33,880  
; REFERENCE/DOCKET NUMBER: 213/003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 714-525-3433  
; TELEFAX: 714-525-3303  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
US-08-529-878B-3

Query Match 100.0%; Score 18; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. NO. 24;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGAGGGGGTGTGGGG 18

Db 1 TTGGAGGGGGTGTGGGG 18

RESULT 2  
US-08-529-878B-44  
; Sequence 44, Application US/08529878B  
; Patent No. 5932556  
; GENERAL INFORMATION:  
; APPLICANT: Tam, Robert C.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
; TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Crockett & Fish  
; STREET: 3000 S. Augusta Court  
; CITY: La Habra  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 90631  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/529,878B  
; FILING DATE: 13-SEP-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fish, Robert D.  
; REGISTRATION NUMBER: 33,880  
; REFERENCE/DOCKET NUMBER: 213/003  
; TELEPHONE: 714-525-3433  
; TELEFAX: 714-525-3303  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 44:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
US-08-529-878B-44

Query Match 100.0%; Score 18; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGAGGGGGTGTGGGG 18  
|||||  
DB 1 TTGAGGGGGTGTGGGG 18

RESULT 3  
US-08-529-878B-4  
; Sequence 4, Application US/08529878B  
; Patent No. 5932556  
; GENERAL INFORMATION:  
; APPLICANT: Tam, Robert C.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
; TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Crockett & Fish  
; STREET: 3000 S. Augusta Court  
; CITY: La Habra  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 90631  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 6.1

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/529,878B  
; FILING DATE: 13-SEP-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fish, Robert D.  
; REGISTRATION NUMBER: 33,880  
; REFERENCE/DOCKET NUMBER: 213/003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 714-525-3433  
; TELEFAX: 714-525-3303  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 21 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
US-08-529-878B-4

Query Match 100.0%; Score 18; DB 2; Length 21;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGAGGGGGTGTGGGG 18  
|||||  
DB 4 TTGAGGGGGTGTGGGG 21

RESULT 4  
US-08-529-878B-45  
; Sequence 45, Application US/08529878B  
; Patent No. 5932556  
; GENERAL INFORMATION:  
; APPLICANT: Tam, Robert C.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
; TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Crockett & Fish  
; STREET: 3000 S. Augusta Court  
; CITY: La Habra  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 90631  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/529,878B  
; FILING DATE: 13-SEP-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fish, Robert D.  
; REGISTRATION NUMBER: 33,880  
; REFERENCE/DOCKET NUMBER: 213/003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 714-525-3433  
; TELEFAX: 714-525-3303  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 45:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 21 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
US-08-529-878B-45

Query Match

100.0%; Score 18; DB 2; Length 21;

```
Best Local Similarity 100.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGTGGTGGG 18
   |||||
Db 4 TTGGAGGGGGTGGTGGG 21

RESULT 5
US-08-476-712-2
; Sequence 2, Application US/08476712
; Patent No. 5962426
; GENERAL INFORMATION:
; APPLICANT: Glazer, Peter, M.
; TITLE OF INVENTION: Triple-Helix Forming Oligonucleotides for
; TITLE OF INVENTION: Targeted Mutagenesis
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,712
; FILING DATE: 7-JUNE-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: YU114
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-873-8794
; TELEFAX: (404)-873-8795
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-476-712-2

Query Match 74.4%; Score 13.4; DB 2; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGGGGTGGTGGG 17
   |||||
Db 6 GGGGGGGTGGTGGG 20

RESULT 6
US-09-411-291-2
; Sequence 2, Application US/09411291
; Patent No. 6303376
; GENERAL INFORMATION:
; APPLICANT: Glazer, Peter, M.
; TITLE OF INVENTION: Triple-Helix Forming Oligonucleotides for
; Targeted Mutagenesis
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta

Best Local Similarity 100.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
STATE: GA
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/411,291
FILING DATE: 04-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,712
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: YU114
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-411-291-2

Query Match 74.4%; Score 13.4; DB 4; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGGGGTGGTGGG 17
   |||||
Db 6 GGGGGGGTGGTGGG 20

RESULT 7
US-09-495-140-26
; Sequence 26, Application US/09495140
; Patent No. 6376182
; GENERAL INFORMATION:
; APPLICANT: CHAO, JULIE
; APPLICANT: CHAO, JULIE
; APPLICANT: SONG, QING
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CORRELATING
; TITLE OF INVENTION: TISSUE KALLIKREIN GENE PROMOTER POLYMORPHISMS WITH TREATMENT
; TITLE OF INVENTION: OF ESSENTIAL HYPERTENSION
; FILE REFERENCE: 19113.0081
; CURRENT APPLICATION NUMBER: US/09/495,140
; CURRENT FILING DATE: 2000-01-31
; EARLIER APPLICATION NUMBER: 09/389,566
; EARLIER FILING DATE: 1999-09-03
; EARLIER APPLICATION NUMBER: 08/856,141
; EARLIER FILING DATE: 1997-05-14
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. 6376182e =
; OTHER INFORMATION: synthetic construct
US-09-495-140-26

Query Match 71.1%; Score 12.8; DB 4; Length 17;
Best Local Similarity 87.5%; Pred. No. 3e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```



QY 3 GGAGGGGGTGGTGGG 18  
|||||  
Db 1 GGAGGGGGGGGGGGG 16

## RESULT 8

US-09-017-974-57  
; Sequence 57, Application US/09017974  
; Patent No. 628042  
; GENERAL INFORMATION:  
; APPLICANT: Rando, Robert F.  
; APPLICANT: Ojwang, Joshua O.  
; APPLICANT: Hogan, Michael E.  
; APPLICANT: Wallace, Thomas L.  
; APPLICANT: Cossum, Paul A.  
; TITLE OF INVENTION: Anti-Viral Guanosine-Rich  
; TITLE OF INVENTION: Tetrad Forming Oligonucleotides  
; NUMBER OF SEQUENCES: 88  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Conley, Rose & Tayon, P.C.  
; STREET: 600 Travis, Suite 1800  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: U.S.A.  
; ZIP: 77002-2912  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: MS Word 97 (saved as .txt file)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/017,974  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/037,374  
; FILING DATE: 04-FEB-97  
; APPLICATION NUMBER:  
; FILING DATE: 09-DEC-97  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mcdaniel, C. Steven  
; REGISTRATION NUMBER: 33,962  
; REFERENCE/DOCKET NUMBER: 1472-06223  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 713/238-8010  
; TELEFAX: 713/238-8008  
; INFORMATION FOR SEQ ID NO: 57:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-09-017-974-57

Query Match 71.1%; Score 12.8; DB 3; Length 18;  
Best Local Similarity 87.5%; Pred. No. 3.le+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGAGGGGGTGGTGGG 17  
|||||  
Db 2 TGGTGGGTGGTGGTGGG 17

## RESULT 9

US-08-682-255A-57  
; Sequence 57, Application US/08682255A  
; Patent No. 6323185  
; GENERAL INFORMATION:  
; APPLICANT: Rando, Robert F.  
; APPLICANT: Fennewald, Susan  
; APPLICANT: Zendegui, Joseph G.

; APPLICANT: Ojwang, Joshua O.  
; APPLICANT: Hogan, Michael E.  
; APPLICANT: Pommier, Yves  
; APPLICANT: Mazumder, Abhijit  
; TITLE OF INVENTION: Anti-Viral Guanosine-Rich  
; TITLE OF INVENTION: Oligonucleotides  
; NUMBER OF SEQUENCES: 87  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Conley, Rose & Tayon, P.C.  
; STREET: 600 Travis, Suite 1850  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: U.S.A.  
; ZIP: 77002-2912  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: MS Windows 95  
; SOFTWARE: MS Word 97 (saved as .txt file)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/682,255A  
; FILING DATE: 17-JULY-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/535,168  
; FILING DATE: 23-OCT-95  
; APPLICATION NUMBER: 60/001,505  
; FILING DATE: 19-JULY-95  
; APPLICATION NUMBER: 60/014,007  
; FILING DATE: 25-MARCH-96  
; APPLICATION NUMBER: 60/013,688  
; FILING DATE: 19-MARCH-96  
; APPLICATION NUMBER: 60/015,714  
; FILING DATE: 17-APRIL-96  
; APPLICATION NUMBER: 60/016,271  
; FILING DATE: 23-APRIL-96  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mcdaniel, C. Steven  
; REGISTRATION NUMBER: 33,962  
; REFERENCE/DOCKET NUMBER: 1472-06214  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 713/238-8010  
; TELEFAX: 713/238-8008  
; INFORMATION FOR SEQ ID NO: 57:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-682-255A-57

Query Match 71.1%; Score 12.8; DB 4; Length 18;  
Best Local Similarity 87.5%; Pred. No. 3.le+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGAGGGGGTGGTGGG 17  
|||||  
Db 2 TGGTGGGTGGTGGTGGG 17

## RESULT 10

US-09-429-130-57  
; Sequence 57, Application US/09429130  
; Patent No. 6355785  
; GENERAL INFORMATION:  
; APPLICANT: Rando, Robert F.  
; APPLICANT: Fennewald, Susan  
; APPLICANT: Zendegui, Joseph G.  
; APPLICANT: Ojwang, Joshua O.  
; APPLICANT: Hogan, Michael E.  
; APPLICANT: Pommier, Yves  
; APPLICANT: Mazumder, Abhijit

60/015,714  
TITLE OF INVENTION: Anti-Viral Guanosine-Rich  
Oligonucleotides  
NUMBER OF SEQUENCES: 87  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Conley, Rose & Tayon, P.C.  
STREET: 600 Travis, Suite 1850  
CITY: Houston  
STATE: Texas  
COUNTRY: U.S.A.  
ZIP: 77002-2912  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: MS Windows 95  
SOFTWARE: MS Word 97 (saved as .txt file)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/429,130  
FILING DATE: 28-Oct-1999  
CLASSIFICATION: <Unknown>  
19-JULY-95  
25-MARCH-96  
19-MARCH-96  
17-APRIL-96  
23-APRIL-96  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/682,255  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 60/001,505  
FILING DATE: 19-JULY-95  
APPLICATION NUMBER: 60/014,007  
FILING DATE: 25-MARCH-96  
APPLICATION NUMBER: 60/013,688  
FILING DATE: 19-MARCH-96  
APPLICATION NUMBER: 60/016,271  
FILING DATE: 17-APRIL-96  
ATTORNEY/AGENT INFORMATION:  
NAME: McDaniel, C. Steven  
REGISTRATION NUMBER: 33,962  
REFERENCE/DOCKET NUMBER: 1472-06214  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713/238-8010  
TELEFAX: 713/238-8008  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 57:  
US-09-429-130-57

Query Match 71.1%; Score 12.8; DB 4; Length 18;  
Best Local Similarity 87.5%; Pred. No. 3.1e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGAGGGGGTGGTGG 17  
|||||  
Db 2 TGGTGGGTGGTGGG 17

RESULT 11  
US-09-490-692-35  
; Sequence 35, Application US/09490692  
; Patent No. 6180353  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas M. Dean  
; APPLICANT: Lex M. Cowser  
; TITLE OF INVENTION: ANTISENSE MODULATION OF DAXX EXPRESSION  
; FILE REFERENCE: RTS-0120  
; CURRENT APPLICATION NUMBER: US/09/490,692  
; CURRENT FILING DATE: 2000-01-24

NUMBER OF SEQ ID NOS: 176  
; SEQ ID NO 35  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-490-692-35

Query Match 71.1%; Score 12.8; DB 3; Length 20;  
Best Local Similarity 87.5%; Pred. No. 3.1e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGTGGTGG 16  
|||||  
Db 3 TTGGAGGTGGTGGCGG 18

RESULT 12  
US-08-632-575B-19  
; Sequence 19, Application US/08632575B  
; Patent No. 5843660  
; GENERAL INFORMATION:  
; APPLICANT: Schumm, James W.  
; TITLE OF INVENTION: Multiplex Amplification of  
; TITLE OF INVENTION: Short Tandem Repeat Loci  
; NUMBER OF SEQUENCES: 61  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Promega Corporation  
; STREET: 2800 Woods Hollow Road  
; CITY: Madison  
; STATE: Wisconsin  
; COUNTRY: U.S.A.  
; ZIP: 53711-5399  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb  
; COMPUTER: IBM compatible PC  
; OPERATING SYSTEM: DOS, version 6.0  
; SOFTWARE: Wordperfect 5.1 (DOS text format)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/632,575B  
; FILING DATE: 04/15/96  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/316,544  
; FILING DATE: 09/30/94  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 21  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; POSITION IN GENOME:  
; MAP POSITION: D14S562  
US-08-632-575B-19

Query Match 71.1%; Score 12.8; DB 2; Length 21;  
Best Local Similarity 87.5%; Pred. No. 3.1e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGTGGTGG 16  
|||||  
Db 2 TTGGAGGTGGTGGTGG 17

RESULT 13  
US-09-199-542B-19  
; Sequence 19, Application US/09199542B  
; Patent No. 6479235  
; GENERAL INFORMATION:  
; APPLICANT: Schumm, James W.  
; APPLICANT: Sprecher, Cynthia J.  
; TITLE OF INVENTION: Multiplex Amplification of Short Tandem Repeat Loci

```

; FILE REFERENCE: 16026/9212
; CURRENT APPLICATION NUMBER: US/09/199,542B
; CURRENT FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: US 08/316,544
; PRIOR FILING DATE: 1994-09-30
; PRIOR APPLICATION NUMBER: US 08/632,575
; PRIOR FILING DATE: 1996-04-15
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: Word97 (converted to DOS text format)
; SEQ ID NO 19
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapien
; LOCATION: D14S562
US-09-199-542B-19

Query Match      71.1%; Score 12.8; DB 4; Length 21;
Best Local Similarity 87.5%; Pred. No. 3.1e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGGAGGGGTGGTGG 16
Db 2 TTGGAGGGGTGGTGG 17

RESULT 14
US-09-809-713-3
; Sequence 3, Application US/09809713
; Patent No. 6428964
; GENERAL INFORMATION:
; APPLICANT: Shuber, Anthony
; TITLE OF INVENTION: Method For Alteration Detection
; FILE REFERENCE: EXT-047
; CURRENT APPLICATION NUMBER: US/09/809,713
; CURRENT FILING DATE: 2001-03-15
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: probe upstream of the 1450 point mutation region
US-09-809-713-3

Query Match      67.8%; Score 12.2; DB 4; Length 17;
Best Local Similarity 82.4%; Pred. No. 5.3e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGGAGGGGTGGTGGG 18
Db 1 TTGAGGAGGTGGTGAG 17

RESULT 15
US-08-013-801-4
; Sequence 4, Application US/08013801
; Patent No. 5420019
; GENERAL INFORMATION:
; APPLICANT: Theofan, Georgia
; APPLICANT: Horwitz, Arnold
; APPLICANT: Burke, David
; APPLICANT: Baltaian, Manik
; APPLICANT: Grinna, Lynn S
; TITLE OF INVENTION: Stable Bactericidal/Permeability-
; TITLE OF INVENTION: Increasing Protein Products and Pharmaceutical
; TITLE OF INVENTION: Compositions Containing the Same
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza
; CITY: Chicago
```

```

; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/013,801
; FILING DATE: 02 FEB 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 27129/30911
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/346-5750
; TELEFAX: 312/346-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-013-801-4

Query Match      67.8%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 5.3e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGGAGGGGTGGTGGG 18
Db 2 TGGAGGGGTGATGGT 18

Search completed: October 27, 2003, 14:03:33
Job time : 42.3143 secs
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:29 ; Search time 1581.77 Seconds  
(without alignments)  
276.576 Million cell updates/sec

Title: US-09-331-204A-4  
Perfect score: 18  
Sequence: 1 ttggaggggtgtgtgggg 13

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 11152

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST: \*  
1: em\_estba: \*  
2: em\_esthum: \*  
3: em\_estin: \*  
4: em\_estmu: \*  
5: em\_estov: \*  
6: em\_estpl: \*  
7: em\_estro: \*  
8: em\_htc: \*  
9: gb\_est1: \*  
10: gb\_est2: \*  
11: gb\_htc: \*  
12: gb\_est3: \*  
13: gb\_est4: \*  
14: gb\_est5: \*  
15: em\_estfun: \*  
16: em\_estom: \*  
17: em\_gss\_hum: \*  
18: em\_gss\_inv: \*  
19: em\_gss\_pln: \*  
20: em\_gss\_vrt: \*  
21: em\_gss\_fun: \*  
22: em\_gss\_mam: \*  
23: em\_gss\_mus: \*  
24: em\_gss\_pro: \*  
25: em\_gss\_rod: \*  
26: em\_gss\_phg: \*  
27: em\_gss\_vrl: \*  
28: gb\_gss1: \*  
29: gb\_gss2: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13.2	73.3	21	28	AZ468862
C 2	12.8	71.1	19	28	AZ760597
C 3	12.8	71.1	20	28	AZ512326
C 4	12.8	71.1	20	28	AZ645269

C 5	12.8	71.1	20	28	AZ659755
C 6	12.8	71.1	20	28	AZ969440
C 7	12.8	71.1	21	28	AZ583408
C 8	12.8	71.1	21	28	AZ774703
C 9	12.8	71.1	21	28	AZ969578
10	12.8	71.1	22	28	AZ307952
C 11	12.8	71.1	22	28	AZ645874
C 12	12.8	71.1	22	28	AZ769521
C 13	12.8	71.1	22	28	AZ871408
14	12.2	67.8	18	13	BQ901245
C 15	12.2	67.8	19	9	AI251781
16	12.2	67.8	19	28	AZ315293
17	12.2	67.8	20	28	AZ622226
C 18	12.2	67.8	20	28	AZ666896
C 19	12.2	67.8	21	28	AZ856540
C 20	12.2	67.8	22	9	AI568336
C 21	12.2	67.8	22	28	AZ766712
22	12.2	67.8	22	28	AZ876923
C 23	11.8	65.6	19	9	AI364573
C 24	11.8	65.6	21	28	AZ476392
C 25	11.8	65.6	21	28	AZ512534
C 26	11.8	65.6	22	9	AI183338
27	11.8	65.6	22	9	AI434548
C 28	11.8	65.6	22	9	AI582080
C 29	11.8	65.6	22	9	AI735392
30	11.8	65.6	22	13	BQ585098
31	11.8	65.6	22	28	AZ331988
C 32	11.8	65.6	22	28	AZ607348
C 33	11.6	64.4	20	28	AZ391065
34	11.6	64.4	20	28	AZ430735
35	11.6	64.4	20	28	AZ845320
36	11.6	64.4	21	28	AZ995847
C 37	11.6	64.4	22	14	D21051
38	11.6	64.4	22	28	AZ792883
C 39	11.4	63.3	16	9	AI590540
C 40	11.4	63.3	19	9	AI807936
41	11.4	63.3	19	28	AZ369361
42	11.4	63.3	19	28	AZ381798
C 43	11.4	63.3	19	28	AZ447936
44	11.4	63.3	19	28	AZ780591
45	11.4	63.3	20	28	AZ405596

ALIGNMENTS

RESULT 1  
AZ468862  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AZ468862  
1M0282004F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0282004 F, genomic survey sequence.  
AZ468862  
AZ468862.1 GI:10626987  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 21)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0282 row: O column: 04  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers  
1. 21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0282O04"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 1 c 15 g 5 t  
ORIGIN  
Query Match 73.3%; Score 13.2; DB 28; Length 21;  
Best Local Similarity 83.3%; Pred. No. 5.6e+05;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 TTGGAGGGGGTGGTGGGG 18  
|||||  
Db 1 TTGGGGGGTGGGTGGGG 18  
|||||  
RESULT 2  
AZ760597/c  
LOCUS  
DEFINITION  
1M0554N21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0554N21 F, genomic survey sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606

Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0554 row: N column: 21  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers  
1. 19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0554N21"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 18 c 0 g 1 t  
ORIGIN  
Query Match 71.1%; Score 12.8; DB 28; Length 19;  
Best Local Similarity 87.5%; Pred. No. 7.6e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 3 GGAGGGGGTGGTGGGG 18  
|||||  
Db 18 GGAGGGGGGGGGGGGG 3  
|||||  
RESULT 3  
AZ512326/c  
LOCUS  
DEFINITION  
1M0357I18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0357I18 R, genomic survey sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0357 row: I column: 18  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers

FEATURES  
source

1. .20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0357I18"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 18 c 0 g 2 t  
ORIGIN

Query Match 71.1%; Score 12.8; DB 28; Length 20;  
Best Local Similarity 87.5%; Pred. No. 7.6e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGGTGGTGGGG 18  
|||||  
Db 18 GGAGGGGGGGGGGGG 3

RESULT 4  
AZ645269/c  
LOCUS  
DEFINITION 1M0510B10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0510B10 R, genomic survey sequence.

ACCESSION AZ645269  
VERSION AZ645269.1 GI:11774602  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 20)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0510 row: B column: 10  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers

FEATURES  
source

1. .20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0510B10"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 19 c 0 g 1 t  
ORIGIN

Query Match 71.1%; Score 12.8; DB 28; Length 20;  
Best Local Similarity 87.5%; Pred. No. 7.6e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGGTGGTGGGG 18  
|||||  
Db 17 GGAGGGGGGGGGGGG 2

RESULT 5  
AZ659755/c

LOCUS  
DEFINITION 1M0537F22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0537F22 F, genomic survey sequence.

ACCESSION AZ659755  
VERSION AZ659755.1 GI:11796901  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0537 row: F column: 22  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 20.

FEATURES  
source

1. .20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0537F22"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 0 a 18 c 0 g 2 t  
ORIGIN

Query Match 71.1%; Score 12.8; DB 28; Length 20;  
Best Local Similarity 87.5%; Pred. No. 7.6e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGAGGGGGTGTGGGG 18  
|||||  
Db 20 GGAGGGGGGGGGGGG 5

RESULT 6  
AZ969440/c  
LOCUS  
DEFINITION  
2M0242012F Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
clone UUGC2M0242012 F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
AZ969440  
GSS.  
Mus musculus (house mouse)  
Mus musculus

REFERENCE  
AUTHORS  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly  
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.  
and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished  
Contact: Robert B. Weiss  
University of Utah Genome Center

TITLE  
JOURNAL  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center

University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0242 row: O column: 12  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 20.

FEATURES  
source

1. .20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0242O12"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC2M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (female) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 0 a 19 c 0 g 1 t  
ORIGIN

Query Match 71.1%; Score 12.8; DB 28; Length 20;  
Best Local Similarity 87.5%; Pred. No. 7.6e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGAGGGGGTGTGGGG 18  
|||||  
Db 16 GGAGGGGGGGGGGGG 1

RESULT 7  
AZ583408/c  
LOCUS  
DEFINITION  
1M0378N23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0378N23 F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
AZ583408  
GSS.  
Mus musculus (house mouse)  
Mus musculus

REFERENCE  
AUTHORS  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly  
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.  
and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished  
Contact: Robert B. Weiss

TITLE  
JOURNAL  
COMMENT  
Contact: Robert B. Weiss



University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0378 row: N column: 23  
Seq primer: CGTTGTAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers

FEATURES

source

1. .21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0378N23"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 0 a 20 c 0 g 1 t  
ORIGIN

Query Match 71.1%; Score 12.8; DB 28; Length 21;  
Best Local Similarity 87.5%; Pred. No. 7.5e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGGTGTGGGG 18  
|||||||  
Db 18 GGAGGGGGGGGGGGG 3

RESULT 8

AZ774703/c

LOCUS

DEFINITION

clone UUGC2M0004G14 F, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 21)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished

COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0004 row: G column: 14  
Seq primer: CGTTGTAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers

FEATURES

source

1. .21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0004G14"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 2 a 19 c 0 g 0 t  
ORIGIN

Query Match 71.1%; Score 12.8; DB 28; Length 21;  
Best Local Similarity 87.5%; Pred. No. 7.5e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGGTGTGGGG 18  
|||||||  
Db 21 GGAGGGGGGGGGGGG 6

RESULT 9

AZ969578/c

LOCUS

DEFINITION

clone UUGC2M0242G20 F, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 21)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts



JOURNAL  
COMMENT

Unpublished  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0242 row: G column: 20  
Seq primer: CGTTGTAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers

FEATURES

source

1. .21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0242G20"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC2M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (female) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 1 a 18 c 0 g 2 t  
ORIGIN

Query Match 71.1%; Score 12.8; DB 28; Length 21;  
Best Local Similarity 87.5%; Pred. No. 7.5e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGGTGGTGGGG 18  
|||||  
Db 21 GGAGGGGGGAGTGGGG 6

RESULT 10

AZ307952  
LOCUS  
DEFINITION  
1M0010L24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0010L24 F, genomic survey sequence.  
AZ307952  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
GSS.  
Mus musculus (house mouse)

GI:10347459

ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 22)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb

TITLE

JOURNAL  
COMMENT

Unpublished  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0010 row: L column: 24  
Seq primer: CGTTGTAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 22.  
Location/Qualifiers

FEATURES

source

1. .22  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0010L24"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 5 a 0 c 14 g 3 t  
ORIGIN

Query Match 71.1%; Score 12.8; DB 28; Length 22;  
Best Local Similarity 87.5%; Pred. No. 7.5e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGGTGGTGGGG 18  
|||||  
Db 4 GGAGGGGGGGTGGGG 19

RESULT 11

AZ645874/c  
LOCUS  
DEFINITION  
1M0511C07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0511C07 R, genomic survey sequence.  
AZ645874  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
GSS.  
Mus musculus (house mouse)

GI:11775791

ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 22)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
JOURNAL plasmid inserts  
COMMENT Unpublished  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0511 row: C column: 07  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 22.

FEATURES  
source

1. .22  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0511C07"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 21 c 0 g 1 t  
ORIGIN  
Query Match 71.1%; Score 12.8; DB 28; Length 22;  
Best Local Similarity 87.5%; Pred. No. 7.5e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGAGGGGTGGTGGG 18  
|||  
Db 17 GGAGGGGGGGGGGG 2

RESULT 12  
AZ769521/c  
LOCUS AZ769521 22 bp DNA linear GSS 16-FEB-2001  
DEFINITION 1M0570018F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0570018 F, genomic survey sequence.  
ACCESSION AZ769521  
VERSION AZ769521.1 GI:12889741  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 22)  
REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

TITLE and Wright,D.,Weiss,R.  
JOURNAL Mouse whole genome scaffolding with paired end reads from 10kb  
COMMENT Unpublished  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0570 row: O column: 18  
Seq primer: CGTTGTAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 22.

FEATURES  
source

1. .22  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0570018"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 1 a 21 c 0 g 0 t  
ORIGIN  
Query Match 71.1%; Score 12.8; DB 28; Length 22;  
Best Local Similarity 87.5%; Pred. No. 7.5e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGAGGGGTGGTGGG 18  
|||  
Db 21 GGAGGGGTGGGGGG 6

RESULT 13  
AZ871408/c  
LOCUS AZ871408 22 bp DNA linear GSS 21-FEB-2001  
DEFINITION 2M0184E16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0184E16 F, genomic survey sequence.  
ACCESSION AZ871408  
VERSION AZ871408.1 GI:13077580  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 22)  
REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly

M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0184 row: E column: 16  
Seq primer: CGTTGTAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 22.

FEATURES source

1. .22  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0184E16"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pW42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 21 c 0 g 1 t  
ORIGIN  
Query Match 71.1%; Score 12.8; DB 28; Length 22;  
Best Local Similarity 87.5%; Pred. NO. 7.5e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGGTGGTGGGG 18  
|||||||  
Db 16 GGAGGGGGGGGGGGG 1

RESULT 14  
BQ901245 18 bp mRNA linear EST 19-AUG-2002  
LOCUS  
DEFINITION  
BQ901245 hasp002xj21f Heterobasidion annosum - Scots pine infection stage subtraction cDNA library (hasp) Pinus sylvestris/Heterobasidion annosum cDNA clone hasp002xj21f, mRNA sequence.  
BQ901245 GI:22300029  
EST.  
Pinus sylvestris/Heterobasidion annosum  
Pinus sylvestris/Heterobasidion annosum  
Eukaryota; mixed EST libraries.  
1 (bases 1 to 18)  
ASIEGBU,F.O., Nahalkova,J. and Dean,R.A.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS

TITLE  
JOURNAL  
COMMENT

Selected Expressed sequence tags of cDNA clones from the interaction of the root rot fungus (Heterobasidion annosum) with seedling roots of Scots pine (Pinus sylvestris)  
Unpublished  
Contact: Fred O. Asiegbu  
Dept. of Forest Mycology & Pathology  
Swedish University of Agriculture, Box 7026,S-750 07, Uppsala, Sweden  
Tel: +46 18 67 15 98  
Fax: +46 18 30 92 45  
Email: Fred.Asiegbu@mykopat.slu.se  
Seq primer: T7 primer.  
Location/Qualifiers  
1. .18  
/organism="Pinus sylvestris/Heterobasidion annosum"  
/mol\_type="mRNA"  
/db\_xref="taxon:169015"  
/clone="hasp002xj21f"  
/dev\_stage="Seedling roots of scots pine were infected for 6 days with H. annosum"  
/clone\_lib="Heterobasidion annosum - Scots pine infection stage subtraction cDNA library (hasp)"  
/note="Vector: pT-Adv; Site 1: EcoRI; The subtractive hybridization cDNA library was constructed from scots pine roots infected for 6-days with mycelia of Heterobasidion annosum (FP5)."

FEATURES source

BASE COUNT 0 a 0 c 17 g 1 t  
ORIGIN  
Query Match 67.8%; Score 12.2; DB 13; Length 18;  
Best Local Similarity 82.4%; Pred. NO. 1.2e+06;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGGAGGGGGTGGTGGGG 18  
|||||||  
Db 2 TGGGGGGGGGGGGGGGG 18

RESULT 15  
AI251781/c  
LOCUS  
DEFINITION

AI251781 19 bp mRNA linear EST 05-NOV-1998  
qu76g01.x1 NCI CGAP Brn35 Homo sapiens cDNA clone IMAGE:1978032.3,  
similar to TR:Q39949 Q39949 HYDROXYPROLINE-RICH PROTEIN.; mRNA  
sequence.  
AI251781  
AI251781.1 GI:3848310  
EST.  
Homo sapiens (human)  
Homo sapiens

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 19)  
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGP), Tumor Gene Index  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
unknown library type  
Trace considered overall poor quality  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .19  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1978032"  
/tissue\_type="tumor, 5 pooled (see description)"  
/lab\_host="DH10B"  
/clone\_lib="NCI\_CGAP\_Brn35"  
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: SalI;

JOURNAL  
COMMENT

FEATURES source

Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.33 kb. Tumor types include:  
meningioma, oligodendroglioma, astrocytoma (grade II),  
medulloblastoma, astrocytoma (grade IV). Life Technologies  
catalog #: 11544-012"

BASE COUNT      4 a    14 C    0 G    1 T  
ORIGIN

Query Match                      67.8%; Score 12.2; DB 9; Length 19;  
Best Local Similarity    82.4%; Pred. NO. 1.2e+06;  
Matches    14; Conservative    0; Mismatches    3; Indels    0; Gaps    0;

OY            1 TTGGAGGGGGTGGTGGG 17  
             ||||| ||||| |||||  
Db            17 TTGGGGGGGGAGGGGGG 1

Search completed: October 27, 2003, 13:59:22  
Job time : 1585.77 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: October 27, 2003, 10:32:29 ; Search time 376.114 Seconds  
(without alignments)  
1957.844 Million cell updates/sec

Title: US-09-331-204A-4  
Perfect score: 18  
Sequence: 1 ttggaggggtgtgtgggg 18

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 681044

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vi:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htg\_mus:\*  
34: em\_htg\_pln:\*  
35: em\_htg\_rod:\*  
36: em\_htg\_mam:\*  
37: em\_htg\_vrt:\*  
38: em\_sy:\*  
39: em\_htgo\_hum:\*  
40: em\_htgo\_mus:\*  
41: em\_htgo\_other:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	18	100.0	18	6	AX023402	AX023402 Sequence
2	18	100.0	18	6	AX023427	AX023427 Sequence
3	13.4	74.4	20	6	AR078333	AR078333 Sequence
4	13.4	74.4	20	6	AR173053	AR173053 Sequence
5	13.4	74.4	21	6	AX384817	AX384817 Sequence
6	12.8	71.1	18	6	AR168831	AR168831 Sequence
7	12.8	71.1	18	6	AR200300	AR200300 Sequence
8	12.8	71.1	18	6	AR262431	AR262431 Sequence
9	12.8	71.1	18	6	E04543	E04543 linker. 9/1
10	12.8	71.1	19	6	AX659401	AX659401 Sequence
11	12.8	71.1	20	6	AR126606	AR126606 Sequence
12	12.8	71.1	21	6	A20477	A20477 oligonucleo
13	12.8	71.1	21	6	A28676	A28676 dsRNA with
14	12.8	71.1	21	6	AR061827	AR061827 Sequence
15	12.8	71.1	21	6	AR252818	AR252818 Sequence
16	12.8	71.1	22	6	BD182437	BD182437 Human art
17	12.8	71.1	22	6	E38866	E38866 Chimeric an
18	12.8	71.1	22	6	E63496	E63496 Non-human a
19	12.4	68.9	20	6	AX488033	AX488033 Sequence
20	12.2	67.8	17	6	A25058	A25058 Nucleoprote
21	12.2	67.8	17	6	AR221900	AR221900 Sequence
22	12.2	67.8	18	6	A02165	A02165 Nucleotide
23	12.2	67.8	18	6	A04686	A04686 Nucleotide
24	12.2	67.8	18	6	AR027664	AR027664 Sequence
25	12.2	67.8	18	6	AR050739	AR050739 Sequence
26	12.2	67.8	18	6	AR165012	AR165012 Sequence
27	12.2	67.8	18	6	AX030648	AX030648 Sequence
28	12.2	67.8	18	6	I13569	I13569 Sequence 13
29	12.2	67.8	18	6	I14323	I14323 Sequence 4
30	12.2	67.8	18	6	I50679	I50679 Sequence 13
31	12.2	67.8	18	6	I68183	I68183 Sequence 4
32	12.2	67.8	18	6	I87067	I87067 Sequence
33	12.2	67.8	19	6	AR012711	AR012711 Sequence
34	12.2	67.8	19	6	AR036657	AR036657 Sequence
35	12.2	67.8	19	6	AR088921	AR088921 Sequence
36	12.2	67.8	19	6	AR152368	AR152368 Sequence
37	12.2	67.8	19	6	AR165304	AR165304 Sequence
38	12.2	67.8	20	6	AR012712	AR012712 Sequence
39	12.2	67.8	20	6	AR036658	AR036658 Sequence
40	12.2	67.8	20	6	AR088922	AR088922 Sequence
41	12.2	67.8	20	6	AR092032	AR092032 Sequence
42	12.2	67.8	20	6	AR112167	AR112167 Sequence
43	12.2	67.8	20	6	AR149209	AR149209 Sequence
44	12.2	67.8	20	6	AR152369	AR152369 Sequence
45	12.2	67.8	20	6	AX418779	AX418779 Sequence

ALIGNMENTS

RESULT 1  
AX023402  
LOCUS AX023402 18 bp DNA  
DEFINITION Sequence 17 from Patent WO0014217.  
ACCESSION AX023402  
VERSION AX023402.1 GI:10183802  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE  
1  
AUTHORS Lipford,G.B., Heeg,K. and Wagner,H.  
TITLE G-motif oligonucleotides and uses thereof  
JOURNAL Patent: WO 0014217-A 17 16-MAR-2000;  
LIPFORD GRAYSON B (DE) ; HEEG KLAUS (DE) ; WAGNER HERMANN (DE) ;

Pred. No. is the number of results predicted by chance to have a





water  
JOURNAL Patent: WO 02102824-A 3 27-DEC-2002;  
Vermicon AG (DB)  
FEATURES  
source Location/Qualifiers  
1.19  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="oligonucleotide" 3 t  
BASE COUNT 4 a 12 c 0 g 3 t  
ORIGIN  
Query Match 71.1%; Score 12.8; DB 6; Length 19;  
Best Local Similarity 87.5%; Pred. No. 6.1e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 TTGGAGGGGGTGGTGG 16  
Db 16 TGGAGAGGGTGGTGG 1  
RESULT 11  
AR126606  
LOCUS AR126606 20 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 35 from patent US 6180353.  
ACCESSION AR126606  
VERSION AR126606.1 GI:14113199  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Dean,N.M. and Cowser,L.M.  
TITLE Antisense modulation of daxx expression  
JOURNAL Patent: US 6180353-A 35 30-JAN-2001;  
FEATURES  
source Location/Qualifiers  
1.20  
/organism="unknown"  
BASE COUNT 3 a 3 c 10 g 4 t  
ORIGIN  
Query Match 71.1%; Score 12.8; DB 6; Length 20;  
Best Local Similarity 87.5%; Pred. No. 6e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 TTGGAGGGGGTGGTGG 16  
Db 3 TTGGAGGTGGTGGCGG 18  
RESULT 12  
A20477/c  
LOCUS A20477 21 bp DNA linear PAT 11-MAR-1996  
DEFINITION Oligonucleotide primer for Sry.  
ACCESSION A20477  
VERSION A20477.1 GI:1566754  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 21)  
AUTHORS SEXE DETERMINING GENE  
TITLE Patent: WO 9200375-A 4 09-JAN-1992;  
JOURNAL Location/Qualifiers  
FEATURES  
source 1.21  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
BASE COUNT 8 a 11 c 1 g 1 t  
ORIGIN  
Query Match 71.1%; Score 12.8; DB 6; Length 21;  
water  
JOURNAL Patent: WO 02102824-A 3 27-DEC-2002;  
Vermicon AG (DB)  
FEATURES  
source Location/Qualifiers  
1.19  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="oligonucleotide" 3 t  
BASE COUNT 4 a 12 c 0 g 3 t  
ORIGIN  
Query Match 71.1%; Score 12.8; DB 6; Length 19;  
Best Local Similarity 87.5%; Pred. No. 6.1e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 TTGGAGGGGGTGGTGG 16  
Db 16 TGGAGAGGGTGGTGG 1  
RESULT 11  
AR126606  
LOCUS AR126606 20 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 35 from patent US 6180353.  
ACCESSION AR126606  
VERSION AR126606.1 GI:14113199  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Dean,N.M. and Cowser,L.M.  
TITLE Antisense modulation of daxx expression  
JOURNAL Patent: US 6180353-A 35 30-JAN-2001;  
FEATURES  
source Location/Qualifiers  
1.20  
/organism="unknown"  
BASE COUNT 3 a 3 c 10 g 4 t  
ORIGIN  
Query Match 71.1%; Score 12.8; DB 6; Length 20;  
Best Local Similarity 87.5%; Pred. No. 6e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 TTGGAGGGGGTGGTGG 16  
Db 3 TTGGAGGTGGTGGCGG 18  
RESULT 12  
A20477/c  
LOCUS A20477 21 bp DNA linear PAT 11-MAR-1996  
DEFINITION Oligonucleotide primer for Sry.  
ACCESSION A20477  
VERSION A20477.1 GI:1566754  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 21)  
AUTHORS SEXE DETERMINING GENE  
TITLE Patent: WO 9200375-A 4 09-JAN-1992;  
JOURNAL Location/Qualifiers  
FEATURES  
source 1.21  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
BASE COUNT 8 a 11 c 1 g 1 t  
ORIGIN  
Query Match 71.1%; Score 12.8; DB 6; Length 21;  
Best Local Similarity 87.5%; Pred. No. 6e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 TTGGAGGGGGTGGTGG 16  
Db 16 TGGAGAGGGTGGTGG 1  
RESULT 13  
A28676/c  
LOCUS A28676 21 bp mRNA linear PAT 04-JUN-1995  
DEFINITION dsRNA with central hinge (comp.).  
ACCESSION A28676  
VERSION A28676.1 GI:1248715  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 21)  
AUTHORS  
TITLE SHORT THERAPEUTIC dsRNA OF DEFINED STRUCTURE  
JOURNAL Patent: WO 9014090-A 4 29-NOV-1990;  
FEATURES  
source Location/Qualifiers  
1.21  
/organism="synthetic construct"  
/mol\_type="mRNA"  
/db\_xref="taxon:32630"  
BASE COUNT 1 a 20 c 0 g 0 t  
ORIGIN  
Query Match 71.1%; Score 12.8; DB 6; Length 21;  
Best Local Similarity 87.5%; Pred. No. 6e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 3 GGAGGGGGTGGTGGG 18  
Db 19 GGGGGGGTGGGGGGG 4  
RESULT 14  
AR061827  
LOCUS AR061827 21 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 19 from patent US 5843660.  
ACCESSION AR061827  
VERSION AR061827.1 GI:5989518  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Schumm,J.W., Micka,K.A. and Rabbach,D.R.  
TITLE Multiplex amplification of short tandem repeat loci  
JOURNAL Patent: US 5843660-A 19 01-DEC-1998;  
FEATURES  
source Location/Qualifiers  
1.21  
/organism="unknown"  
BASE COUNT 3 a 2 c 11 g 5 t  
ORIGIN  
Query Match 71.1%; Score 12.8; DB 6; Length 21;  
Best Local Similarity 87.5%; Pred. No. 6e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 TTGGAGGGGGTGGTGG 16  
Db 2 TTGGAGGGTGGGGTGG 17  
RESULT 15  
AR252818  
LOCUS AR252818 21 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 19 from patent US 6479235.  
ACCESSION AR252818



VERSION AR252818.1 GI:27301167  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Schumm,J.W. and Sprecher,C.J.  
TITLE Multiplex amplification of short tandem repeat loci  
JOURNAL Patent: US 6479235-A 19 12-NOV-2002;  
FEATURES Location/Qualifiers  
          1..21  
          source /organism="unknown"  
BASE COUNT 3 a 2 c 11 g 5 t  
ORIGIN  
  
Query Match 71.1%; Score 12.8; DB 6; Length 21;  
Best Local Similarity 87.5%; Pred. No. 6e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 TTGGAGGGGGTGGTGG 16  
   |||||||  
Db 2 TTGGAGGGGTGGGGTGG 17

Search completed: October 27, 2003, 11:09:22  
Job time : 380.114 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:29 ; Search time 162 Seconds  
(without alignments)  
299.938 Million cell updates/sec

Title: US-09-331-204A-4  
Perfect score: 18  
Sequence: 1 ttggaggggggtgtggggg 18

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 1643890

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N Geneseq 19Jun03: \*  
1: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT: \*  
2: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT: \*  
3: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT: \*  
4: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT: \*  
5: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT: \*  
6: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT: \*  
7: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT: \*  
8: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT: \*  
9: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT: \*  
10: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT: \*  
11: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT: \*  
12: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT: \*  
13: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT: \*  
14: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT: \*  
15: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT: \*  
16: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT: \*  
17: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT: \*  
18: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT: \*  
19: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT: \*  
20: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT: \*  
21: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT: \*  
22: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT: \*  
23: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT: \*  
24: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT: \*  
25: /SIDSL1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	17	AAT36196
2	18	100.0	18	20	AAAX90328
3	18	100.0	18	20	AAAX90290
4	18	100.0	18	21	AAZ99625
5	18	100.0	18	21	AAZ99650
6	18	100.0	21	17	AAT36197
7	18	100.0	21	20	AAAX90329
8	18	100.0	21	20	AAAX90291

9	16.4	91.1	18	17	AAT36243	CD28 expression in
10	16.4	91.1	18	20	AAAX90336	CD28 inhibiting ph
11	14.8	82.2	18	17	AAT36242	CD28 expression in
12	14.8	82.2	18	17	AAT36244	CD28 expression in
13	14.8	82.2	18	20	AAAX90335	CD28 inhibiting ph
14	14.8	82.2	18	20	AAAX90337	CD28 inhibiting ph
15	13.6	75.6	22	22	AAF16593	Gastric acid produ
C	16	13.4	15	24	AAD25952	ASO probe #5 to de
17	13.4	74.4	20	16	AAQ81074	supF gene triplex
18	13.4	74.4	20	18	AAT70012	Triplex-forming ol
19	13.4	74.4	20	18	AAT47061	Oligonucleotide AG
C	20	13.4	20	24	ABK89176	Human jAZF1/jAZ1
21	13.4	74.4	21	24	AAD30438	Human androgen rec
22	13	72.2	15	24	ABL39459	Human E2F1 allele-
23	12.8	71.1	16	17	AAT36247	CD28 expression in
24	12.8	71.1	16	20	AAAX90340	CD28 inhibiting ph
25	12.8	71.1	17	20	AAV55680	Human tissue kall
C	26	12.8	17	21	AAF01954	Hammerhead ribozym
27	12.8	71.1	17	24	AAL43484	Human tissue kall
28	12.8	71.1	18	17	AAT36245	CD28 expression in
29	12.8	71.1	18	18	AAT51673	Viral integrase in
30	12.8	71.1	18	19	AAAX9255	Oligonucleotide #4
31	12.8	71.1	18	20	AAAX90338	CD28 inhibiting ph
C	32	12.8	19	25	ABX94534	23S/16S rRNA detec
33	12.8	71.1	20	22	AAF72934	Human daxx inhibit
C	34	12.8	21	13	AAQ22561	Sry primer (B). H
35	12.8	71.1	21	18	AAV06186	Primer used when o
36	12.8	71.1	21	21	AAA47231	Primer 1 for human
C	37	12.8	22	18	AAT92773	Primer #2 for immu
C	38	12.8	22	19	AAV52770	Immunoglobulin lam
C	39	12.8	22	19	AAV52822	Ig-lambda #2 PCR p
40	12.8	71.1	22	20	AAZ22690	STAR (5' sense) pr
C	41	12.8	22	21	AAA09933	Primer 2 for human
C	42	12.8	22	21	AAA09983	Primer for human i
C	43	12.8	22	21	AAA10015	Primer IG-lambda-R
C	44	12.8	22	22	AAI71728	PCR primer Ig lamb
C	45	12.8	22	24	ABT11926	Human immunoglobul

ALIGNMENTS

RESULT 1

AAT36196

ID AAT36196 standard; DNA; 18 BP.

XX AAT36196;

XX AAT36196;

DT 25-MAR-2003 (updated)

DT 15-APR-1997 (first entry)

XX	Triplex forming oligo targetting CD28 5'-UTR (nt 58-75).
DE	Reduction; T cell; CD28; gene expression; treatment; immune system;
XX	disorder; graft versus host disease; septic shock; viral disease;
KW	psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;
KW	multiple sclerosis; uveitis; rheumatoid arthritis; 5'-UTR;
KW	systemic lupus erythematosus; inflammatory bowel disease;
KW	triplex forming; oligonucleotide; 5'-untranslated region; ss
XX	Synthetic.
OS	WO9624380-A1.
PN	15-AUG-1996.
XX	05-FEB-1996; 96WO-US01507.
XX	09-FEB-1995; 95US-0387041.
XX	18-SEP-1995; 95US-0529878.
XX	09-FEB-1995; 95US-0387041.
XX	18-SEP-1995; 95US-0529878.

USN 5,932,558

PA (ICNC ) ICN PHARM INC.  
XX Tam RC;  
PI  
XX WPI; 1996-384228/38.  
XX  
XX Oligo:nucleotide which reduces CD28 gene expression in T cells -  
PT for treating immune system diseases, e.g. graft vs. host disease,  
PT septic shock, psoriasis, etc.  
XX  
XX Claim 9; Page 54; 77pp; English.  
PS  
XX The present oligonucleotide reduces T cell CD28 gene expression,  
CC useful in the treatment of CD28 mediated diseases, particularly  
CC immune system disorders, e.g. graft versus host disease, septic  
CC shock, viral disease, psoriasis, type I diabetes mellitus,  
CC thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid  
CC arthritis, systemic lupus erythematosus, inflammatory bowel  
CC disease, etc.. Reducing CD28 expression may reduce the effects of  
CC antigenic stimulation of CD28 positive T cells, with a consequent  
CC reduction in cytokine release.  
CC (Updated on 25-MAR-2003 to correct PR field.)  
XX  
XX Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;  
SQ  
Query Match 100.0%; Score 18; DB 17; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGGAGGGGGTGGTGGG 18  
Db 1 TTGGAGGGGGTGGTGGG 18  
RESULT 2  
AAX90328  
ID AAX90328 standard; DNA; 18 BP.  
XX  
XX AAX90328;  
AC  
XX 24-SEP-1999 (first entry)  
DT  
XX  
DE CD28 inhibiting phosphorothioate oligonucleotide RT03S.  
XX  
XX CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;  
KW immune system mediated disease; gamma-interferon; IL-8;  
KW phosphorothioate; ss.  
XX  
XX Synthetic.  
OS  
XX US5932556-A.  
PN  
XX 03-AUG-1999.  
PD  
XX 18-SEP-1995; 95US-0529878.  
PF  
XX 18-SEP-1995; 95US-0529878.  
PR  
XX (TAMR/) TAM R C.  
PA  
XX Tam RC;  
PI  
XX WPI; 1999-443609/37.  
DR  
XX Treatment of immune system-mediated diseases by inhibiting  
PT expression of CD28, IL-2, gamma-interferon or IL-8  
XX  
XX Claim 5; Column 21; 45pp; English.  
PS  
XX The present invention describes a method for inhibiting the expression  
CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method  
CC comprises subcutaneous administration of an oligonucleotide (OGN).  
CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the  
CC method. The OGNs are used for the treatment of immune system-mediated  
CC diseases.  
XX  
XX Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;  
SQ  
Query Match 100.0%; Score 18; DB 20; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGGAGGGGGTGGTGGG 18  
Db 1 TTGGAGGGGGTGGTGGG 18  
RESULT 4  
AAX99625  
ID AAX99625 standard; DNA; 18 BP.  
XX  
XX AAX99625;  
AC

CC method. The OGNs are used for the treatment of immune system-mediated  
CC diseases. The present sequence represents a CD28 inhibiting  
CC phosphorothioate oligonucleotide used in the exemplification of the  
CC present invention.  
XX  
SQ Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;  
Query Match 100.0%; Score 18; DB 20; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGGAGGGGGTGGTGGG 18  
Db 1 TTGGAGGGGGTGGTGGG 18  
RESULT 3  
AAX90290  
ID AAX90290 standard; DNA; 18 BP.  
XX  
XX AAX90290;  
AC  
XX 24-SEP-1999 (first entry)  
DT  
XX  
DE CD28 inhibition oligonucleotide RT03.  
XX  
XX CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;  
KW immune system mediated disease; gamma-interferon; IL-8; ss.  
XX  
XX Synthetic.  
OS  
XX US5932556-A.  
PN  
XX 03-AUG-1999.  
PD  
XX 18-SEP-1995; 95US-0529878.  
PF  
XX 18-SEP-1995; 95US-0529878.  
PR  
XX (TAMR/) TAM R C.  
PA  
XX Tam RC;  
PI  
XX WPI; 1999-443609/37.  
DR  
XX Treatment of immune system-mediated diseases by inhibiting  
PT expression of CD28, IL-2, gamma-interferon or IL-8  
XX  
XX Claim 5; Column 29; 45pp; English.  
PS  
XX The present invention describes a method for inhibiting the expression  
CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method  
CC comprises subcutaneous administration of an oligonucleotide (OGN).  
CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the  
CC method. The OGNs are used for the treatment of immune system-mediated  
CC diseases.  
XX  
XX Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;  
SQ  
Query Match 100.0%; Score 18; DB 20; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGGAGGGGGTGGTGGG 18  
Db 1 TTGGAGGGGGTGGTGGG 18  
RESULT 4  
AAX99625  
ID AAX99625 standard; DNA; 18 BP.  
XX  
XX AAX99625;  
AC

```
XX 12-JUL-2000 (first entry)
XX DE Nucleotide sequence of G-motif oligonucleotide GR1.
XX KW G-motif oligonucleotide; vaccine; Toxoplasmosis; viral infection;
XX KW antigen presenting cell activation; natural killer cell; septic shock;
XX KW cytotoxic T-lymphocyte; inflammation; autoimmune disease;
XX KW rheumatoid arthritis; Crohn's disease; sarcoidosis; multiple sclerosis;
XX KW Kawasaki syndrome; graft-versus-host disease; transplant rejection;
XX KW helper T cell response 1-mediated disease; Lyme arthritis;
XX KW Streptococcal induced arthritis; chronic inflammatory bowel disease;
XX KW psoriasis vulgaris; experimental allergic encephalomyelitis;
XX KW insulin-dependent diabetes mellitus; bacterial infection;
XX KW parasitic infection; Leishmaniasis; spontaneous abortion; tumour; ss.
XX OS Synthetic.
XX PN WO200014217-A2.
XX PD 16-MAR-2000.
XX PF 03-SEP-1999; 99WO-EP06502.
XX PR 03-SEP-1998; 98EP-0116652.
XX PA (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.
XX PI Wagner H, Lipford GB, Heeg K;
XX WPI; 2000-256970/22.
XX PT Compositions comprising G-motif oligonucleotides useful for treating
XX PT e.g. septic shock, rheumatoid arthritis, diabetes and human
XX PT immunodeficiency virus infections -
XX PS Example 14; Page 32; 75pp; English.
XX CC The present sequence represents a G-motif oligonucleotide of the
XX CC invention. The specification describes compositions comprising G-motif
XX CC oligonucleotides. The G-motif oligonucleotides inhibit activation of
XX CC antigen presenting cells by inhibiting the uptake of DNA by a cell, by
XX CC stimulating natural killer cells, or by co-stimulating cytotoxic
XX CC T-lymphocytes. The G-motif oligonucleotides may be used for the
XX CC productions of vaccines for treating septic shock, inflammation,
XX CC autoimmune diseases (e.g. rheumatoid arthritis, Crohn's disease,
XX CC sarcoidosis, multiple sclerosis, Kawasaki syndrome, graft-versus-host
XX CC disease and transplant rejection), helper T cell response 1-mediated
XX CC diseases (e.g. Streptococcal induced arthritis, Lyme arthritis, chronic
XX CC inflammatory bowel disease, psoriasis vulgaris, experimental allergic
XX CC encephalomyelitis, and insulin-dependent diabetes mellitus), bacterial
XX CC infections, parasitic infections (e.g. Leishmaniasis or Toxoplasmosis),
XX CC viral infections (e.g. Cytomegalovirus and human immunodeficiency virus
XX CC (HIV)-infections), spontaneous abortions and tumours. They may also be
XX CC used to induce proliferation of bone marrow cells, especially macrophage
XX CC precursor cells.
XX SQ Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 Other;
Query Match 100.0%; Score 18; DB 21; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTGAGGGGGTGGTGGG 18
Db 1 TTGAGGGGGTGGTGGG 18
RESULT 5
AAZ99650/c
ID AAZ99650 standard; DNA; 18 BP.
XX AC AAZ99650;
```

---

```
XX 12-JUL-2000 (first entry)
XX DE Nucleotide sequence of non-G-motif oligonucleotide GR1comp.
XX KW G-motif oligonucleotide; vaccine; Toxoplasmosis; viral infection;
XX KW antigen presenting cell activation; natural killer cell; septic shock;
XX KW cytotoxic T-lymphocyte; inflammation; autoimmune disease;
XX KW rheumatoid arthritis; Crohn's disease; sarcoidosis; multiple sclerosis;
XX KW Kawasaki syndrome; graft-versus-host disease; transplant rejection;
XX KW helper T cell response 1-mediated disease; Lyme arthritis;
XX KW Streptococcal induced arthritis; chronic inflammatory bowel disease;
XX KW psoriasis vulgaris; experimental allergic encephalomyelitis;
XX KW insulin-dependent diabetes mellitus; bacterial infection;
XX KW parasitic infection; Leishmaniasis; spontaneous abortion; tumour; ss.
XX OS Synthetic.
XX PN WO200014217-A2.
XX PD 16-MAR-2000.
XX PF 03-SEP-1999; 99WO-EP06502.
XX PR 03-SEP-1998; 98EP-0116652.
XX PA (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.
XX PI Wagner H, Lipford GB, Heeg K;
XX WPI; 2000-256970/22.
XX PT Compositions comprising G-motif oligonucleotides useful for treating
XX PT e.g. septic shock, rheumatoid arthritis, diabetes and human
XX PT immunodeficiency virus infections -
XX PS Example 14; Page 32; 75pp; English.
XX CC The present sequence represents a non-G-motif oligonucleotide of the
XX CC invention. The specification describes compositions comprising G-motif
XX CC oligonucleotides. The G-motif oligonucleotides inhibit activation of
XX CC antigen presenting cells by inhibiting the uptake of DNA by a cell, by
XX CC stimulating natural killer cells, or by co-stimulating cytotoxic
XX CC T-lymphocytes. The G-motif oligonucleotides may be used for the
XX CC productions of vaccines for treating septic shock, inflammation,
XX CC autoimmune diseases (e.g. rheumatoid arthritis, Crohn's disease,
XX CC sarcoidosis, multiple sclerosis, Kawasaki syndrome, graft-versus-host
XX CC disease and transplant rejection), helper T cell response 1-mediated
XX CC diseases (e.g. Streptococcal induced arthritis, Lyme arthritis, chronic
XX CC inflammatory bowel disease, psoriasis vulgaris, experimental allergic
XX CC encephalomyelitis, and insulin-dependent diabetes mellitus), bacterial
XX CC infections, parasitic infections (e.g. Leishmaniasis or Toxoplasmosis),
XX CC viral infections (e.g. Cytomegalovirus and human immunodeficiency virus
XX CC (HIV)-infections), spontaneous abortions and tumours. They may also be
XX CC used to induce proliferation of bone marrow cells, especially macrophage
XX CC precursor cells.
XX SQ Sequence 18 BP; 4 A; 13 C; 0 G; 1 T; 0 Other;
Query Match 100.0%; Score 18; DB 21; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTGAGGGGGTGGTGGG 18
Db 18 TTGAGGGGGTGGTGGG 1
RESULT 6
AAT36197
ID AAT36197 standard; DNA; 21 BP.
XX AC AAT36197;
```

```
XX 25-MAR-2003 (updated)
DT 15-APR-1997 (first entry)
XX
DE Triplex forming oligo targetting CD28 5'-UTR (nt 58-78).
XX
KW Reduction; T cell; CD28; gene expression; treatment; immune system;
KW disorder; graft versus host disease; septic shock; viral disease;
KW psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;
KW multiple sclerosis; uveitis; rheumatoid arthritis; 5'-UTR;
KW systemic lupus erythematosus; inflammatory bowel disease;
KW triplex forming; oligonucleotide; 5'-untranslated region; ss
XX
OS Synthetic.
XX
XX WO9624380-A1.
PN
XX
PD 15-AUG-1996.
XX
XX 05-FEB-1996; 96WO-US01507.
PF
XX 09-FEB-1995; 95US-0387041.
PR
PR 18-SEP-1995; 95US-0529878.
PR
PR 09-FEB-1995; 95US-0387041.
PR
PR 18-SEP-1995; 95US-0529878.
XX
PA (ICNC ) ICN PHARM INC.
XX
XX Tam RC;
PI
XX
XX WPI; 1996-384228/38.
DR
XX
XX Oligo:nucleotide which reduces CD28 gene expression in T cells -
PT for treating immune system diseases, e.g. graft vs. host disease,
PT septic shock, psoriasis, etc.
XX
XX Claim 10; Page 54; 77pp; English.
PS
XX
XX The present oligonucleotide reduces T cell CD28 gene expression,
CC useful in the treatment of CD28 mediated diseases, particularly
CC immune system disorders, e.g. graft versus host disease, septic
CC shock, viral disease, psoriasis, type I diabetes mellitus,
CC thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid
CC arthritis, systemic lupus erythematosus, inflammatory bowel
CC disease, etc.. Reducing CD28 expression may reduce the effects of
CC antigenic stimulation of CD28 positive T cells, with a consequent
CC reduction in cytokine release.
CC (Updated on 25-MAR-2003 to correct PR field.)
XX
XX Sequence 21 BP; 1 A; 0 C; 16 G; 4 T; 0 other;
SQ
Query Match 100.0%; Score 18; DB 17; Length 21;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGTGGTGGGG 18
Db 4 TTGGAGGGGGTGGTGGGG 21

RESULT 7
AAX90329
ID AAX90329 standard; DNA; 21 BP.
XX
AC AAX90329;
XX
XX 24-SEP-1999 (first entry)
DT
XX
DE CD28 inhibiting phosphorothioate oligonucleotide RT04S.
XX
KW CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
KW immune system mediated disease; gamma-interferon; IL-8;
KW phosphorothioate; ss.
```

```
XX Synthetic.
OS
XX US5932556-A.
PN
XX 03-AUG-1999.
PD
XX
XX 18-SEP-1995; 95US-0529878.
PF
XX 18-SEP-1995; 95US-0529878.
PR
XX (TAMR/) TAM R C.
PA
XX Tam RC;
PI
XX
XX WPI; 1999-443609/37.
DR
XX
XX Treatment of immune system-mediated diseases by inhibiting
PT expression of CD28, IL-2, gamma-interferon or IL-8
PT
XX
XX Example; Column 21; 45pp; English.
PS
XX
XX The present invention describes a method for inhibiting the expression
CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method
CC comprises subcutaneous administration of an oligonucleotide (OGN).
CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the
CC method. The OGNs are used for the treatment of immune system-mediated
CC diseases. The present sequence represents a CD28 inhibiting
CC phosphorothioate oligonucleotide used in the exemplification of the
CC present invention.
XX
XX Sequence 21 BP; 1 A; 0 C; 16 G; 4 T; 0 other;
SQ
Query Match 100.0%; Score 18; DB 20; Length 21;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGTGGTGGGG 18
Db 4 TTGGAGGGGGTGGTGGGG 21

RESULT 8
AAX90291
ID AAX90291 standard; DNA; 21 BP.
XX
AC AAX90291;
XX
XX 24-SEP-1999 (first entry)
DT
XX
DE CD28 inhibition oligonucleotide RT04.
XX
XX CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
KW immune system mediated disease; gamma-interferon; IL-8; ss.
XX
XX Synthetic.
OS
XX US5932556-A.
PN
XX 03-AUG-1999.
PD
XX
XX 18-SEP-1995; 95US-0529878.
PF
XX 18-SEP-1995; 95US-0529878.
PR
XX (TAMR/) TAM R C.
PA
XX Tam RC;
PI
XX
XX WPI; 1999-443609/37.
DR
XX
XX Treatment of immune system-mediated diseases by inhibiting
PT expression of CD28, IL-2, gamma-interferon or IL-8
PT
```

XX PS Claim 6; Column 29; 45pp; English.

XX CC The present invention describes a method for inhibiting the expression

CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method

CC comprises subcutaneous administration of an oligonucleotide (OGN).

CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the

CC method. The OGNs are used for the treatment of immune system-mediated

CC diseases.

XX SQ Sequence 21 BP; 1 A; 0 C; 16 G; 4 T; 0 other;

Query Match 100.0%; Score 18; DB 20; Length 21;

Best Local Similarity 100.0%; Pred. No. 3e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGTGGTGGG 18

Db 4 TTGGAGGGGGTGGTGGG 21

RESULT 9

AAT36243

ID AAT36243 standard; DNA; 18 BP.

XX AC AAT36243;

XX DT 25-MAR-2003 (updated)

DT 16-APR-1997 (first entry)

XX DE CD28 expression inhibiting oligonucleotide, RT09s.

XX KW Reduction; T cell; CD28; gene expression; treatment; immune system;

KW disorder; graft versus host disease; septic shock; viral disease;

KW psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;

KW multiple sclerosis; uveitis; rheumatoid arthritis; interleukin 2;

KW systemic lupus erythematosus; inflammatory bowel disease;

KW IL-2; production; antisense; inhibition; ss

XX OS Synthetic.

XX PN WO9624380-A1.

XX PD 15-AUG-1996.

XX PF 05-FEB-1996; 95WO-US01507.

XX PR 09-FEB-1995; 95US-0387041.

PR 18-SEP-1995; 95US-0529878.

PR 09-FEB-1995; 95US-0387041.

PR 18-SEP-1995; 95US-0529878.

XX PA (ICNC) ICN PHARM INC.

XX PI Tam RC;

XX WI WPI; 1996-384228/38.

XX PT Oligo:nucleotide which reduces CD28 gene expression in T cells -

PT for treating immune system diseases, e.g. graft vs. host disease,

PT septic shock, psoriasis, etc.

XX PS Example 2; Page 45; 77pp; English.

XX CC The present oligonucleotide reduces CD28 dependent interleukin-2

CC (IL-2) production and T cell CD28 gene expression, useful in the

CC treatment of CD28 mediated diseases, particularly immune system

CC disorders, e.g. graft versus host disease, septic shock, viral

CC disease, psoriasis, type I diabetes mellitus, thyroiditis,

CC sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis,

CC systemic lupus erythematosus, inflammatory bowel disease, etc..

CC Reducing CD28 expression may reduce the effects of antigenic

CC stimulation of CD28 positive T cells, with a consequent reduction

CC in cytokine release.

CC (Updated on 25-MAR-2003 to correct PR field.)

XX SQ Sequence 18 BP; 2 A; 0 C; 13 G; 3 T; 0 other;

Query Match 91.1%; Score 16.4; DB 17; Length 18;

Best Local Similarity 94.4%; Pred. No. 1.3e+03;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGTGGTGGG 18

Db 1 TTGGAGGGGGAGGTGGG 18

RESULT 10

AAX90336

ID AAX90336 standard; DNA; 18 BP.

XX AC AAX90336;

XX DT 24-SEP-1999 (first entry)

XX DE CD28 inhibiting phosphorothioate oligonucleotide RT09S.

XX KW CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;

KW immune system mediated disease; gamma-interferon; IL-8;

KW phosphorothioate; ss.

XX OS Synthetic.

XX PN US932556-A.

XX PD 03-AUG-1999.

XX PF 18-SEP-1995; 95US-0529878.

XX PR 18-SEP-1995; 95US-0529878.

XX PA (TAMR/) TAM R C.

XX PI Tam RC;

XX DR WPI; 1999-443609/37.

XX PT Treatment of immune system-mediated diseases by inhibiting

PT expression of CD28, IL-2, gamma-interferon or IL-8

XX PS Example; Column 24; 45pp; English.

XX CC The present invention describes a method for inhibiting the expression

CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method

CC comprises subcutaneous administration of an oligonucleotide (OGN).

CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the

CC method. The OGNs are used for the treatment of immune system-mediated

CC diseases. The present sequence represents a CD28 inhibiting

CC phosphorothioate oligonucleotide used in the exemplification of the

CC present invention.

XX SQ Sequence 18 BP; 2 A; 0 C; 13 G; 3 T; 0 other;

Query Match 91.1%; Score 16.4; DB 20; Length 18;

Best Local Similarity 94.4%; Pred. No. 1.3e+03;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGTGGTGGG 18

Db 1 TTGGAGGGGGAGGTGGG 18

RESULT 11

AAT36242

ID AAT36242 standard; DNA; 18 BP.

XX

AC AAT36242;  
XX  
DT 25-MAR-2003 (updated)  
DT 16-APR-1997 (first entry)  
XX  
DE CD28 expression inhibiting oligonucleotide, RT05s.  
XX  
KW Reduction; T cell; CD28; gene expression; treatment; immune system;  
KW disorder; graft versus host disease; septic shock; viral disease;  
KW psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;  
KW multiple sclerosis; uveitis; rheumatoid arthritis; interleukin 2;  
KW systemic lupus erythematosus; inflammatory bowel disease;  
KW IL-2; production; antisense; inhibition; ss  
XX  
OS Synthetic.  
XX  
PN WO9624380-A1.  
XX  
PD 15-AUG-1996.  
XX  
PF 05-FEB-1996; 96WO-US01507.  
XX  
PR 09-FEB-1995; 95US-0387041.  
PR 18-SEP-1995; 95US-0529878.  
PR 09-FEB-1995; 95US-0387041.  
PR 18-SEP-1995; 95US-0529878.  
XX  
PA (ICNC ) ICN PHARM INC.  
XX  
PI Tam RC;  
XX  
XX WPI; 1996-384228/38.  
XX  
PT Oligo:nucleotide which reduces CD28 gene expression in T cells -  
PT for treating immune system diseases, e.g. graft vs. host disease,  
PT septic shock, psoriasis, etc.  
XX  
PS Example 2; Page 45; 77pp; English.  
XX  
CC The present oligonucleotide reduces CD28 dependent interleukin-2  
CC (IL-2) production and T cell CD28 gene expression, useful in the  
CC treatment of CD28 mediated diseases, particularly immune system  
CC disorders, e.g. graft versus host disease, septic shock, viral  
CC disease, psoriasis, type I diabetes mellitus, thyroiditis,  
CC sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis,  
CC systemic lupus erythematosus, inflammatory bowel disease, etc..  
CC Reducing CD28 expression may reduce the effects of antigenic  
CC stimulation of CD28 positive T cells, with a consequent reduction  
CC in cytokine release.  
CC (Updated on 25-MAR-2003 to correct PR field.)  
XX  
SQ Sequence 18 BP; 3 A; 0 C; 13 G; 2 T; 0 other;  
Query Match 82.2%; Score 14.8; DB 17; Length 18;  
Best Local Similarity 88.9%; Pred. No. 5.2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 TTGGAGGGGGTGGTGGGG 18  
Db 1 TTGGAGGGGGGAGGGGG 18  
RESULT 12  
AAT36244  
ID AAT36244 standard; DNA; 18 BP.  
XX  
AC AAT36244;  
XX  
DT 25-MAR-2003 (updated)  
DT 16-APR-1997 (first entry)  
XX  
DE CD28 expression inhibiting oligonucleotide, RT10s.

KW Reduction; T cell; CD28; gene expression; treatment; immune system;  
KW disorder; graft versus host disease; septic shock; viral disease;  
KW psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;  
KW multiple sclerosis; uveitis; rheumatoid arthritis; interleukin 2;  
KW systemic lupus erythematosus; inflammatory bowel disease;  
KW IL-2; production; antisense; inhibition; ss  
XX  
OS Synthetic.  
XX  
PN WO9624380-A1.  
XX  
PD 15-AUG-1996.  
XX  
PF 05-FEB-1996; 96WO-US01507.  
XX  
PR 09-FEB-1995; 95US-0387041.  
PR 18-SEP-1995; 95US-0529878.  
PR 09-FEB-1995; 95US-0387041.  
PR 18-SEP-1995; 95US-0529878.  
XX  
PA (ICNC ) ICN PHARM INC.  
XX  
PI Tam RC;  
XX  
XX WPI; 1996-384228/38.  
XX  
PT Oligo:nucleotide which reduces CD28 gene expression in T cells -  
PT for treating immune system diseases, e.g. graft vs. host disease,  
PT septic shock, psoriasis, etc.  
XX  
PS Example 2; Page 45; 77pp; English.  
XX  
CC The present oligonucleotide reduces CD28 dependent interleukin-2  
CC (IL-2) production and T cell CD28 gene expression, useful in the  
CC treatment of CD28 mediated diseases, particularly immune system  
CC disorders, e.g. graft versus host disease, septic shock, viral  
CC disease, psoriasis, type I diabetes mellitus, thyroiditis,  
CC sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis,  
CC systemic lupus erythematosus, inflammatory bowel disease, etc..  
CC Reducing CD28 expression may reduce the effects of antigenic  
CC stimulation of CD28 positive T cells, with a consequent reduction  
CC in cytokine release.  
CC (Updated on 25-MAR-2003 to correct PR field.)  
XX  
SQ Sequence 18 BP; 1 A; 2 C; 11 G; 4 T; 0 other;  
Query Match 82.2%; Score 14.8; DB 17; Length 18;  
Best Local Similarity 88.9%; Pred. No. 5.2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 TTGGAGGGGGTGGTGGGG 18  
Db 1 TTGGAGGGGGTGGTGGCG 18  
RESULT 13  
AAX90335  
ID AAX90335 standard; DNA; 18 BP.  
XX  
AC AAX90335;  
XX  
DT 24-SEP-1999 (first entry)  
XX  
DE CD28 inhibiting phosphorothioate oligonucleotide RT05S.  
XX  
KW CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;  
KW immune system mediated disease; gamma-interferon; IL-8;  
KW phosphorothioate; ss.  
XX  
OS Synthetic.  
XX  
PN US5932556-A.

PD 03-AUG-1999.  
XX  
PF 18-SEP-1995; 95US-0529878.  
XX  
PR 18-SEP-1995; 95US-0529878.  
XX (TAMR/) TAM R C.  
XX  
PI Tam RC;  
XX  
DR WPI; 1999-443609/37.  
XX  
XX Treatment of immune system-mediated diseases by inhibiting  
PT expression of CD28, IL-2, gamma-interferon or IL-8  
XX  
PS Example; Column 24; 45pp; English.  
XX  
CC The present invention describes a method for inhibiting the expression  
CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method  
CC comprises subcutaneous administration of an oligonucleotide (OGN).  
CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the  
CC method. The OGNs are used for the treatment of immune system-mediated  
CC diseases. The present sequence represents a CD28 inhibiting  
CC phosphorothioate oligonucleotide used in the exemplification of the  
CC present invention.  
XX  
SQ Sequence 18 BP; 3 A; 0 C; 13 G; 2 T; 0 other;  
  
Query Match 82.2%; Score 14.8; DB 20; Length 18;  
Best Local Similarity 88.9%; Pred. No. 5.2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 1 TTGGAGGGGGTGGTGGG 18  
Db 1 TTGGAGGGGGAGGAGGGG 18  
  
RESULT 14  
AAX90337  
ID AAX90337 standard; DNA; 18 BP.  
XX  
AC AAX90337;  
XX  
DT 24-SEP-1999 (first entry)  
XX  
DE CD28 inhibiting phosphorothioate oligonucleotide RT10S.  
XX  
KW CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;  
KW immune system mediated disease; gamma-interferon; IL-8;  
KW phosphorothioate; ss.  
XX  
OS Synthetic.  
XX  
PN US5932556-A.  
XX  
PD 03-AUG-1999.  
XX  
PF 18-SEP-1995; 95US-0529878.  
XX  
PR 18-SEP-1995; 95US-0529878.  
XX (TAMR/) TAM R C.  
XX  
PI Tam RC;  
XX  
DR WPI; 1999-443609/37.  
XX  
XX Treatment of immune system-mediated diseases by inhibiting  
PT expression of CD28, IL-2, gamma-interferon or IL-8  
XX  
PS Example; Column 24; 45pp; English.  
XX  
CC The present invention describes a method for inhibiting the expression

CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method  
CC comprises subcutaneous administration of an oligonucleotide (OGN).  
CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the  
CC method. The OGNs are used for the treatment of immune system-mediated  
CC diseases. The present sequence represents a CD28 inhibiting  
CC phosphorothioate oligonucleotide used in the exemplification of the  
CC present invention.  
XX  
SQ Sequence 18 BP; 1 A; 2 C; 11 G; 4 T; 0 other;  
  
Query Match 82.2%; Score 14.8; DB 20; Length 18;  
Best Local Similarity 88.9%; Pred. No. 5.2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 1 TTGGAGGGGGTGGTGGG 18  
Db 1 TTGGAGGGGGTGGTGGG 18  
  
RESULT 15  
AAF16593  
ID AAF16593 standard; DNA; 22 BP.  
XX  
AC AAF16593;  
XX  
DT 13-MAR-2001 (first entry)  
XX  
DE Gastric acid production inhibiting oligonucleotide SEQ ID NO: 79.  
XX  
KW Gastric acid disturbance; gastric reflux; gastritis; dyspepsia;  
KW stomach ulcer; duodenal ulcer; Helicobacter pylori; antisense;  
KW DNA-RNA hybrid; ss.  
XX  
OS Synthetic.  
XX  
PN WO200071164-A1.  
XX  
PD 30-NOV-2000.  
XX  
PF 24-MAY-2000; 2000WO-AU00498.  
XX  
PR 24-MAY-1999; 99AU-0000510.  
XX (TACH/) TACHAS G.  
XX  
PI Tachas G;  
XX  
DR WPI; 2001-025093/03.  
XX  
PT Treating gastric acid disturbance by administering an oligonucleotide  
PT which modulates the activity of a polypeptide involved in gastric acid  
PT production or secretion -  
XX  
PS Example 3; Page 145; 164pp; English.  
XX  
CC The present invention provides oligonucleotides, and methods for their  
CC use, which are useful in modulating the action of proteins involved in  
CC gastric acid production. The target protein is preferably the histamine  
CC H2 receptor or one of the proteins which form part of the gastric proton  
CC pump. The sequences and methods of the invention are useful in the  
CC treatment of gastric reflux, gastritis, dyspepsia, stomach ulcers,  
CC duodenal ulcers and other gastric acid disturbances, most of which are  
CC caused by Helicobacter pylori.  
XX  
SQ Sequence 22 BP; 0 A; 0 C; 16 G; 3 T; 3 other;  
  
Query Match 75.6%; Score 13.6; DB 22; Length 22;  
Best Local Similarity 81.2%; Pred. No. 1.5e+04;  
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 2 TGGAGGGGGTGGTGGG 17  
Db 2 TGGMGGGGGGMGGKGG 17



Search completed: October 27, 2003, 11:25:18  
Job time : 163 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: October 27, 2003, 10:32:29 ; Search time 376.114 Seconds  
(without alignments)  
1957.844 Million cell updates/sec

Title: US-09-331-204A-5  
Perfect score: 18  
Sequence: 1 ggggaggagggtgga 18  
Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 2888711 seqs, 20454813386 residues  
Total number of hits satisfying chosen parameters: 681044

Minimum DB seq length: 0  
Maximum DB seq length: 22  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vi:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htg\_mus:\*  
34: em\_htg\_pln:\*  
35: em\_htg\_rod:\*  
36: em\_htg\_mam:\*  
37: em\_htg\_vrt:\*  
38: em\_sy:\*  
39: em\_htgo\_hum:\*  
40: em\_htgo\_mus:\*  
41: em\_htgo\_other:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
C 1	13.8	76.7	17	6	AR029939	AR029939 Sequence
C 2	13.8	76.7	21	6	AX096246	AX096246 Sequence
C 3	13.4	74.4	20	6	AR103774	AR103774 Sequence
C 4	13.4	74.4	20	6	BD130004	BD130004 Asthma-as
C 5	13.4	74.4	22	6	A27787	A27787 Oligonucleo
C 6	12.8	71.1	17	6	AX215456	AX215456 Sequence
C 7	12.8	71.1	17	6	AX215457	AX215457 Sequence
C 8	12.8	71.1	17	6	AX422501	AX422501 Sequence
C 9	12.8	71.1	17	6	AX422502	AX422502 Sequence
C 10	12.8	71.1	19	6	AX001112	AX001112 Sequence
C 11	12.8	71.1	20	6	AR029133	AR029133 Sequence
C 12	12.8	71.1	20	6	AR036517	AR036517 Sequence
C 13	12.8	71.1	20	6	AR073952	AR073952 Sequence
C 14	12.8	71.1	20	6	AR096050	AR096050 Sequence
C 15	12.8	71.1	20	6	AR105507	AR105507 Sequence
C 16	12.8	71.1	20	6	AR212283	AR212283 Sequence
C 17	12.8	71.1	20	6	AR215974	AR215974 Sequence
C 18	12.8	71.1	20	6	AR231417	AR231417 Sequence
C 19	12.8	71.1	20	6	E49531	E49531 Antisense O
C 20	12.8	71.1	20	6	I27251	I27251 Sequence 21
C 21	12.8	71.1	22	6	A44397	A44397 Sequence 27
C 22	12.8	71.1	22	6	AR193523	AR193523 Sequence
C 23	12.4	68.9	17	6	AX532422	AX532422 Sequence
C 24	12.4	68.9	17	6	AX532423	AX532423 Sequence
C 25	12.4	68.9	17	6	AX532424	AX532424 Sequence
C 26	12.4	68.9	17	6	AX532425	AX532425 Sequence
C 27	12.4	68.9	18	6	A97983	A97983 Sequence 13
C 28	12.4	68.9	20	6	AR208749	AR208749 Sequence
C 29	12.4	68.9	20	6	AR208750	AR208750 Sequence
C 30	12.4	68.9	21	6	BD173872	BD173872 Novel pro
C 31	12.2	67.8	17	6	AX216967	AX216967 Sequence
C 32	12.2	67.8	18	6	A97312	A97312 Sequence 29
C 33	12.2	67.8	19	6	AX119341	AX119341 Sequence
C 34	12.2	67.8	20	6	AR080189	AR080189 Sequence
C 35	12.2	67.8	20	6	AX664949	AX664949 Sequence
C 36	12.2	67.8	20	6	I60656	I60656 Sequence 6
C 37	12	66.7	16	6	I26792	I26792 Sequence 15
C 38	12	66.7	16	6	I91533	I91533 Sequence 15
C 39	12	66.7	17	6	AR029938	AR029938 Sequence
C 40	12	66.7	17	6	AX214604	AX214604 Sequence
C 41	12	66.7	17	6	AX214605	AX214605 Sequence
C 42	12	66.7	17	6	AX215458	AX215458 Sequence
C 43	12	66.7	17	6	AX215459	AX215459 Sequence
C 44	12	66.7	17	6	AX532426	AX532426 Sequence
C 45	12	66.7	17	6	AX532427	AX532427 Sequence

ALIGNMENTS

RESULT 1  
AR029939/c  
LOCUS AR029939 Sequence 128 from patent US 5861244.  
DEFINITION Sequence 128 from patent US 5861244.  
ACCESSION AR029939  
VERSION AR029939.1 GI:5943153  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Wang, C.-G. and Hepburn, A.G.  
TITLE Genetic sequence assay using DNA triple strand formation  
JOURNAL Patent: US 5861244-A 128 19-JAN-1999;  
FEATURES Location/Qualifiers

AR029939 17 bp DNA  
Sequence 128 from patent US 5861244.  
AR029939  
AR029939.1 GI:5943153  
Unknown.  
Unknown.  
Unclassified.  
1 (bases 1 to 17)  
Wang, C.-G. and Hepburn, A.G.  
Genetic sequence assay using DNA triple strand formation  
Patent: US 5861244-A 128 19-JAN-1999;  
Location/Qualifiers

Pred. No. is the number of results predicted by chance to have a

```

source      1..17
            /organism="unknown"
BASE COUNT  0 a 12 c 0 g 5 t
ORIGIN
Query Match      76.7%; Score 13.8; DB 6; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTGGA 17
Db 17 GGGGAGGAGGGGAAGGA 1

RESULT 2
AX096246/c
LOCUS      AX096246      21 bp      DNA      linear      PAT 30-MAR-2001
DEFINITION Sequence 1424 from Patent WO0118250.
ACCESSION  AX096246
VERSION     AX096246.1 GI:13512473
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens

REFERENCE 1
AUTHORS   Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
           Mccarthy,J.J.
TITLE     Single nucleotide polymorphisms in genes
JOURNAL   Patent: WO 0118250-A 1424 15-MAR-2001;
           WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
           Pharmaceuticals, Inc. (US)
FEATURES   Location/Qualifiers
            source      1..21
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
BASE COUNT  2 a 12 c 1 g 5 t 1 others
ORIGIN
Query Match      76.7%; Score 13.8; DB 6; Length 21;
Best Local Similarity 88.2%; Pred. No. 1.7e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTGGA 17
Db 21 GGGGAGGAGAYGCTGGA 5

RESULT 3
AR103774
LOCUS      AR103774      20 bp      DNA      linear      PAT 14-FEB-2001
DEFINITION Sequence 298 from patent US 6087485.
ACCESSION  AR103774
VERSION     AR103774.1 GI:12815362
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS   Brooks-Wilson,A.R., Buckler,A., Cardon,L., Carey,A.H., Galvin,M.,
           Miller,A. and North,M.
TITLE     Asthma related genes
JOURNAL   Patent: US 6087485-A 298 11-JUL-2000;
           Location/Qualifiers
FEATURES   Location/Qualifiers
            source      1..20
            /organism="unknown"
            /mol_type="genomic DNA"
BASE COUNT  3 a 2 c 12 g 3 t
ORIGIN
Query Match      74.4%; Score 13.4; DB 6; Length 20;
Best Local Similarity 93.3%; Pred. No. 2.6e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTG 15
Db 5 GGTGAGGAGGGGCTG 19

RESULT 4
BD130004
LOCUS      BD130004      22 bp      DNA      linear      PAT 18-SEP-2002
DEFINITION Asthma-associated gene.
ACCESSION  BD130004
VERSION     BD130004.1 GI:23224949
KEYWORDS   JP 2002500895-A/294.
SOURCE     unidentified
ORGANISM   unidentified
            unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS   Willson,A.R.B., Buckler,A., Cardon,L., Carey,A.H., Galvin,M.,
           Miller,A. and North,M.
TITLE     Asthma-associated gene
JOURNAL   Patent: JP 2002500895-A 294 15-JAN-2002;
           AKYS PHARMACEUTICALS INC
COMMENT    OS Unidentified
            PN JP 2002500895-A/294
            PD 15-JAN-2002
            PF 21-JAN-1998 JP 2000528715
            PI ANGELA R BROOKS WILSON,ALAN BUCKLER,LON
            CARDON,ALISOUN H CAREY,
            PI MARGARET GALVIN,ANDREW MILLER,MICHAEL NORTH
            PC C12Q1/68,A01K67/027,C07K14/47,C12N15/09,C12N15/00 CC
            Strandedness: Single;
            CC Topology: Linear;
            CC Asthma-associated gene
            FH Key Location/Qualifiers
            FT source      1..20
            /organism='Unidentified'.
            Location/Qualifiers
            source      1..20
            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"
BASE COUNT  3 a 2 c 12 g 3 t
ORIGIN
Query Match      74.4%; Score 13.4; DB 6; Length 20;
Best Local Similarity 93.3%; Pred. No. 2.6e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTG 15
Db 5 GGTGAGGAGGGGCTG 19

RESULT 5
A27787
LOCUS      A27787      22 bp      DNA      linear      PAT 11-MAY-1995
DEFINITION Oligonucleotide DNA (33.6 AL) from patent EP0422861.
ACCESSION  A27787
VERSION     A27787.1 GI:905260
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   synthetic construct
            artificial sequences.
REFERENCE 1 (bases 1 to 22)
AUTHORS   Garman,A.J.
TITLE     Probes
JOURNAL   Patent: EP 0422861-A 1 17-APR-1991;
           IMPERIAL CHEMICAL INDUSTRIES PLC; ZENECA LIMITED
           Location/Qualifiers
FEATURES   Location/Qualifiers
            source      1..22
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
```

BASE COUNT 5 a 1 c 14 g 2 t

Query Match 74.4%; Score 13.4; DB 6; Length 22;  
Best Local Similarity 93.3%; Pred. No. 2.6e+05;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGAGGGGCTGA 17  
Db 2 GGAGGAAGGGCTGA 16

RESULT 6  
AX215456/c  
LOCUS AX215456 17 bp mRNA linear PAT 07-SEP-2001  
DEFINITION Sequence 898 from Patent WO0159103.  
ACCESSION AX215456  
VERSION AX215456.1 GI:1525499  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1  
AUTHORS Blatt, L., Mcswiggen, J. and Chowrira, B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression  
JOURNAL Patent: WO 0159103-A 898 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);  
McsWiggen, James (US); Chowrira, Bharat M. (US)  
FEATURES  
source  
1..17  
/organism="synthetic construct"  
/mol\_type="mRNA"  
/db\_xref="taxon:32630"  
/note="Nucleic Acid"

BASE COUNT 0 a 13 c 1 g 3 t

Query Match 71.1%; Score 12.8; DB 6; Length 17;  
Best Local Similarity 87.5%; Pred. No. 4.9e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGCTGG 16  
Db 17 GGGGAGGAGGGGAGG 2

RESULT 7  
AX215457/c  
LOCUS AX215457 17 bp mRNA linear PAT 07-SEP-2001  
DEFINITION Sequence 899 from Patent WO0159103.  
ACCESSION AX215457  
VERSION AX215457.1 GI:1525500  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1  
AUTHORS Blatt, L., Mcswiggen, J. and Chowrira, B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression  
JOURNAL Patent: WO 0159103-A 899 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);  
McsWiggen, James (US); Chowrira, Bharat M. (US)  
FEATURES  
source  
1..17  
/organism="synthetic construct"  
/mol\_type="mRNA"  
/db\_xref="taxon:32630"  
/note="Nucleic Acid"

BASE COUNT 0 a 14 c 0 g 3 t

Query Match 71.1%; Score 12.8; DB 6; Length 17;  
Best Local Similarity 87.5%; Pred. No. 4.9e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTGG 16  
Db 16 GGGGAGGAGGGGAGG 1

RESULT 8  
AX422501/c  
LOCUS AX422501 17 bp mRNA linear PAT 18-JUN-2002  
DEFINITION Sequence 837 from Patent WO0188124.  
ACCESSION AX422501  
VERSION AX422501.1 GI:21525883  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and Randi, A.M.  
TITLE Method and reagent for the inhibition of erg  
JOURNAL Patent: WO 0188124-A 837 22-NOV-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)  
FEATURES  
source  
1..17  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"

BASE COUNT 2 a 13 c 1 g 1 t

Query Match 71.1%; Score 12.8; DB 6; Length 17;  
Best Local Similarity 87.5%; Pred. No. 4.9e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGGAGGAGGGGCTGGA 17  
Db 17 GGGGGTGGGGGCTGGA 2

RESULT 9  
AX422502/c  
LOCUS AX422502 17 bp mRNA linear PAT 18-JUN-2002  
DEFINITION Sequence 838 from Patent WO0188124.  
ACCESSION AX422502  
VERSION AX422502.1 GI:21525884  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and Randi, A.M.  
TITLE Method and reagent for the inhibition of erg  
JOURNAL Patent: WO 0188124-A 838 22-NOV-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)  
FEATURES  
source  
1..17  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"

BASE COUNT 2 a 12 c 2 g 1 t

Query Match 71.1%; Score 12.8; DB 6; Length 17;  
Best Local Similarity 87.5%; Pred. No. 4.9e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGGAGGAGGGGCTGGA 17

Db 16 GGGGGTGGGGCTGGA 1  
||| || ||||| |||  
RESULT 10  
AX001112 LOCUS AX001112 19 bp DNA linear PAT 10-MAR-2000  
DEFINITION Sequence 2 from Patent WO9901574.  
ACCESSION AX001112  
VERSION AX001112.1 GI:7241311  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Amouyel, P. and Chartier-Harlin, M.  
TITLE METHOD FOR DIAGNOSING ALZHEIMER DISEASE  
JOURNAL Patent: WO 9901574-A 2 14-JAN-1999;  
INST NAT SANTE RECH MED (FR); AMOUEL PHILIPPE (FR)  
FEATURES  
source  
1..19  
/organism="unidentified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644" 4 t  
BASE COUNT 3 a 2 c 10 g 4 t  
ORIGIN  
Query Match 71.1%; Score 12.8; DB 6; Length 19;  
Best Local Similarity 87.5%; Pred. No. 4.8e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 3 GGAGGAGGGCTGGAA 18  
||| ||||| |||||  
Db 1 GGGGAGGTGCTGGAA 16  
RESULT 11  
AR029133/c LOCUS AR029133 20 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 9 from patent US 5859221.  
ACCESSION AR029133  
VERSION AR029133.1 GI:5941106  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Cook, P. Dan. and Kawasaki, A. Mamoru.  
TITLE 2'-O-modified oligonucleotides  
JOURNAL Patent: US 5859221-A 9 12-JAN-1999;  
FEATURES  
source  
1..20  
/organism="unknown" 4 t  
BASE COUNT 0 a 14 c 2 g 4 t  
ORIGIN  
Query Match 71.1%; Score 12.8; DB 6; Length 20;  
Best Local Similarity 87.5%; Pred. No. 4.7e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GGGGAGGAGGGCTGG 16  
||| ||||| |||||  
Db 20 GGGGAGGAGGAGCGGG 5  
RESULT 12  
AR036517/c LOCUS AR036517 20 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 9 from patent US 5872232.  
ACCESSION AR036517  
VERSION AR036517.1 GI:5953185  
KEYWORDS  
SOURCE Unknown.  
Query Match 71.1%; Score 12.8; DB 6; Length 20;  
Best Local Similarity 87.5%; Pred. No. 4.7e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GGGGAGGAGGGCTGG 16  
||| ||||| |||||  
Db 20 GGGGAGGAGGAGCGGG 5  
RESULT 13  
AR073952/c LOCUS AR073952 20 bp DNA linear PAT 28-AUG-2000  
DEFINITION Sequence 21 from patent US 5952229.  
ACCESSION AR073952  
VERSION AR073952.1 GI:10000712  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Monia, B. P. and Boggs, R. T.  
TITLE Antisense oligonucleotide modulation of raf gene expression  
JOURNAL Patent: US 5952229-A 21 14-SEP-1999;  
FEATURES  
source  
1..20  
/organism="unknown" 4 t  
BASE COUNT 0 a 14 c 2 g 4 t  
ORIGIN  
Query Match 71.1%; Score 12.8; DB 6; Length 20;  
Best Local Similarity 87.5%; Pred. No. 4.7e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GGGGAGGAGGGCTGG 16  
||| ||||| |||||  
Db 20 GGGGAGGAGGAGCGGG 5  
RESULT 14  
AR096050/c LOCUS AR096050 20 bp DNA linear PAT 08-SEP-2000  
DEFINITION Sequence 9 from patent US 6005087.  
ACCESSION AR096050  
VERSION AR096050.1 GI:10024498  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Cook, P. Dan. and Kawasaki, A. Mamoru.  
TITLE 2'-modified oligonucleotides  
JOURNAL Patent: US 6005087-A 9 21-DEC-1999;  
FEATURES  
source  
1..20  
/organism="unknown" 4 t  
BASE COUNT 0 a 14 c 2 g 4 t  
ORIGIN  
Query Match 71.1%; Score 12.8; DB 6; Length 20;  
Best Local Similarity 87.5%; Pred. No. 4.7e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GGGGAGGAGGGCTGG 16  
||| ||||| |||||  
Db 20 GGGGAGGAGGAGCGGG 5  
RESULT 15  
AR096050/c LOCUS AR096050 20 bp DNA linear PAT 08-SEP-2000  
DEFINITION Sequence 9 from patent US 6005087.  
ACCESSION AR096050  
VERSION AR096050.1 GI:10024498  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Cook, P. Dan. and Kawasaki, A. Mamoru.  
TITLE 2'-modified oligonucleotides  
JOURNAL Patent: US 6005087-A 9 21-DEC-1999;  
FEATURES  
source  
1..20  
/organism="unknown" 4 t  
BASE COUNT 0 a 14 c 2 g 4 t  
ORIGIN  
Query Match 71.1%; Score 12.8; DB 6; Length 20;  
Best Local Similarity 87.5%; Pred. No. 4.7e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GGGGAGGAGGGCTGG 16  
||| ||||| |||||  
Db 20 GGGGAGGAGGAGCGGG 5

QY 1 GGGGAGGAGGGGCTGG 16  
| | | | | | | | | | | | | | | |  
Db 20 GGGGAGGAGGAGCGGG 5

RESULT 15  
AR105507/c  
LOCUS AR105507 20 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 7 from patent US 6096720.  
ACCESSION AR105507  
VERSION AR105507.1 GI:12819104  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Love,W.Guy., Nicklin,P.Leslie., Hamilton,K.Ophelia. and  
Phillips,J.Ann.  
TITLE Liposomal oligonucleotide compositions  
JOURNAL Patent: US 6096720-A 7 01-AUG-2000;  
FEATURES Location/Qualifiers  
source 1..20  
/organism="unknown"  
BASE COUNT 0 a 14 c 2 g 4 t  
ORIGIN

Query Match 71.1%; Score 12.8; DB 6; Length 20;  
Best Local Similarity 87.5%; Pred. No. 4.7e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTGG 16  
| | | | | | | | | | | | | | | |  
Db 20 GGGGAGGAGGAGCGGG 5

Search completed: October 27, 2003, 11:09:24  
Job time : 378.114 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:29 ; Search time 162 Seconds  
(without alignments)  
299.938 Million cell updates/sec

Title: US-09-331-204A-5  
Perfect score: 18  
Sequence: 1 ggggaggggggctggaa 18  
Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 1643890

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_19Jun03.\*  
1: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1980.DAT:\*  
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:\*  
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1982.DAT:\*  
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1983.DAT:\*  
5: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1984.DAT:\*  
6: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1985.DAT:\*  
7: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1986.DAT:\*  
8: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1987.DAT:\*  
9: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1988.DAT:\*  
10: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1989.DAT:\*  
11: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1990.DAT:\*  
12: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1991.DAT:\*  
13: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1992.DAT:\*  
14: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1993.DAT:\*  
15: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1994.DAT:\*  
16: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1995.DAT:\*  
17: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1996.DAT:\*  
18: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1997.DAT:\*  
19: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1998.DAT:\*  
20: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:\*  
21: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:\*  
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:\*  
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:\*  
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:\*  
25: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	17 AAT36241	CD28 expression in
C 2	18	100.0	18	17 AAT36255	CD28 expression in
3	18	100.0	18	20 AAX90334	CD28 inhibiting ph
C 4	18	100.0	18	20 AAX90346	CD28 inhibiting ph
C 5	13.8	76.7	17	20 AAX14741	Triple helix third
C 6	13.8	76.7	18	15 AAQ70343	Antisense oligonuc
C 7	13.8	76.7	21	15 AAQ70342	Antisense oligonuc
C 8	13.8	76.7	21	15 AAQ70345	Antisense oligonuc

C	9	13.8	76.7	21	22	AAF96659	Human gene single
	10	13.4	74.4	20	20	AAZ18648	ASTH1 gene intron/
	11	13.4	74.4	20	21	AAA93151	Clone vql5 1 seque
	12	13.4	74.4	20	21	AAA80555	Human ASTH1 gene
	13	13	72.2	21	21	AAC68417	Primer #2 used to
C	14	12.8	71.1	17	23	ABK00898	Human NOGO inozyme
C	15	12.8	71.1	17	23	ABK00899	Human NOGO inozyme
	16	12.8	71.1	17	24	ABN07492	Human GDMLP-1 17-m
	17	12.8	71.1	17	24	ABN07493	Human GDMLP-1 17-m
C	18	12.8	71.1	17	24	ABK18190	Human ERG hammerhe
C	19	12.8	71.1	17	24	ABK18191	Human ERG hammerhe
C	20	12.8	71.1	20	17	AAT27501	Human c-raf kinase
C	21	12.8	71.1	20	18	AAX36460	Chimeric 2'-O-meth
C	22	12.8	71.1	20	18	AAT62151	Human c-raf and de
C	23	12.8	71.1	20	18	AAT59722	Human raf inhibito
C	24	12.8	71.1	20	20	AAZ11531	Human c-raf kinase
C	25	12.8	71.1	20	20	AAZ10292	Oligonucleotide us
C	26	12.8	71.1	20	20	AAX05464	Chimeric antisense
C	27	12.8	71.1	20	20	AAX15066	c-raf antisense ch
C	28	12.8	71.1	20	21	AAA73509	Human c-raf kinase
C	29	12.8	71.1	20	21	AAZ48162	Human c-raf kinase
C	30	12.8	71.1	20	24	AAD44734	C-raf chimeric pho
C	31	12.8	71.1	22	16	AAQ88739	Human FGF receptor
	32	12.8	71.1	22	19	AAT99482	Human ST receptor
	33	12.8	71.1	22	19	AAT99484	Human ST receptor
	34	12.8	71.1	22	19	AAT99486	Human ST receptor
	35	12.8	71.1	22	19	AAT99488	Human ST receptor
	36	12.8	71.1	22	19	AAT99480	Human ST receptor
C	37	12.8	71.1	22	24	AAL46753	FGF receptor antis
C	38	12.4	68.9	15	22	AAH91757	Human inflammatory
C	39	12.4	68.9	17	24	ABV91218	Human POSHL1 scann
C	40	12.4	68.9	17	24	ABV91219	Human POSHL1 scann
C	41	12.4	68.9	17	24	ABV91220	Human POSHL1 scann
C	42	12.4	68.9	17	24	ABV91221	Human POSHL1 scann
	43	12.4	68.9	17	24	ABN07494	Human GDMLP-1 17-m
	44	12.4	68.9	17	24	ABN07495	Human GDMLP-1 17-m
	45	12.4	68.9	18	20	AAX23093	Primer #16. Synth

ALIGNMENTS

RESULT 1

AAT36241  
ID AAT36241 standard; DNA; 18 BP.

XX AAT36241;

XX 25-MAR-2003 (updated)

DT 16-APR-1997 (first entry)

XX CD28 expression inhibiting oligonucleotide, RT11s.

XX Reduction; T cell; CD28; gene expression; treatment; immune system;  
KW disorder; graft versus host disease; septic shock; viral disease;  
KW psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;  
KW multiple sclerosis; uveitis; rheumatoid arthritis; interleukin 2;  
KW systemic lupus erythematosus; inflammatory bowel disease;  
KW IL-2; production; antisense; inhibition; ss

XX Synthetic.

PN WO9624380-A1.

XX 15-AUG-1996.

PD 05-FEB-1996; 96WO-US01507.

XX 09-FEB-1995; 95US-0387041.

PR 18-SEP-1995; 95US-0529878.

PR 09-FEB-1995; 95US-0387041.

PR 18-SEP-1995; 95US-0529878.

XX

```
PA (ICNC ) ICN PHARM INC.
XX
PI Tam RC;
XX
XX WPI; 1996-384228/38.
XX
XX Oligonucleotide which reduces CD28 gene expression in T cells -
PT for treating immune system diseases, e.g. graft vs. host disease,
PT septic shock, psoriasis, etc.
XX
XX Example 2; Page 45; 77pp; English.
XX
XX The present oligonucleotide reduces CD28 dependent interleukin-2
CC (IL-2) production and T cell CD28 gene expression, useful in the
CC treatment of CD28 mediated diseases, particularly immune system
CC disorders, e.g. graft versus host disease, septic shock, viral
CC disease, psoriasis, type I diabetes mellitus, thyroiditis,
CC sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis,
CC systemic lupus erythematosus, inflammatory bowel disease, etc..
CC Reducing CD28 expression may reduce the effects of antigenic
CC stimulation of CD28 positive T cells, with a consequent reduction
CC in cytokine release.
CC (Updated on 25-MAR-2003 to correct PR field.)
XX
XX Sequence 18 BP; 4 A; 1 C; 12 G; 1 T; 0 other;
SQ Query Match 100.0%; Score 18; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTGGAA 18
Db 1 GGGGAGGAGGGGCTGGAA 18

RESULT 2
AAT36255/c
ID AAT36255 standard; DNA; 18 BP.
XX
XX AAT36255;
XX
XX 25-MAR-2003 (updated)
DT 16-APR-1997 (first entry)
XX
XX CD28 expression inhibiting oligonucleotide, RT06s.
XX
XX Reduction; T cell; CD28; gene expression; treatment; immune system;
KW disorder; graft versus host disease; septic shock; viral disease;
KW psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;
KW multiple sclerosis; uveitis; rheumatoid arthritis; interleukin 2;
KW systemic lupus erythematosus; inflammatory bowel disease;
KW IL-2; production; antisense; inhibition; ss
XX
XX Synthetic.
XX
XX WO9624380-A1.
XX
XX 15-AUG-1996.
XX
XX 05-FEB-1996; 96WO-US01507.
XX
XX 09-FEB-1995; 95US-0387041.
XX 18-SEP-1995; 95US-0529878.
XX 09-FEB-1995; 95US-0387041.
XX 18-SEP-1995; 95US-0529878.
XX
XX (ICNC ) ICN PHARM INC.
XX
XX Tam RC;
XX
XX WPI; 1996-384228/38.
XX
XX Oligonucleotide which reduces CD28 gene expression in T cells -
```

```
PT for treating immune system diseases, e.g. graft vs. host disease,
PT septic shock, psoriasis, etc.
XX
XX Example 2; Page 45; 77pp; English.
XX
XX The present oligonucleotide reduces CD28 dependent interleukin-2
CC (IL-2) production and T cell CD28 gene expression, useful in the
CC treatment of CD28 mediated diseases, particularly immune system
CC disorders, e.g. graft versus host disease, septic shock, viral
CC disease, psoriasis, type I diabetes mellitus, thyroiditis,
CC sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis,
CC systemic lupus erythematosus, inflammatory bowel disease, etc..
CC Reducing CD28 expression may reduce the effects of antigenic
CC stimulation of CD28 positive T cells, with a consequent reduction
CC in cytokine release.
CC (Updated on 25-MAR-2003 to correct PR field.)
XX
XX Sequence 18 BP; 1 A; 12 C; 1 G; 4 T; 0 other;
SQ Query Match 100.0%; Score 18; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTGGAA 18
Db 18 GGGGAGGAGGGGCTGGAA 1

RESULT 3
AAX90334
ID AAX90334 standard; DNA; 18 BP.
XX
XX AAX90334;
XX
XX 24-SEP-1999 (first entry)
DT
DE CD28 inhibiting phosphorothioate oligonucleotide RT11S.
XX
XX CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
KW immune system mediated disease; gamma-interferon; IL-8;
KW phosphorothioate; ss.
XX
XX Synthetic.
XX
XX US5932556-A.
XX
XX 03-AUG-1999.
PD
XX 18-SEP-1995; 95US-0529878.
XX
XX 18-SEP-1995; 95US-0529878.
XX
XX (TAMR/) TAM R C.
XX
XX Tam RC;
XX
XX WPI; 1999-443609/37.
XX
XX Treatment of immune system-mediated diseases by inhibiting
PT expression of CD28, IL-2, gamma-interferon or IL-8
XX
XX Example; Column 24; 45pp; English.
XX
XX The present invention describes a method for inhibiting the expression
CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method
CC comprises subcutaneous administration of an oligonucleotide (OGN).
CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the
CC method. The OGNs are used for the treatment of immune system-mediated
CC diseases. The present sequence represents a CD28 inhibiting
CC phosphorothioate oligonucleotide used in the exemplification of the
CC present invention.
XX
XX Sequence 18 BP; 4 A; 1 C; 12 G; 1 T; 0 other;
```



Query Match 100.0%; Score 18; DB 20; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTGGAA 18  
| | | | | | | | | | | | | | | |  
Db 1 GGGGAGGAGGGGCTGGAA 18

RESULT 4  
AAX90346/c  
ID AAX90346 standard; DNA; 18 BP.  
XX  
AC AAX90346;  
XX  
DT 24-SEP-1999 (first entry)  
XX  
DE CD28 inhibiting phosphorothioate oligonucleotide RT06S.  
XX  
KW CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;  
KW immune system mediated disease; gamma-interferon; IL-8;  
KW phosphorothioate; ss.  
XX  
OS Synthetic.  
XX  
PN US5932556-A.  
XX  
PD 03-AUG-1999.  
XX  
PF 18-SEP-1995; 95US-0529878.  
XX  
PR 18-SEP-1995; 95US-0529878.  
XX  
PA (TAMR/) TAM R C.  
XX  
PI Tam RC;  
XX  
DR WPI; 1999-443609/37.  
XX  
XX  
PT Treatment of immune system-mediated diseases by inhibiting  
PT expression of CD28, IL-2, gamma-interferon or IL-8  
XX  
PS Example; Column 24; 45pp; English.  
XX

The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleotide (OGN). AAX90288 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated diseases. The present sequence represents a CD28 inhibiting phosphorothioate oligonucleotide used in the exemplification of the present invention.

Sequence 18 BP; 1 A; 12 C; 1 G; 4 T; 0 other;  
Query Match 100.0%; Score 18; DB 20; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTGGAA 18  
| | | | | | | | | | | | | | | |  
Db 18 GGGGAGGAGGGGCTGGAA 1

RESULT 5  
AAX14741/c  
ID AAX14741 standard; DNA; 17 BP.  
XX  
AC AAX14741;  
XX  
DT 24-MAR-1999 (first entry)  
XX

Triple helix third strand of alpha-globin gene nucleotides 827-843.  
XX  
KW Triplex formation; DNA detection; triple helix; identification;  
KW bacteria; oncogene; virus; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN US5861244-A.  
XX  
PD 19-JAN-1999.  
XX  
PF 22-DEC-1993; 93US-0173489.  
XX  
PR 22-DEC-1993; 93US-0173489.  
PR 29-OCT-1992; 92US-0968436.  
XX  
PA (PROF-) PROFILE DIAGNOSTIC SCI INC.  
XX  
PI Hepburn AG, Wang C;  
XX  
DR WPI; 1999-130384/11.  
XX  
PT Assay of genetic sequences based on triplex formation from double  
PT stranded analyte - and hybrid of anchor and reporter sequences, with  
PT reporter released if triplex formation occurs, used e.g. to identify  
PT bacteria  
XX  
PS Disclosure; Columns 17-18; 168pp; English.  
XX  
CC The present sequence represents a polynucleotide that is able to  
CC form a triple helix with a double stranded sequence. Cytosine bases  
CC in the present can be replaced with 5-methylcytosine for increased  
CC triplex stability. The present sequence is used in the assay of the  
CC invention, where it can be part of the anchor DNA or reporter DNA  
CC sequence. The assay comprises adding a sample containing double-stranded  
CC DNA test sequences to an aqueous medium containing at least one complex  
CC of anchor DNA, attached to a solid support, and reporter DNA, where  
CC either a part of the anchor DNA or reporter DNA is designed to form  
CC a triple-strand structure with part of the test sequence. Triplex  
CC formation results in displacement of the reporter DNA which is  
CC detected as an indication of the presence of the DNA test sequence.  
CC The method is used to detect DNA sequences, particularly for  
CC identification of bacteria (by detecting genes for ribosomal RNA) in  
CC clinical samples, but also detection of oncogenes and Hepatitis B virus.  
XX  
SQ Sequence 17 BP; 0 A; 12 C; 0 G; 5 T; 0 other;  
Query Match 76.7%; Score 13.8; DB 20; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.5e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GGGGAGGAGGGGCTGGA 17  
| | | | | | | | | | | | | | | |  
Db 17 GGGGAGGAGGGGAGGGA 1  
RESULT 6  
AAX70343/c  
ID AAX70343 standard; DNA; 18 BP.  
XX  
AC AAX70343;  
XX  
DT 25-MAR-2003 (updated)  
DT 15-FEB-1995 (first entry)  
XX  
DE Antisense oligonucleotide for mouse FGF.  
XX  
KW Fibroblast growth factor; hybridisation; laser procedures;  
KW vascular smooth muscle cell; proliferation;  
KW SMC; vascular stenosis; post angioplasty restenosis;  
KW atherosclerosis; cardiac hypertrophy; organ transplant; ss.  
XX

OS Synthetic.  
XX WO9415945-A1.  
XX 21-JUL-1994.  
XX 28-DEC-1993; 93WO-US12600.  
XX 31-DEC-1992; 92US-0999706.  
XX (TEXA-) TEXAS BIOTECHNOLOGY CORP.  
XX Denner LA, Dixon RAF, Rege AA, Dixon RA;  
XX WPI; 1994-249123/30.  
XX New anti-sense polynucleotide(s) to fibroblast growth factor  
PT receptor - used for inhibiting vascular smooth muscle cell  
PT proliferation, partic. for treating restenosis  
XX Claim 3; Page 9; 53pp; English.  
XX The sequence is an antisense molecule directed against position -3  
CC to +15, relative to the start codon of the gene for  
CC mouse fibroblast growth factor 1. The polynucleotide can be used for  
CC inhibiting vascular smooth muscle cell proliferation and for treating  
CC a disease e.g. vascular stenosis, post angioplasty restenosis,  
CC atherectomy, atherosclerosis, atrial venous shunt failure, cardiac  
CC hypertrophy, vascular surgery and organ transplant.  
CC See also AAQ70333-60.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX Sequence 18 BP; 3 A; 11 C; 1 G; 3 T; 0 other;  
SQ Query Match 76.7%; Score 13.8; DB 15; Length 18;  
Best Local Similarity 88.2%; Pred. No. 1.5e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 GGGAGGAGGGGCTGGAA 18  
Db 18 GGGATGTGGGGCTGGAA 2  
RESULT 7  
AAQ70342/c  
ID AAQ70342 standard; DNA; 21 BP.  
XX AC AAQ70342;  
XX 25-MAR-2003 (updated)  
DT 15-FEB-1995 (first entry)  
XX Antisense oligonucleotide for mouse FGF.  
XX Fibroblast growth factor; hybridisation; laser procedures;  
KW vascular smooth muscle cell; proliferation;  
KW SMC; vascular stenosis; post angioplasty restenosis;  
KW atherosclerosis; cardiac hypertrophy; organ transplant; ss.  
XX Synthetic.  
XX WO9415945-A1.  
XX 21-JUL-1994.  
XX 28-DEC-1993; 93WO-US12600.  
XX 31-DEC-1992; 92US-0999706.  
XX (TEXA-) TEXAS BIOTECHNOLOGY CORP.  
XX Denner LA, Dixon RAF, Rege AA, Dixon RA;  
XX WPI; 1994-249123/30.  
XX New anti-sense polynucleotide(s) to fibroblast growth factor  
PT receptor - used for inhibiting vascular smooth muscle cell  
PT proliferation, partic. for treating restenosis  
XX Claim 3; Page 9; 53pp; English.  
XX The sequence is an antisense molecule directed against position -3  
CC to +15, relative to the start codon of the gene for  
CC mouse fibroblast growth factor 1. The polynucleotide can be used for  
CC inhibiting vascular smooth muscle cell proliferation and for treating  
CC a disease e.g. vascular stenosis, post angioplasty restenosis,  
CC atherectomy, atherosclerosis, atrial venous shunt failure, cardiac  
CC hypertrophy, vascular surgery and organ transplant.  
CC See also AAQ70333-60.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX Sequence 18 BP; 3 A; 11 C; 1 G; 3 T; 0 other;  
SQ Query Match 76.7%; Score 13.8; DB 15; Length 18;  
Best Local Similarity 88.2%; Pred. No. 1.5e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 GGGAGGAGGGGCTGGAA 18  
Db 18 GGGATGTGGGGCTGGAA 2

DR WPI; 1994-249123/30.  
XX New anti-sense polynucleotide(s) to fibroblast growth factor  
PT receptor - used for inhibiting vascular smooth muscle cell  
PT proliferation, partic. for treating restenosis  
XX Claim 3; Page 9; 53pp; English.  
XX The sequence is an antisense molecule directed against position -3  
CC to +18, relative to the start codon of the gene for  
CC mouse fibroblast growth factor 1. The polynucleotide can be used for  
CC inhibiting vascular smooth muscle cell proliferation and for treating  
CC a disease e.g. vascular stenosis, post angioplasty restenosis,  
CC atherectomy, atherosclerosis, atrial venous shunt failure, cardiac  
CC hypertrophy, vascular surgery and organ transplant.  
CC See also AAQ70333-60.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX Sequence 21 BP; 4 A; 12 C; 2 G; 3 T; 0 other;  
SQ Query Match 76.7%; Score 13.8; DB 15; Length 21;  
Best Local Similarity 88.2%; Pred. No. 1.5e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 GGGAGGAGGGGCTGGAA 18  
Db 21 GGGATGTGGGGCTGGAA 5  
RESULT 8  
AAQ70345/c  
ID AAQ70345 standard; DNA; 21 BP.  
XX AC AAQ70345;  
XX 25-MAR-2003 (updated)  
DT 15-FEB-1995 (first entry)  
XX Antisense oligonucleotide for mouse FGF.  
DE Fibroblast growth factor; hybridisation; laser procedures;  
XX vascular smooth muscle cell; proliferation;  
KW SMC; vascular stenosis; post angioplasty restenosis;  
KW atherosclerosis; cardiac hypertrophy; organ transplant; ss.  
XX Synthetic.  
XX WO9415945-A1.  
XX 21-JUL-1994.  
XX 28-DEC-1993; 93WO-US12600.  
XX 31-DEC-1992; 92US-0999706.  
XX (TEXA-) TEXAS BIOTECHNOLOGY CORP.  
XX Denner LA, Dixon RAF, Rege AA, Dixon RA;  
XX WPI; 1994-249123/30.  
XX New anti-sense polynucleotide(s) to fibroblast growth factor  
PT receptor - used for inhibiting vascular smooth muscle cell  
PT proliferation, partic. for treating restenosis  
XX Claim 3; Page 9; 53pp; English.  
XX The sequence is an antisense molecule directed against position -6  
CC to +15, relative to the start codon of the gene for  
CC mouse fibroblast growth factor 1. The polynucleotide can be used for  
CC inhibiting vascular smooth muscle cell proliferation and for treating  
CC a disease e.g. vascular stenosis, post angioplasty restenosis,  
CC atherectomy, atherosclerosis, atrial venous shunt failure, cardiac

CC hypertrophy, vascular surgery and organ transplant.  
CC See also AAQ70333-60.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX

SQ Sequence 21 BP; 4 A; 11 C; 2 G; 4 T; 0 other;  
Query Match 76.7%; Score 13.8; DB 15; Length 21;  
Best Local Similarity 88.2%; Pred. No. 1.5e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGAGGAGGGGCTGGAA 18  
DB 18 GGGATGTGGGGCTGGAA 2

RESULT 9  
AAF96659/c  
ID AAF96659 standard; DNA; 21 BP.

AC AAF96659;  
XX  
DT 06-JUN-2001 (first entry)  
DE Human gene single nucleotide polymorphism #1420.

XX Human; variant thrombospondin 1; variant thrombospondin 4; SNP;  
KW polymorphism; vascular disease; coronary artery disease; forensics;  
KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;  
KW pulmonary embolism; paternity test; ds.

OS Homo sapiens.

XX  
FH Key Location/Qualifiers  
FT Variation replace(11,A)  
FT /\*tag= a  
FT /standard\_name= "single nucleotide polymorphism"

XX WO200118250-A2.  
XX  
PD 15-MAR-2001.

PF 07-SEP-2000; 2000WO-US24503.

XX  
PR 10-SEP-1999; 99US-0153357.  
PR 26-JUL-2000; 2000US-0220947.  
PR 16-AUG-2000; 2000US-0225724.

XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.  
PA (MILL-) MILLENNIUM PHARM INC.

XX Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;  
WPI; 2001-226749/23.

XX Nucleic acids comprising single nucleotide polymorphisms, useful in  
PT applications such as forensics, paternity testing, medicine, genetic  
PT analysis and phenotype correlations to diseases such as diabetes and  
PT atherosclerosis -

XX Examples; Page 145; 242pp; English.

XX The present invention provides a method of diagnosing a vascular disease  
CC in an individual, involving determining the sequence at various  
CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4  
CC genes. The sequences at a number of polymorphic sites are also provided  
CC in the specification. In particular, the method can be used in the  
CC diagnosis of atherosclerosis, myocardial infarction, coronary heart  
CC disease, stroke, peripheral vascular diseases, venous thromboembolism  
CC and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also  
CC useful in forensics, paternity testing, genetic analysis and phenotype  
CC correlations to diseases. The present sequence is an example of one of  
CC the human gene SNPs shown in the specification.

XX

SQ Sequence 21 BP; 2 A; 12 C; 2 G; 5 T; 0 other;

Query Match 76.7%; Score 13.8; DB 22; Length 21;  
Best Local Similarity 88.2%; Pred. No. 1.5e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGAGGAGGGGCTGGA 17  
DB 21 GGGAGGAGACGCTGGA 5

RESULT 10  
AAZ18648  
ID AAZ18648 standard; DNA; 20 BP.

XX AAZ18648;

XX 19-OCT-1999 (first entry)

XX ASTH1 gene intron/exon junction sequence.

XX ASTH1; asthma; human; chromosome 11p; ASTH1I; ASTH1J; genetic locus;  
KW therapeutic; immunogen; polymorphism; junction; ss.

XX Homo sapiens.

XX WO9937809-A1.

XX 29-JUL-1999.

XX 21-JAN-1998; 98WO-US01260.

XX 21-JAN-1998; 98WO-US01260.

XX (AXYS-) AXYS PHARM INC.

PI Brooks-Wilson AR, Buckler A, Cardon L, Carey AH;  
PI Galvin M, Miller A, North M;

XX WPI; 1999-479058/40.

XX Mammalian asthma related genes, useful for diagnosis of a  
PT predisposition to development of asthma

XX Disclosure; Page 57; 195pp; English.

XX The invention identifies a genetic locus ASTH1, associated with asthma,  
CC mapped to human chromosome 11p. ASTH1I and ASTH1J are genes present  
CC within the locus, located close to each other on human chromosome 11p,  
CC and have similar patterns of expression, and common sequence motifs. The  
CC ASTH1 genes and fragments, encoded protein, genomic regulatory regions  
CC and anti-ASTH1 antibodies are useful in the identification of  
CC individuals predisposed to development of asthma, and for the modulation  
CC of gene activity in vivo for prophylactic and therapeutic purposes. The  
CC ASTH1 protein is useful as an immunogen to raise specific antibodies, in  
CC drug screening for compositions that mimic or modulate ASTH1 activity or  
CC expression, including altered forms of ASTH1 protein, and as a  
CC therapeutic. Sequences AAZ18643-Z18685 intron/exon junction sequences of  
CC ASTH1I and ASTH1J genes.

XX Sequence 20 BP; 3 A; 2 C; 12 G; 3 T; 0 other;

Query Match 74.4%; Score 13.4; DB 20; Length 20;  
Best Local Similarity 93.3%; Pred. No. 2.1e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGAGGAGGGGCTG 15

DB 5 GGTGAGGAGGGGCTG 19

RESULT 11  
AAA93151

ID AAA93151 standard; DNA; 20 BP.  
AC AAA93151;  
XX  
DT 12-JAN-2001 (first entry)  
XX  
DE Clone vql5\_1 secreted protein coding sequence probe SEQ ID NO: 82.  
XX  
KW Human secreted protein; cytokine; cell proliferation;  
KW nutritional supplement; immune modulation; autoimmune disorder;  
KW haematopoiesis regulation; tissue growth; haemostasis; inflammation;  
KW probe; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200049134-A1.  
XX  
PD 24-AUG-2000.  
XX  
PF 18-FEB-2000; 2000WO-US04340.  
XX  
PR 19-FEB-1999; 99US-0120680.  
PR 23-APR-1999; 99US-0298733.  
PR 17-AUG-1999; 99US-0149639.  
PR 23-SEP-1999; 99US-0155686.  
PR 01-OCT-1999; 99US-0157247.  
PR 29-NOV-1999; 99US-0167822.  
PR 29-NOV-1999; 99US-0167823.  
PR 15-FEB-2000; 2000US-0298733.  
XX  
PA (ALPH-) ALPHAGENE INC.  
XX  
PI Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;  
XX  
XX WPI; 2000-549267/50.  
DR  
XX  
PT New secreted proteins and polynucleotides encoding them, which are  
PT derived from Homo sapiens, useful for therapy, diagnosis, and research,  
PT as well as nutritional sources or supplements -  
XX  
XX Disclosure; Page 294; 309pp; English.  
PS  
XX The present invention is concerned with a number of secreted proteins  
CC and their coding sequences isolated from various human cDNA libraries.  
CC The probes shown in the specification (AAA93132-A93156) can be used to  
CC obtain the cloned sequences from bacterial cells. The proteins and  
CC coding sequences can be used in the isolation of similar genes and  
CC proteins, in the elucidation of their function in vivo, and to treat a  
CC number of conditions. It is possible that they may have uses as  
CC nutritional supplements, as cytokine or cell proliferation factors, in  
CC immune modulation, where they may be used to treat immune and autoimmune  
CC diseases, as haematopoiesis regulators (treating myeloid or lymphoid  
CC cell deficiencies), in the promotion of tissue growth, they may have  
CC chemokine or chemotactic activity, haemostatic or thrombolytic activity,  
CC or anti-inflammatory activity.  
XX  
SQ Sequence 20 BP; 7 A; 1 C; 10 G; 2 T; 0 other;  
  
Query Match 74.4%; Score 13.4; DB 21; Length 20;  
Best Local Similarity 93.3%; Pred. No. 2.1e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 3 GGAGGAGGGGCTGGA 17  
|||||  
Db 4 GGAGGAGGGTCTGGA 18  
  
RESULT 12  
AAA80555  
ID AAA80555 standard; DNA; 20 BP.  
XX  
AC AAA80555;  
XX

DT 22-NOV-2000 (first entry)  
XX  
DE Human ASTH1I gene exon k 5' boundary region.  
XX  
KW ASTH1 locus; ASTH1I; human; chromosome 11p; asthma;  
KW bronchial hyperreactivity; ets family; transcription factor;  
KW splice variant; genetic predisposition; polymorphism; antibody;  
KW drug screening; prophylaxis; therapy; diagnosis; exon boundary; ss.  
XX  
OS Homo sapiens.  
XX  
PN US6087485-A.  
XX  
PD 11-JUL-2000.  
XX  
PF 21-JAN-1998; 98US-0009913.  
XX  
PR 21-JAN-1997; 97US-0035663.  
PR 01-JUL-1997; 97US-0051432.  
XX  
PA (AXYS-) AXYS PHARM INC.  
XX  
PI Galvin M, Miller A, North M, Cardon L, Buckler A;  
PI Brooks-Wilson AR, Carey AH;  
XX  
DR WPI; 2000-505109/45.  
XX  
PT New nucleic acids other than naturally occurring chromosomes encoding  
PT ASTH1 protein, for e.g. screening compositions that modulate expression  
PT or function of ASTH1 proteins or as diagnostics for genetic  
PT predisposition to asthma -  
XX  
PS Examples; Column 37; 131pp; English.  
XX  
CC The invention relates to the ASTH1 locus on the short arm of human  
CC chromosome (11p). This locus comprises the ASTH1I and ASTH1J genes,  
CC which are associated with a genetic predisposition to asthma and  
CC bronchial hyperreactivity. The ASTH1I and ASTH1J genes are oriented in  
CC opposite directions with the ASTH1 locus, and have similar patterns of  
CC expression and common sequence motifs. They are both expressed in  
CC trachea, lung and several other tissues. ASTH1I and ASTH1J are novel  
CC members of the ets family of transcription factors, which have been  
CC implicated in the activation of a variety of genes, including the TCRa  
CC gene and cytokine genes known to be important in the aetiology of  
CC asthma. Both ASTH1I and ASTH1J mRNAs are alternatively spliced.  
CC Alternative splicing of transcripts has no effect on the open reading  
CC frame of ASTH1J, as the exons involved are all 5' to the start codon in  
CC exon b. In contrast, alternative splicing of ASTH1I transcripts results  
CC in 3 different ASTH1I isoforms. The invention also encompasses mouse  
CC asth1j protein. The ASTH1 nucleic acids are useful as diagnostics to  
CC identify a hereditary predisposition to asthma, as probes for identifying  
CC ASTH1 related genes, for identifying expression of the gene in a  
CC biological specimen, and for generating genetically modified non-human  
CC animals or site specific gene modifications in cell lines. The encoded  
CC ASTH1 proteins are useful as immunogens to raise specific antibodies; in  
CC drug screening for compositions that mimic or modulate activity or  
CC expression of ASTH1I and/or ASTH1J (including altered forms of these  
CC proteins); and as a therapeutic. The ASTH1 genes or fragments thereof,  
CC encoded proteins, ASTH1 genomic regulatory regions, and anti-ASTH1I and  
CC anti-ASTH1J antibodies are useful in the identification of individuals  
CC predisposed to development of asthma, and for modulation of gene activity  
CC in vivo for prophylactic and therapeutic purposes. The intact ASTH1I or  
CC ASTH1J proteins or active fragments thereof may be used to modulate or  
CC reduce bronchial hyperreactivity. Sequences AAA80550-A80570 represent the  
CC exon boundary regions of the human ASTH1I gene.  
XX  
SQ Sequence 20 BP; 3 A; 2 C; 12 G; 3 T; 0 other;  
  
Query Match 74.4%; Score 13.4; DB 21; Length 20;  
Best Local Similarity 93.3%; Pred. No. 2.1e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GGGGAGGAGGGGCTG 15

Db 5 GGTGAGGAGGGGCTG 19  
RESULT 13  
AAC68417  
ID AAC68417 standard; DNA; 21 BP.  
XX  
AC AAC68417;  
XX  
DT 21-FEB-2001 (first entry)  
XX  
DE Primer #2 used to isolate human ECE-3.  
XX  
KW ECE-3; endothelin converting enzyme 3; hypertension;  
KW arteriosclerosis; vascular restenosis;  
KW myocardial ischemia; cerebral vasospasm; subarachnoid hemorrhage;  
KW congestive heart failure; diabetes; endotoxic shock; migraine;  
KW Raynaud's disease; pulmonary disease; ss.  
XX  
OS Synthetic.  
XX  
PN WO200065025-A2.  
XX  
PD 02-NOV-2000.  
XX  
PF 21-APR-2000; 2000WO-US10828.  
XX  
PR 23-APR-1999; 99US-0130691.  
XX  
PA (MERI ) MERCK & CO INC.  
XX  
PI Austin CP, Bailey WJ, Ma L;  
XX  
DR WPI; 2000-687323/67.  
XX  
PT Nucleic acid molecule encoding human endothelin converting enzyme-3  
PT protein, useful for screening modulators that are useful for treating  
PT arteriosclerosis, myocardial and cerebral ischemia, and diabetes  
XX  
PS Example 1; Page 40; 78pp; English.  
XX  
CC The present invention relates to human endothelin converting  
CC enzyme-3 protein (ECE-3). ECE-3 is useful for screening selective  
CC modulators of vertebrate ECE-3 function, that are useful for treating  
CC diseases such as hypertension, arteriosclerosis, vascular restenosis,  
CC myocardial ischemia, cerebral vasospasm and subarachnoid hemorrhage,  
CC congestive heart failure, diabetes, endotoxic shock, migraine,  
CC Raynaud's disease, and also for treating pulmonary disease such as  
CC asthma, pulmonary hypertension and adult respiratory distress  
CC syndrome.  
SQ Sequence 21 BP; 3 A; 3 C; 12 G; 3 T; 0 other;  
Query Match 72.2%; Score 13; DB 21; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3e+04;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 GGAGGGGCTGGAA 18  
Db 7 GGAGGGGCTGGAA 19  
RESULT 14  
ABK00898/c  
ID ABK00898 standard; RNA; 17 BP.  
XX  
AC ABK00898;  
XX  
DT 12-MAR-2002 (first entry)  
XX  
DE Human NOGO Inozyme #169.  
XX  
KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;  
KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;  
KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;  
KW DNzyme; inozyme; G-cleaver; amberzyme; zinczyme; lymphoma; leukaemia;  
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;  
KW inflammatory arthropathy; central nervous system injury;  
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
KW Parkinson's disease; ataxia; Huntington's disease;  
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200159103-A2.  
XX  
PD 16-AUG-2001.  
XX  
PF 09-FEB-2001; 2001WO-US04273.  
XX  
PR 11-FEB-2000; 2000US-181797P.  
PR 28-FEB-2000; 2000US-185516P.  
PR 06-MAR-2000; 2000US-187128P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
PA (MCSW/) MCSWIGGEN J.  
PA (CHOW/) CHOWRIRA B M.  
XX  
PI Blatt L, McSwiggen J, Chowrira BM;  
XX  
DR WPI; 2001-607195/69.  
XX  
PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
PT constructs, which down regulate expression of a CD20 gene or neurite  
PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia,  
PT and central nervous system injury  
XX  
PS Claim 88; Page 80; 200pp; English.  
XX  
CC The invention relates to a nucleic acid molecule which down regulates  
CC expression of a CD20 gene and a nucleic acid molecule which down  
CC regulates expression of a neurite growth inhibitor gene (NOGO).  
CC The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a  
CC DNzyme) an Inozyme (an endolytic nucleic acid cleaving a RNA molecule  
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NVN  
CC motif) pr an amberzyme (cleaving RNA with an NGN triplet), a zinczyme  
CC (cleaving RNA with a YGY motif). The CD20-targetting nucleic acid is used  
CC to cleave RNA of CD20 in the presence of a divalent cation that is  
CC preferably Mg<sup>2+</sup>. Furthermore, it may be contacted with a cell to reduce  
CC CD20 activity of the cell and treat a patient having a condition  
CC associated with the level of CD20. The treatment may further comprise the  
CC use of one or more therapies. In particular, the CD20 targeting  
CC nucleic acid may be used to treat lymphoma, leukaemia, B-cell  
CC lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky  
CC low-grade or follicular NHL, lymphocytic leukaemia, HIV (human  
CC immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL),  
CC immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune  
CC thrombocytopaenia, and inflammatory arthropathy. The NOGO-targetting  
CC nucleic acid is used to cleave RNA of the NOGO gene in the presence of a  
CC divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the nucleic acid  
CC may be contacted with a cell to reduce NOGO activity of the cell and  
CC treat a patient having a condition associated with the level of NOGO. The  
CC treatment may further comprise the use of one or more therapies.  
CC In particular, the NOGO-targetting nucleic acid may be used to treat  
CC central nervous system (CNS) injury and cerebrovascular accident (CVA,  
CC stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
CC disease, muscular dystrophy, and/or other neurodegenerative disease  
CC states which respond to the modulation of NOGO expression. The

```
CC present sequence is an inozyme of the invention.
XX
SQ Sequence 17 BP; 0 A; 13 C; 1 G; 3 U; 0 other;
    Query Match      71.1%; Score 12.8; DB 23; Length 17;
    Best Local Similarity 87.5%; Pred. No. 3.6e+04;
    Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGGAGGAGGGGCTGG 16
Db 17 GGGGAGGAGGGGAGG 2

RESULT 15
ABK00899/c
ID ABK00899 standard; RNA; 17 BP.
XX
AC ABK00899;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human NOGO Inozyme #169.
XX
KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
KW DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KW MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;
KW inflammatory arthropathy; central nervous system injury;
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KW Parkinson's disease; ataxia; Huntington's disease;
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200159103-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US04273.
XX
PR 11-FEB-2000; 2000US-181797P.
PR 28-FEB-2000; 2000US-185516P.
PR 06-MAR-2000; 2000US-187128P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J.
PA (CHOW/) CHOWRIRA B M.
XX
PI Blatt L, McSwiggen J, Chowrira BM;
XX
WPI; 2001-607195/69.
XX
Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
constructs, which down regulate expression of a CD20 gene or neurite
growth inhibitor gene useful for treating, e.g., lymphoma, leukemia,
and central nervous system injury -
XX
Claim 88; Page 80; 200pp; English.
XX
The invention relates to a nucleic acid molecule which down regulates
expression of a CD20 gene and a nucleic acid molecule which down
regulates expression of a neurite growth inhibitor gene (NOGO).
XX
The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
DNazyme) an inozyme (an endolytic nucleic acid cleaving a an RNA molecule
possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN
motif) pr an amberzyme (cleaving RNA with an NGN triplet), a zinzyme
(cleaving RNA with a YGY motif). The CD20-targetting nucleic acid is used
```

```
CC to cleave RNA of CD20 in the presence of a divalent cation that is
CC preferably Mg2+. Furthermore, it may be contacted with a cell to reduce
CC CD20 activity of the cell and treat a patient having a condition
CC associated with the level of CD20. The treatment may further comprise the
CC use of one or more therapies. In particular, the CD20 targetting
CC nucleic acid may be used to treat lymphoma, leukaemia, B-cell
CC lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky
CC low-grade or follicular NHL, lymphocytic leukaemia, HIV (human
CC immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL),
CC immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune
CC thrombocytopenia, and inflammatory arthropathy. The NOGO-targetting
CC nucleic acid is used to cleave RNA of the NOGO gene in the presence of a
CC divalent cation that is preferably Mg2+. Furthermore, the nucleic acid
CC may be contacted with a cell to reduce NOGO activity of the cell and
CC treat a patient having a condition associated with the level of NOGO. The
CC treatment may further comprise the use of one or more therapies.
CC In particular, the NOGO-targetting nucleic acid may be used to treat
CC central nervous system (CNS) injury and cerebrovascular accident (CVA,
CC stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NOGO expression. The
CC present sequence is an inozyme of the invention.
XX
SQ Sequence 17 BP; 0 A; 14 C; 0 G; 3 U; 0 other;
    Query Match      71.1%; Score 12.8; DB 23; Length 17;
    Best Local Similarity 87.5%; Pred. No. 3.6e+04;
    Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 1 GGGGAGGAGGGGCTGG 16
Db 16 GGGGAGGAGGGGAGG 1
```

Search completed: October 27, 2003, 11:25:19  
Job time : 163 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:29 ; Search time 1581.77 Seconds  
(without alignments)  
276.576 Million cell updates/sec

Title: US-09-331-204A-5  
Perfect score: 19  
Sequence: 1 gggaggaggctgaa 18

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 11152

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12.4	68.9	22	AZ307952	AZ307952 1M0010L24
2	12	66.7	16	AA968729	AA968729 or69h11.s
3	12	66.7	21	AU254493	AU254493 AU254493
4	11.8	65.6	19	AI696833	AI696833 wc74e09.x

5	11.8	65.6	20	28	AZ579495	1M0367C13
C 6	11.6	64.4	21	28	AZ512534	1M0358B07
7	11.4	63.3	19	28	AZ345792	1M0080G12
C 8	11.2	62.2	19	28	AZ493581	1M0328A24
C 9	11.2	62.2	20	28	AZ512326	1M0357I18
C 10	11.2	62.2	20	28	AZ645269	1M0510B10
C 11	11.2	62.2	20	28	AZ772707	1M0583L18
C 12	11.2	62.2	20	28	AZ969440	2M0242O12
C 13	11.2	62.2	21	28	AZ433710	1M0219P12
C 14	11.2	62.2	21	28	AZ476392	1M0295F12
C 15	11.2	62.2	21	28	AZ495585	1M0331H02
C 16	11.2	62.2	21	28	AZ583408	1M0378N23
C 17	11.2	62.2	21	28	AZ653464	1M0527G11
C 18	11.2	62.2	21	28	AZ871715	2M0184B13
C 19	11.2	62.2	22	28	AZ331988	1M0331H02
C 20	11.2	62.2	22	28	AZ607348	1M0429D18
C 21	11.2	62.2	22	28	AZ645874	1M0511C07
C 22	11.2	62.2	22	28	AZ805739	2M0067K14
C 23	11.2	62.2	22	28	AZ861868	2M0168I19
C 24	11.2	62.2	22	28	AZ871408	2M0184E16
C 25	11.1	61.1	21	28	AZ967090	2M0237D24
26	10.8	60.0	19	28	AZ326174	1M0048A07
27	10.8	60.0	20	28	AZ405596	1M0174B06
C 28	10.8	60.0	21	28	AZ836049	2M0130E11
29	10.6	58.9	19	9	AI702520	tz67G05.X
30	10.6	58.9	19	28	AZ493714	1M0328I04
31	10.6	58.9	19	28	AZ775540	2M0008H15
32	10.6	58.9	20	28	AZ623037	1M0460K16
C 33	10.6	58.9	20	28	AZ659755	1M0537F22
34	10.6	58.9	21	28	AZ321746	1M0042N20
C 35	10.6	58.9	21	28	AZ419284	1M0195A16
C 36	10.6	58.9	21	28	AZ467734	1M0279N18
C 37	10.6	58.9	21	28	AZ499846	1M0337E23
C 38	10.6	58.9	21	28	AZ657144	1M0533E12
C 39	10.6	58.9	21	28	AZ961893	2M0230E06
40	10.6	58.9	22	28	AZ307488	1M0009B13
C 41	10.6	58.9	22	28	AZ611419	1M0437D15
C 42	10.6	58.9	22	28	AZ650470	1M0520J12
C 43	10.6	58.9	22	28	AZ775193	2M0007P16
C 44	10.6	58.9	22	28	AZ974046	2M0248C01
C 45	10.4	57.8	16	9	AI569544	tz28d10.X

ALIGNMENTS

RESULT 1  
AZ307952  
LOCUS AZ307952 22 bp DNA linear GSS 29-SEP-2000  
DEFINITION 1M0010L24F Mouse 10kb plasmid UUGCLM library Mus musculus genomic clone UUGCLM0010L24 F, genomic survey sequence.  
ACCESSION AZ307952 GI:10347459  
VERSION AZ307952.1  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177



Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0010 row: L column: 24  
Seq primer: CGTTGTAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 22.  
Location/Qualifiers  
1. .22  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUC1M0010L24"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 5 a 0 c 14 g 3 t  
ORIGIN

Query Match 68.9%; Score 12.4; DB 28; Length 22;  
Best Local Similarity 92.9%; Pred. No. 7.9e+05;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGAGGGGGCTGG 16  
|||||  
Db 4 GGAGGAGGGGGTGG 17

RESULT 2  
AA968729  
LOCUS  
DEFINITION  
AA968729 16 bp mRNA linear EST 27-AUG-1998  
OR69hl1.s1 NCI CGAP GC3 Homo sapiens cDNA clone IMAGE:1601157 3', similar to SW:FRPE\_HUMAN P02811 BASIC PROLINE-RICH PEPTIDE P-E ;contains element MSR1 repetitive element ;, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 16)  
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CCAP clone distribution information can be

AA968729  
LOCUS  
DEFINITION  
AA968729 16 bp mRNA linear EST 27-AUG-1998  
OR69hl1.s1 NCI CGAP GC3 Homo sapiens cDNA clone IMAGE:1601157 3', similar to SW:FRPE\_HUMAN P02811 BASIC PROLINE-RICH PEPTIDE P-E ;contains element MSR1 repetitive element ;, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 16)  
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CCAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
Insert Length: 514 Std Error: 0.00  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .16  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1601157"  
/tissue\_type="pooled germ cell tumors"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP GC3"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 2 a 1 c 13 g 0 t  
ORIGIN

Query Match 66.7%; Score 12; DB 9; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.1e+06;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGG 12  
|||||  
Db 4 GGGGAGGAGGGG 15

RESULT 3  
AU254493  
LOCUS  
DEFINITION  
AU254493 21 bp mRNA linear EST 25-APR-2002  
AU254493 3'-directed mouse cDNA library Mus musculus cDNA clone  
BED0002246 3', mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 21)  
Kato,K. and Matoba,R.  
Generation of expressed sequence tags from mouse brain  
Unpublished  
Contact: Kikuya Kato  
Graduate School of Biological Sciences  
Nara Institute of Science and Technology  
8916-5 Takayama, Ikoma, Nara 630-0101, Japan  
Tel: 81-743-72-5581  
Fax: 81-743-72-5589  
Email: kkato@bs.aist-nara.ac.jp,  
URL:http://love2.aist-nara.ac.jp/BED/index.html.

Location/Qualifiers  
1. .21  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="BED0002246"  
/tissue\_type="brain"  
/clone\_lib="3'-directed mouse cDNA library"

BASE COUNT 3 a 2 c 14 g 2 t  
ORIGIN

Query Match 66.7%; Score 12; DB 9; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.1e+06;



Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGG 12  
|||||

Db 10 GGGGAGGAGGG 21

RESULT 4  
AI696833  
LOCUS  
DEFINITION  
wc74e09.x1 NCI CGAP Pan1 Homo sapiens cDNA clone IMAGE:2324392 3',  
similar to TR:Q01942 Q01942 EXTENSIN ;contains element TAR1  
repetitive element ;, mRNA sequence.

ACCESSION  
AI696833  
VERSION  
AI696833.1 GI:4984733  
KEYWORDS  
EST.

SOURCE  
Homo sapiens (human)

ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
1 (bases 1 to 19)

AUTHORS  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

JOURNAL  
Unpublished

COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Life Technologies catalog #: 11548-013  
DNA sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality  
Insert Length: 1542 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.

FEATURES  
source  
1. .19  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2324392"  
/tissue\_type="adenocarcinoma"  
/lab\_host="DH10B"  
/clone\_lib="NCI\_CGAP\_Pan1"  
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: SalI;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.72 kb. Life Technologies catalog #:  
11548-013"

BASE COUNT 4 a 1 c 14 g 0 t

ORIGIN  
Query Match 65.6%; Score 11.8; DB 9; Length 19;  
Best Local Similarity 86.7%; Pred. No. 1.3e+06;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGAGGGGCTGGA 17  
|||||

Db 3 GGAGGAGGGGGGGA 17

RESULT 5  
AZ579495  
LOCUS  
DEFINITION  
iM0367C13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0367C13 F, genomic survey sequence.

ACCESSION  
AZ579495  
VERSION  
AZ579495.1 GI:11693924  
KEYWORDS  
GSS.

SOURCE  
Mus musculus (house mouse)

ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
AUTHORS  
1 (bases 1 to 20)  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.,  
and Wright,D.,Weiss,R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
Unpublished

COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: [ddunne@genetics.utah.edu](mailto:ddunne@genetics.utah.edu)  
Insert Length: 10000 Std Error: 0.00  
Plate: 0367 row: C column: 13  
Seq primer: CGTTGTAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 20.

FEATURES  
source  
1. .20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0367C13"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 1 a 2 c 17 g 0 t

ORIGIN  
Query Match 65.6%; Score 11.8; DB 28; Length 20;  
Best Local Similarity 86.7%; Pred. No. 1.3e+06;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTG 15  
|||||

Db 6 GGGGGGAGGGGGCGG 20

RESULT 6  
AZ512534/c  
LOCUS  
DEFINITION  
AZ512534 21 bp DNA linear GSS 05-OCT-2000  
iM0358B07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0358B07 F, genomic survey sequence.

ACCESSION  
AZ512534  
VERSION  
AZ512534.1 GI:10693850  
KEYWORDS  
GSS.

SOURCE  
Mus musculus (house mouse)

ORGANISM  
Mus musculus

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 21)  
REFERENCE  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL  
COMMENT  
Unpublished  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0358 row: B column: 07  
Seq primer: CGTTGTAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers  
1. 21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0358B07"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

FEATURES  
source

FEATURES  
source

1. 19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0080G12"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 2 a 18 c 0 g 1 t  
ORIGIN

BASE COUNT 1 a 1 c 17 g 0 t  
ORIGIN

Query Match 64.4%; Score 11.6; DB 28; Length 21;  
Best Local Similarity 77.8%; Pred. No. 1.5e+06;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Query Match 63.3%; Score 11.4; DB 28; Length 19;  
Best Local Similarity 92.3%; Pred. No. 1.7e+06;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGCTGGAA 18  
|||||  
Db 21 GGGGGGGGGGGGTGGGA 4

QY 1 GGGGAGGAGGGGC 13  
|||||  
Db 6 GGGGAGGGGGGGC 18

RESULT 7  
AZ345792  
LOCUS  
DEFINITION  
AZ345792  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE

AZ345792  
1M0080G12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0080G12 R, genomic survey sequence.  
AZ345792  
GSS.  
Mus musculus (house mouse)

RESULT 8  
AZ493581/c  
LOCUS  
DEFINITION  
AZ493581  
ACCESSION  
VERSION  
KEYWORDS

AZ493581  
1M0328A24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0328A24 F, genomic survey sequence.  
AZ493581  
GSS.  
GI:10667400

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
REFERENCE  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL  
COMMENT  
Unpublished  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0080 row: G column: 12  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers  
1. 19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0080G12"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS 1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0328 row: A column: 24  
Seq primer: CGTGTAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.  
FEATURES Location/Qualifiers  
1..19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0328A24"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."  
BASE COUNT 0 a 18 c 1 g 0 t  
ORIGIN  
Query Match 62.2%; Score 11.2; DB 28; Length 19;  
Best Local Similarity 81.2%; Pred. No. 2e+06;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GGGGAGGAGGGGGCTGG 16  
|||||  
Db 19 GGGGGGGGGGGCGGG 4  
RESULT 9  
AZ512326/c  
LOCUS AZ512326 20 bp DNA linear GSS 05-OCT-2000  
DEFINITION 1M0357118R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0357118 R, genomic survey sequence.  
ACCESSION AZ512326  
VERSION AZ512326.1 GI:10693642

KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS 1 (bases 1 to 20)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0357 row: I column: 18  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.  
FEATURES Location/Qualifiers  
1..20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0357I18"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."  
BASE COUNT 0 a 18 c 0 g 2 t  
ORIGIN  
Query Match 62.2%; Score 11.2; DB 28; Length 20;  
Best Local Similarity 81.2%; Pred. No. 2e+06;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GGGGAGGAGGGGGCTGG 16  
|||||  
Db 20 GGGGAGGGGGGGGGG 5  
RESULT 10  
AZ645269/c  
LOCUS AZ645269 20 bp DNA linear GSS 14-DEC-2000  
DEFINITION 1M0510B10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0510B10 R, genomic survey sequence.  
ACCESSION AZ645269

ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCES AUTHORS	TITLE	JOURNAL COMMENT	FEATURES source
AZ645269.1 GSS. Mus musculus (house mouse) Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20) Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly , M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0510 row: B column: 10 Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends High quality sequence stop: 20. Location/Qualifiers 1. .20 /organism="Mus musculus"	REFERENCE AUTHORS	TITLE	JOURNAL COMMENT	FEATURES source

FEATURES  
SOURCE[illegible][illegible]

AZ772707  
AZ772707.1 GI:12896303  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
EuKaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 20)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.,  
and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0583 row: L column: 18  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence spot: 20.

```
BASE COUNT      0 a    19 c    0 g    1 t  
ORIGIN
```

and selected for ampicillin resistance.

RESULT 12	AZ969440/c	LOCUS	AZ969440	20 bp	DNA	linear	GSS 27-APR-2001
DEFINITION	2M0242O12F	Mouse	10kb	plasmid	UUGC2M	library	Mus musculus genomic

clone UUGC2M0242012 F, genomic survey sequence.  
AZ969440  
AZ969440.1 GI:13840667  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0242 row: O column: 12  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers  
1. .20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0242012"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC2M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (female) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

FEATURES

source

DEFINITION 1M0219P12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0219P12 R, genomic survey sequence.  
ACCESSION AZ433710  
VERSION AZ433710.1 GI:10557723  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 21)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0219 row: P column: 12  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers  
1. .21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0219P12"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

FEATURES

source

BASE COUNT 0 a 19 c 0 g 1 t  
ORIGIN  
Query Match 62.2%; Score 11.2; DB 28; Length 20;  
Best Local Similarity 81.2%; Pred. No. 2e+06;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GGGGAGGAGGGGCTGG 16  
|||||  
Db 18 GGGGAGGGGGGGGGG 3  
|||||

RESULT 13  
AZ433710/c  
LOCUS

21 bp DNA linear GSS 03-OCT-2000

BASE COUNT

ORIGIN

Query Match 62.2%; Score 11.2; DB 28; Length 21;  
Best Local Similarity 81.2%; Pred. No. 2e+06;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GGGGAGGAGGGGCTGG 16  
|||||  
Db 17 GGGGGGGGGGGGGGG 2  
|||||

RESULT 14  
AZ476392/c

LOCUS AZ476392 21 bp DNA linear GSS 04-OCT-2000  
DEFINITION IM0295F12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0295F12 F, genomic survey sequence.  
ACCESSION AZ476392  
VERSION AZ476392.1 GI:10634517  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 21)  
REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
AUTHORS Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0295 row: F column: 12  
Seq primer: CGTTGTAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers  
1. .21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0295F12"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

FEATURES  
source

1. .21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0295F12"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 0 a 20 c 0 g 1 t  
ORIGIN

Query Match 62.2%; Score 11.2; DB 28; Length 21;  
Best Local Similarity 81.2%; Pred. No. 2e+06;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGCGCTGG 16  
||| ||||| |||  
Db 20 GGGGGGAGGGGGGGG 5

RESULT 15

AZ495585/c  
LOCUS  
DEFINITION IM0331H02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0331H02 R, genomic survey sequence.  
ACCESSION AZ495585  
VERSION AZ495585.1 GI:10671122  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 21)  
REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
AUTHORS Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0331 row: H column: 02  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers  
1. .21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0331H02"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

FEATURES  
source

1. .21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0331H02"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 2 a 16 c 1 g 2 t  
ORIGIN

Query Match 62.2%; Score 11.2; DB 28; Length 21;  
Best Local Similarity 81.2%; Pred. No. 2e+06;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGCGCTGG 16  
||| ||||| |||  
Db 21 GGGGTGGGGGGCGGG 6

Search completed: October 27, 2003, 13:59:24  
Job time : 1583.77 secs

---



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:34 ; Search time 41.3143 Seconds  
(without alignments)  
192.304 Million cell updates/sec

Title: US-09-331-204A-5  
Perfect score: 18  
Sequence: 1 999gaggagggttgaa 18

Scoring table: IDENTITY\_NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 376294

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA: \*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq: \*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq: \*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq: \*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq: \*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq: \*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	13.8	76.7	17	2	US-08-173-489C-128
C 2	13.8	76.7	18	5	PCT-US93-12600-11
C 3	13.8	76.7	21	5	PCT-US93-12600-10
C 4	13.8	76.7	21	5	PCT-US93-12600-13
C 5	13.4	74.4	20	3	US-09-009-913-298
C 6	12.8	71.1	20	1	US-08-250-856A-21
C 7	12.8	71.1	20	2	US-08-468-037A-9
C 8	12.8	71.1	20	2	US-08-471-973A-9
C 9	12.8	71.1	20	2	US-08-756-806A-21
C 10	12.8	71.1	20	2	US-08-465-880-9
C 11	12.8	71.1	20	3	US-09-035-357-9
C 12	12.8	71.1	20	3	US-09-143-214-21
C 13	12.8	71.1	20	3	US-09-000-136-7
C 14	12.8	71.1	20	4	US-09-135-202-9
C 15	12.8	71.1	20	4	US-09-506-073-21
C 16	12.8	71.1	20	4	US-08-802-331-9
C 17	12.8	71.1	20	4	US-09-389-283-9
C 18	12.8	71.1	20	5	PCT-US95-07111A-21
C 19	12.8	71.1	22	4	US-08-337-120A-27
C 20	12.4	68.9	20	4	US-09-659-791A-48
C 21	12.4	68.9	20	4	US-09-659-791A-49
C 22	12.2	67.8	18	5	PCT-US93-12600-26
C 23	12.2	67.8	20	1	US-08-290-936-6
C 24	12.2	67.8	20	2	US-08-343-443B-126
C 25	12.2	67.8	21	5	PCT-US93-12600-19
C 26	12.2	67.8	21	5	PCT-US93-12600-25
C 27	12	66.7	16	1	US-08-152-313-15

C 28	12	66.7	16	1	US-08-579-223-15	Sequence 15, Appl
C 29	12	66.7	16	5	PCT-US94-12947A-15	Sequence 15, Appl
C 30	12	66.7	17	2	US-08-173-489C-127	Sequence 127, App
C 31	12	66.7	21	2	US-08-859-998-128	Sequence 128, App
C 32	12	66.7	21	4	US-09-225-928-128	Sequence 128, App
C 33	12	66.7	21	4	US-09-225-201B-128	Sequence 128, App
C 34	11.8	65.6	15	3	US-08-557-210A-2	Sequence 2, Appli
C 35	11.8	65.6	15	5	PCT-US93-12600-12	Sequence 12, Appl
C 36	11.8	65.6	18	5	PCT-US93-12600-17	Sequence 17, Appl
C 37	11.8	65.6	20	1	US-07-977-284A-68	Sequence 68, Appl
C 38	11.8	65.6	20	1	US-08-483-122-5	Sequence 5, Appli
C 39	11.8	65.6	20	1	US-08-483-122-5	Sequence 6, Appli
C 40	11.8	65.6	20	2	US-08-486-648-5	Sequence 5, Appli
C 41	11.8	65.6	20	2	US-08-486-648-6	Sequence 6, Appli
C 42	11.8	65.6	20	2	US-08-256-426B-68	Sequence 68, Appl
C 43	11.8	65.6	20	2	US-08-486-307-5	Sequence 5, Appli
C 44	11.8	65.6	20	2	US-08-486-307-5	Sequence 6, Appli
C 45	11.8	65.6	20	3	US-09-357-070-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1  
US-08-173-489C-128/c  
; Sequence 128, Application US/08173489C  
; Patent No. 5861244  
; GENERAL INFORMATION:  
; APPLICANT: WANG, C. -G.  
; APPLICANT: HEPBURN, A. G.  
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA  
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.  
; NUMBER OF SEQUENCES: 365  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,  
; STREET: 510 EAST 73RD STREET,  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10021.  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage  
; COMPUTER: IBM PC/XT/AT  
; OPERATING SYSTEM: MS-DOS version 6.2  
; SOFTWARE: Wordperfect Version 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/173,489C  
; FILING DATE: 22 DEC 1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/968,436  
; FILING DATE: 29 OCT 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Handelman, Joseph H.  
; REGISTRATION NUMBER: 26,179  
; REFERENCE/DOCKET NUMBER: U9518-6  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (attorney) (212) 708-1880  
; TELEFAX: (attorney) (212) 246-8959  
; INFORMATION FOR SEQ ID NO: 128:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 bases  
; TYPE: nucleic acid  
; STRANDEDNESS: single stranded  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: third strand derived from alpha-1-  
; DESCRIPTION: Globin sequence region in Seq ID No. 5861244127  
; HYPOTHETICAL: yes  
; ANTI-SENSE: no  
; PUBLICATION INFORMATION:  
; RELEVANT RESIDUES IN SEQ ID NO: 128 :FROM 1 TO 17  
US-08-173-489C-128



Query Match 76.7%; Score 13.8; DB 2; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.4e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGAGGAGGGGCTGGA 17  
|||||  
Db 17 GGGAGGAGGGGAAGGA 1

## RESULT 2

PCT-US93-12600-11/c  
; Sequence 11, Application PC/TUS9312600  
; GENERAL INFORMATION:  
; APPLICANT: Denner, Larry A.  
; APPLICANT: Rege, Ajay A.  
; APPLICANT: Dixon, Richard A.F.  
; TITLE OF INVENTION: ANTISENSE MOLECULES DIRECTED AGAINST A  
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR RECEPTOR GENE FAMILY  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dressler, Goldsmith, Shore &  
; ADDRESSEE: Milnamow, Ltd.  
; STREET: 180 North Stetson, Suite 4700  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60601

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/12600  
FILING DATE: 28-DEC-1993

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/999,706  
FILING DATE: December 31, 1992

ATTORNEY/AGENT INFORMATION:  
NAME: Katz, Martin L.  
REGISTRATION NUMBER: 25,011

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312)616-5400  
TELEFAX: (312)616-5460

SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)  
PCT-US93-12600-11

Query Match 76.7%; Score 13.8; DB 5; Length 18;  
Best Local Similarity 88.2%; Pred. No. 1.4e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGAGGAGGGGCTGGA 18  
|||||  
Db 18 GGGATGTGGGCTGGA 2

## RESULT 3

PCT-US93-12600-10/c  
; Sequence 10, Application PC/TUS9312600  
; GENERAL INFORMATION:  
; APPLICANT: Denner, Larry A.  
; APPLICANT: Rege, Ajay A.  
; APPLICANT: Dixon, Richard A.F.  
; TITLE OF INVENTION: ANTISENSE MOLECULES DIRECTED AGAINST A  
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR RECEPTOR GENE FAMILY

NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dressler, Goldsmith, Shore &  
ADDRESSEE: Milnamow, Ltd.  
STREET: 180 North Stetson, Suite 4700  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/12600  
FILING DATE: 28-DEC-1993

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/999,706  
FILING DATE: December 31, 1992

ATTORNEY/AGENT INFORMATION:  
NAME: Katz, Martin L.  
REGISTRATION NUMBER: 25,011

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312)616-5400  
TELEFAX: (312)616-5460

SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)  
PCT-US93-12600-10

Query Match 76.7%; Score 13.8; DB 5; Length 21;  
Best Local Similarity 88.2%; Pred. No. 1.4e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGAGGAGGGGCTGGA 18  
|||||  
Db 21 GGGATGTGGGCTGGA 5

## RESULT 4

PCT-US93-12600-13/c  
; Sequence 13, Application PC/TUS9312600  
; GENERAL INFORMATION:  
; APPLICANT: Denner, Larry A.  
; APPLICANT: Rege, Ajay A.  
; APPLICANT: Dixon, Richard A.F.  
; TITLE OF INVENTION: ANTISENSE MOLECULES DIRECTED AGAINST A  
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR RECEPTOR GENE FAMILY

NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dressler, Goldsmith, Shore &  
ADDRESSEE: Milnamow, Ltd.  
STREET: 180 North Stetson, Suite 4700  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60601

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/12600  
FILING DATE: 28-DEC-1993

CLASSIFICATION:  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/999,706  
FILING DATE: December 31, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Katz, Martin L.  
REGISTRATION NUMBER: 25,011  
TELEPHONE: (312)616-5400  
TELEFAX: (312)616-5460  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
PCT-US93-12600-13

Query Match 76.7%; Score 13.8; DB 5; Length 21;  
Best Local Similarity 88.2%; Pred. No. 1.4e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGAGGAGGGGCTGGAA 18  
Db 18 GGGATGTGGGGCTGGAA 2

RESULT 5  
US-09-009-913-298  
Sequence 298, Application US/09009913  
Patent No. 6087485  
GENERAL INFORMATION:  
APPLICANT: AYS Pharmaceuticals, Inc.  
TITLE OF INVENTION: Asthma Related Genes  
NUMBER OF SEQUENCES: 339  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bozicevic & Reed, LLP  
STREET: 285 Hamilton Ave, Suite 200  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/009,913  
FILING DATE: 21-JAN-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: Sherwood, Pamela J  
REGISTRATION NUMBER: 36,677  
REFERENCE/DOCKET NUMBER: SEQ-4P  
TELEPHONE: 650-327-3231  
TELEFAX: 650-327-3231  
TELEX:  
INFORMATION FOR SEQ ID NO: 298:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-09-009-913-298  
Query Match 74.4%; Score 13.4; DB 3; Length 20;  
Best Local Similarity 93.3%; Pred. No. 2.1e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGAGGAGGGGCTG 15  
Db 5 GGTGAGGAGGGGCTG 19  
RESULT 6  
US-08-250-856A-21/c  
Sequence 21, Application US/08250856A  
Patent No. 5563255  
GENERAL INFORMATION:  
APPLICANT: Monia, Brett P. and Boggs, Russell T.  
TITLE OF INVENTION: Antisense Oligonucleotide Modulation  
TITLE OF INVENTION: of raf Gene Expression  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Law Offices of Jane Massey Licata  
STREET: 210 Lake Drive East, Suite 201  
CITY: Cherry Hill  
STATE: NJ  
COUNTRY: USA  
ZIP: 08002  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/250,856A  
FILING DATE: May 31, 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane Massey Licata  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-0094  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 779-2400  
TELEFAX: (609) 779-8488  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: Yes  
US-08-250-856A-21

Query Match 71.1%; Score 12.8; DB 1; Length 20;  
Best Local Similarity 87.5%; Pred. No. 3.7e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGAGGAGGGGCTGG 16  
Db 20 GGGAGGAGGGGCGG 5

RESULT 7  
US-08-468-037A-9/c  
Sequence 9, Application US/08468037A  
Patent No. 5859221  
GENERAL INFORMATION:  
APPLICANT: Phillip Dan Cook  
APPLICANT: A. Kawasaki  
TITLE OF INVENTION: 2'-Modified Oligonucleotides  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5859221  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: U.S.A.

ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch disk, 720 Kb  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,037A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 835,932  
FILING DATE: 05-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Joseph Lucci  
REGISTRATION NUMBER: 33,307  
REFERENCE/DOCKET NUMBER: ISIS-2004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
ANTI-SENSE: yes  
US-08-468-037A-9

Query Match 71.1%; Score 12.8; DB 2; Length 20;  
Best Local Similarity 87.5%; Pred. No. 3.7e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTGG 16  
|||||  
DB 20 GGGGAGGAGGAGCGGG 5

RESULT 8  
US-08-471-973A-9/c  
Sequence 9, Application US/08471973A  
Patent No. 5872232  
GENERAL INFORMATION:  
APPLICANT: Phillip Dan Cook  
APPLICANT: Andrew Kawasaki  
TITLE OF INVENTION: Sugar Modified Oligonucleotides  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5872232ris  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: U.S.A.  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch disk, 720 Kb  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,973A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 835,932  
FILING DATE: 05-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Joseph Lucci  
REGISTRATION NUMBER: 33,307  
REFERENCE/DOCKET NUMBER: ISIS-2005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
ANTI-SENSE: yes  
US-08-471-973A-9

Query Match 71.1%; Score 12.8; DB 2; Length 20;  
Best Local Similarity 87.5%; Pred. No. 3.7e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTGG 16  
|||||  
DB 20 GGGGAGGAGGAGCGGG 5

RESULT 9  
US-08-756-806A-21/c  
Sequence 21, Application US/08756806A  
Patent No. 5952229  
GENERAL INFORMATION:  
APPLICANT: Monia, Brett P. and Boggs, Russell T.  
TITLE OF INVENTION: Antisense Oligonucleotide Modulation  
TITLE OF INVENTION: of raf Gene Expression  
NUMBER OF SEQUENCES: 65  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Law Offices of Jane Massey Licata  
STREET: 66 East Main Street  
CITY: Marlton  
STATE: NJ  
COUNTRY: USA  
ZIP: 08053  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/756,806A  
FILING DATE: No. 5952229ember 26, 1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/07111  
FILING DATE: May 31, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/250,856  
FILING DATE: May 31, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane Massey Licata  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-0200  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 779-2400  
TELEFAX: (609) 810-1454  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: Yes  
US-08-756-806A-21

Query Match 71.1%; Score 12.8; DB 2; Length 20;  
Best Local Similarity 87.5%; Pred. No. 3.7e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTGG 16  
|||||  
DB 20 GGGGAGGAGGAGCGGG 5

```
RESULT 10
US-08-465-880-9/c
; Sequence 9, Application US/08465880
; Patent No. 595589
; GENERAL INFORMATION:
; APPLICANT: Philip Dan Cook
; TITLE OF INVENTION: Gapped 2' Modified Oligonucleotides
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 595589ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,880
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 244,993
; FILING DATE: 21-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-2002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: Yes
US-08-465-880-9

Query Match 71.1%; Score 12.8; DB 2; Length 20;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTGG 16
Db 20 GGGGAGGAGGAGCGGG 5

RESULT 11
US-09-035-357-9/c
; Sequence 9, Application US/09035357
; Patent No. 6005087
; GENERAL INFORMATION:
; APPLICANT: Phillip Dan Cook
; APPLICANT: A. Kawasaki
; TITLE OF INVENTION: 2'-Modified Oligonucleotides
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6005087ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

```
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/035,357
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/468,037
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Joseph Lucci
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: ISIS-2004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: yes
US-09-035-357-9

Query Match 71.1%; Score 12.8; DB 3; Length 20;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTGG 16
Db 20 GGGGAGGAGGAGCGGG 5

RESULT 12
US-09-143-214-21/c
; Sequence 21, Application US/09143214
; Patent No. 6090626
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P. and Boggs, Russell T.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation
; TITLE OF INVENTION: of raf Gene Expression
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/143,214
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/756,806
; FILING DATE: No. 6090626ember 26, 1996
; APPLICATION NUMBER: PCT/US95/07111
; FILING DATE: May 31, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/250,856
; FILING DATE: May 31, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0200
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 810-1454
```

```
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 20
;   TYPE: Nucleic Acid
;   STRANDEDNESS: Single
;   TOPOLOGY: Linear
;   ANTI-SENSE: Yes
; US-09-143-214-21
;
; Query Match          71.1%; Score 12.8; DB 3; Length 20;
; Best Local Similarity 87.5%; Pred. No. 3.7e+03;
; Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 1 GGGGAGGAGGGGCTGG 16
;    |||||
; Db 20 GGGGAGGAGGAGCGGG 5
;
; RESULT 13
; US-09-000-136-7/c
; Sequence 7, Application US/090000136
; Patent No. 6096720
; GENERAL INFORMATION:
; APPLICANT: Love, William G
; APPLICANT: Sharman, Thomas
; APPLICANT: Phillips, Judith A
; APPLICANT: Nicklin, Paul L
; APPLICANT: Hamilton, Karen O
; TITLE OF INVENTION: Liposomal Oligonucleotide Compositions
; FILE REFERENCE: 4-20536/A/MA 2112
; CURRENT APPLICATION NUMBER: US/09/000,136
; CURRENT FILING DATE: 1998-04-23
; EARLIER APPLICATION NUMBER: GB 9515743.4
; EARLIER FILING DATE: 1995-08-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 7
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: oligonucleotide
; FEATURE:
; OTHER INFORMATION: phosphorothioate backbone
; FEATURE:
; OTHER INFORMATION: alternative oligonucleotide with uniform
; OTHER INFORMATION: phosphorothioate backbone with nucleotides 10-20
; OTHER INFORMATION: being substituted by methoxy at the 2' position of
; OTHER INFORMATION: the sugar moiety
; US-09-000-136-7
;
; Query Match          71.1%; Score 12.8; DB 3; Length 20;
; Best Local Similarity 87.5%; Pred. No. 3.7e+03;
; Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 1 GGGGAGGAGGGGCTGG 16
;    |||||
; Db 20 GGGGAGGAGGAGCGGG 5
;
; RESULT 14
; US-09-135-202-9/c
; Sequence 9, Application US/09135202
; Patent No. 6399754
; GENERAL INFORMATION:
; APPLICANT: Phillip Dan Cook
; APPLICANT: Andrew Kawasaki
; TITLE OF INVENTION: Sugar Modified Oligonucleotides
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 6399754ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
;
; Query Match          71.1%; Score 12.8; DB 4; Length 20;
; Best Local Similarity 87.5%; Pred. No. 3.7e+03;
; Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/135,202
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/471,973
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-2005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: yes
; US-09-135-202-9
;
; Query Match          71.1%; Score 12.8; DB 4; Length 20;
; Best Local Similarity 87.5%; Pred. No. 3.7e+03;
; Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 1 GGGGAGGAGGGGCTGG 16
;    |||||
; Db 20 GGGGAGGAGGAGCGGG 5
;
; RESULT 15
; US-09-506-073-21/c
; Sequence 21, Application US/09506073
; Patent No. 6410518
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/506,073
; CURRENT FILING DATE: 2000-02-18
; EARLIER APPLICATION NUMBER: US 09/143,214
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: PCT/US98/13961
; EARLIER FILING DATE: 1998-07-06
; EARLIER APPLICATION NUMBER: US 08/888,982
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US 08/756,806
; EARLIER FILING DATE: 1996-11-26
; EARLIER APPLICATION NUMBER: PCT/US95/07111
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/250,856
; EARLIER FILING DATE: 1994-05-31
; NUMBER OF SEQ ID NOS: 130
; SEQ ID NO 21
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
; US-09-506-073-21
;
; Query Match          71.1%; Score 12.8; DB 4; Length 20;
; Best Local Similarity 87.5%; Pred. No. 3.7e+03;
```

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGGAGGAGGGGCTGG 16  
| | | | | | | | | |  
Db 20 GGGGAGGAGGGGCGGG 5

Search completed: October 27, 2003, 14:03:34  
Job time : 42.3143 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 11:25:34 ; Search time 387.943 Seconds  
(without alignments)  
124.432 Million cell updates/sec

Title: US-09-331-204A-5  
Perfect score: 18  
Sequence: 1 gggaggagggtgaa 18  
Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1792395 seqs, 1340300451 residues

Total number of hits satisfying chosen parameters: 408622

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*
- 16: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*
- 17: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	12.8	71.1	17	9	US-09-866-108-7484 Sequence 7484, Ap
2	12.8	71.1	17	9	US-09-866-108-7485 Sequence 7485, Ap
3	12.8	71.1	17	11	US-09-780-533A-898 Sequence 898, Ap
4	12.8	71.1	17	11	US-09-780-533A-899 Sequence 899, Ap
5	12.8	71.1	17	12	US-10-133-779-45 Sequence 45, Appl
6	12.8	71.1	20	11	US-09-996-263-9 Sequence 9, Appl
7	12.8	71.1	20	12	US-10-352-586-9 Sequence 9, Appl
8	12.8	71.1	20	14	US-10-057-550-21 Sequence 21, Appl
9	12.8	71.1	20	14	US-10-173-225B-21 Sequence 21, Appl
10	12.4	68.9	17	9	US-09-866-108-7486 Sequence 7486, Ap
11	12.4	68.9	17	9	US-09-866-108-7487 Sequence 7487, Ap
12	12.4	68.9	17	12	US-10-061-201-1931 Sequence 1931, Ap
13	12.4	68.9	17	12	US-10-061-201-1932 Sequence 1932, Ap
14	12.4	68.9	17	12	US-10-061-201-1933 Sequence 1933, Ap
15	12.4	68.9	17	12	US-10-061-201-1934 Sequence 1934, Ap
16	12.2	67.8	17	11	US-09-780-533A-2409 Sequence 2409, Ap

C 17	12	66.7	17	11	US-09-780-533A-46	Sequence 46, Appl
C 18	12	66.7	17	11	US-09-780-533A-47	Sequence 47, Appl
C 19	12	66.7	17	11	US-09-780-533A-900	Sequence 900, App
C 20	12	66.7	17	11	US-09-780-533A-901	Sequence 901, App
C 21	12	66.7	17	12	US-10-061-201-1935	Sequence 1935, Ap
C 22	12	66.7	17	12	US-10-061-201-1936	Sequence 1936, Ap
C 23	12	66.7	19	10	US-09-225-904-22	Sequence 22, Appl
C 24	12	66.7	19	12	US-10-167-241-1	Sequence 1, Appl
C 25	12	66.7	19	12	US-10-108-732-14	Sequence 14, Appl
C 26	12	66.7	21	10	US-09-934-060A-11	Sequence 11, Appl
C 27	11.8	65.6	17	9	US-09-866-108-7483	Sequence 7483, Ap
C 28	11.8	65.6	17	9	US-09-866-108-8084	Sequence 8084, Ap
C 29	11.8	65.6	17	9	US-09-866-108-8085	Sequence 8085, Ap
C 30	11.8	65.6	17	9	US-09-864-785-339	Sequence 8086, Ap
C 31	11.8	65.6	17	10	US-09-864-785-339	Sequence 339, App
C 32	11.8	65.6	17	10	US-09-864-785-340	Sequence 340, App
C 33	11.8	65.6	17	10	US-09-864-785-341	Sequence 341, App
C 34	11.8	65.6	17	11	US-09-780-533A-897	Sequence 897, App
C 35	11.8	65.6	17	11	US-09-780-533A-922	Sequence 922, App
C 36	11.8	65.6	17	11	US-09-780-533A-923	Sequence 923, App
C 37	11.8	65.6	17	11	US-09-780-533A-2415	Sequence 2415, Ap
C 38	11.8	65.6	18	9	US-09-730-617-16	Sequence 16, Appl
C 39	11.8	65.6	19	11	US-09-943-416A-11	Sequence 11, Appl
C 40	11.8	65.6	20	11	US-09-925-911-5	Sequence 5, Appl
C 41	11.8	65.6	20	11	US-09-925-911-6	Sequence 6, Appl
C 42	11.8	65.6	20	14	US-10-199-830-5	Sequence 5, Appl
C 43	11.8	65.6	20	14	US-10-199-830-6	Sequence 6, Appl
C 44	11.8	65.6	21	14	US-10-219-616-16	Sequence 16, Appl
C 45	11.8	65.6	22	14	US-10-209-372-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1

US-09-866-108-7484  
; Sequence 7484, Application US/09866108  
; Patent No. US20020048900A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7484
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7484

Query Match 71.1%; Score 12.8; DB 9; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.5e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGAGGAGGGGCTGGA 17
| | | | | | | | | | | | | | |
Db 2 GCGAGGAGAGGCTGGA 17

RESULT 2
US-09-866-108-7485
; Sequence 7485, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7485

; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7485
Query Match 71.1%; Score 12.8; DB 9; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.5e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 GGGAGGAGGGGCTGGA 17
| | | | | | | | | | | | | | |
Db 1 GCGAGGAGAGGCTGGA 16

RESULT 3
US-09-780-533A-898/c
; Sequence 898, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 898
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-898

Query Match 71.1%; Score 12.8; DB 11; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.5e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GGGAGGAGGGGCTGG 16
| | | | | | | | | | | | | |
Db 17 GGGAGGAGGGGGAGG 2

RESULT 4
US-09-780-533A-899/c
; Sequence 899, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 899
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-899

Query Match 71.1%; Score 12.8; DB 11; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.5e+04;



```
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GGGGAGGAGGGGCTGG 16
    |||||
Db 16 GGGGAGGAGGGGAGG 1
    |||||

RESULT 5
US-10-133-779-45
; Sequence 45, Application US/10133779
; Publication No. US20030165884A1
; GENERAL INFORMATION:
; APPLICANT: Chow, Robert
; APPLICANT: Tonai, Richard
; APPLICANT: StemCyt, Inc.
; TITLE OF INVENTION: High Throughput Methods of HLA Typing
; FILE REFERENCE: 020035-000210US
; CURRENT APPLICATION NUMBER: US/10/133,779
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/747,391
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/172,768
; PRIOR FILING DATE: 1999-12-20
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 45
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-133-779-45

Query Match 71.1%; Score 12.8; DB 12; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.5e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 GGAGGAGGGGCTGGAA 18
    |||||
Db 2 GCAGGAGGGGCGGAA 17
    |||||

RESULT 6
US-09-996-263-9/c
; Sequence 9, Application US/09996263
; Publication No. US20030004325A1
; GENERAL INFORMATION:
; APPLICANT: Phillip Dan Cook
; APPLICANT: Andrew Kawasaki
; TITLE OF INVENTION: Sugar Modified Oligonucleotides
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. US20030004325A1ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/996,263
; FILING DATE: 28-Nov-00 US20030004325A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/471,973
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-2005
; TELECOMMUNICATION INFORMATION:
```

```
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: yes
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-996-263-9

Query Match 71.1%; Score 12.8; DB 11; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GGGGAGGAGGGGCTGG 16
    |||||
Db 20 GGGGAGGAGGAGCGGG 5
    |||||

RESULT 7
US-10-352-586-9/c
; Sequence 9, Application US/10352586
; Publication No. US20030187240A1
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Kawasaki, Andrew
; TITLE OF INVENTION: 2'-Modified Oligonucleotides
; FILE REFERENCE: ISIS137
; CURRENT APPLICATION NUMBER: US/10/352,586
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 09/389,283
; PRIOR FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-352-586-9

Query Match 71.1%; Score 12.8; DB 12; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GGGGAGGAGGGGCTGG 16
    |||||
Db 20 GGGGAGGAGGAGCGGG 5
    |||||

RESULT 8
US-10-057-550-21/c
; Sequence 21, Application US/10057550
; Publication No. US20030032607A1
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/057,550
; CURRENT FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: 09/506,073
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: US 09/143,214
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: PCT/US98/13961
; PRIOR FILING DATE: 1998-07-06
; PRIOR APPLICATION NUMBER: US 08/888,982
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: US 08/756,806
; PRIOR FILING DATE: 1996-11-26
```

```

; PRIOR APPLICATION NUMBER: PCT/US95/071111
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/250,856
; PRIOR FILING DATE: 1994-05-31
; NUMBER OF SEQ ID NOS: 130
; SEQ ID NO 21
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-10-057-550-21

```

```
Query Match          71.1%; Score 12.8; DB 14; Length 20;
Best Local Similarity 87.5%; Pred. NO. 2.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 1 GGGGAGGAGGGCTGG 16  
Db 20 GGGGAGGAGGAGCGGG 5

```

RESULT 9
US-10-173-225B-21/c
; Sequence 21, Application US/10173225B
; Publication No. US20030119769A1
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression
; FILE REFERENCE: ISPH-0665
; CURRENT APPLICATION NUMBER: US/10/173,225B
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 10/057,550
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 09/143,214
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: PCT/US98/13961
; PRIOR FILING DATE: 1998-07-06
; PRIOR APPLICATION NUMBER: US 08/888,982
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: US 08/756,806
; PRIOR FILING DATE: 1996-11-26
; PRIOR APPLICATION NUMBER: PCT/US95/07111
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/250,856
; PRIOR FILING DATE: 1994-05-31
; NUMBER OF SEQ ID NOS: 109
; SEQ ID NO 21
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-10-173-225B-21

```

Query Match	71.1%;	Score 12.8;	DB 14;	Length 20;
Best Local Similarity	87.5%;	Pred. No. 2.4e+04;		
Matches 14;	Conservative	0;	Mismatches 2;	Indels 0;
				Gaps 0;

Qy 1 GCGGAGGAGGGGCTGG 16  
|||  
Db 20 GCGGAGGAGGAGCGGG 5

RESULT 10  
US-09-866-108-7486  
; Sequence 7486, Application US/09866108  
; Patent No. US20020048800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.

```

; APPLICANT: RANK, David R.
; APPLICANT: CHEN, wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7486
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108-7486

Query Match          68.9%; Score 12.4; DB 9; Length 17;
Best Local Similarity 92.9%; Pred. No. 3.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps

```

Qy 4 GAGGAGGGGCTGA 17  
|||  
Db 2 GAGGAGGGGCTGA 15

RESULT 11  
US-09-866-108-7487  
; Sequence 7487, Application US/09866108  
; Patent No. US20020048800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEONICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7487
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7487

Query Match 68.9%; Score 12.4; DB 9; Length 17;
Best Local Similarity 92.9%; Pred. No. 3.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAGGAGGGGCTGGA 17
Db 1 GAGGAGAGGCTGGA 14

RESULT 12
US-10-061-201-1931/c
; Sequence 1931, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; PRIOR FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205

; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1931
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-1931

Query Match 68.9%; Score 12.4; DB 12; Length 17;
Best Local Similarity 92.9%; Pred. No. 3.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCT 14
Db 17 GGGGAGGAGGGGAT 4

RESULT 13
US-10-061-201-1932/c
; Sequence 1932, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; PRIOR FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1932
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-1932

Query Match 68.9%; Score 12.4; DB 12; Length 17;
Best Local Similarity 92.9%; Pred. No. 3.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCT 14
Db 16 GGGGAGGAGGGGAT 3

RESULT 14
US-10-061-201-1933/c
; Sequence 1933, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178

; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1933
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-1933

Query Match 68.9%; Score 12.4; DB 12; Length 17;
Best Local Similarity 92.9%; Pred. No. 3.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCT 14
Db 15 GGGGAGGAGGGGAT 2

RESULT 15
US-10-061-201-1934/c
; Sequence 1934, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1934
; LENGTH: 17

; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-1934
Query Match 68.9%; Score 12.4; DB 12; Length 17;
Best Local Similarity 92.9%; Pred. No. 3.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGGGAGGAGGGGCT 14
Db 14 GGGGAGGAGGGGAT 1
Search completed: October 27, 2003, 19:00:52
Job time : 387.943 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:35 ; Search time 2356.29 Seconds  
(without alignments)  
253.343 Million cell updates/sec

Title: US-09-331-204A-5  
Perfect score: 18  
Sequence: 1 gggaggaggggctggaa 18

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 33363688 seqs, 16581889874 residues

Total number of hits satisfying chosen parameters: 2938060

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents\_NA Main:\*

1: /cgn2\_6/ptodata/1/pna/PCTUS COMB.seq:\*

2: /cgn2\_6/ptodata/1/pna/PCTUS COMB.seq:old:\*

3: /cgn2\_6/ptodata/1/pna/US06 COMB.seq:\*

4: /cgn2\_6/ptodata/1/pna/US07 COMB.seq:\*

5: /cgn2\_6/ptodata/1/pna/US08 COMB.seq:\*

6: /cgn2\_6/ptodata/1/pna/US081 COMB.seq:\*

7: /cgn2\_6/ptodata/1/pna/US082 COMB.seq:\*

8: /cgn2\_6/ptodata/1/pna/US083 COMB.seq:\*

9: /cgn2\_6/ptodata/1/pna/US084 COMB.seq:\*

10: /cgn2\_6/ptodata/1/pna/US085 COMB.seq:\*

11: /cgn2\_6/ptodata/1/pna/US086 COMB.seq:\*

12: /cgn2\_6/ptodata/1/pna/US087 COMB.seq:\*

13: /cgn2\_6/ptodata/1/pna/US088 COMB.seq:\*

14: /cgn2\_6/ptodata/1/pna/US089 COMB.seq:\*

15: /cgn2\_6/ptodata/1/pna/US090 COMB.seq:\*

16: /cgn2\_6/ptodata/1/pna/US091 COMB.seq:\*

17: /cgn2\_6/ptodata/1/pna/US092A COMB.seq:\*

18: /cgn2\_6/ptodata/1/pna/US092B COMB.seq:\*

19: /cgn2\_6/ptodata/1/pna/US093A COMB.seq:\*

20: /cgn2\_6/ptodata/1/pna/US093B COMB.seq:\*

21: /cgn2\_6/ptodata/1/pna/US094 COMB.seq:\*

22: /cgn2\_6/ptodata/1/pna/US095A COMB.seq:\*

23: /cgn2\_6/ptodata/1/pna/US095B COMB.seq:\*

24: /cgn2\_6/ptodata/1/pna/US095C COMB.seq:\*

25: /cgn2\_6/ptodata/1/pna/US095D COMB.seq:\*

26: /cgn2\_6/ptodata/1/pna/US096A COMB.seq:\*

27: /cgn2\_6/ptodata/1/pna/US096B COMB.seq:\*

28: /cgn2\_6/ptodata/1/pna/US096C COMB.seq:\*

29: /cgn2\_6/ptodata/1/pna/US096D COMB.seq:\*

30: /cgn2\_6/ptodata/1/pna/US096E COMB.seq:\*

31: /cgn2\_6/ptodata/1/pna/US097A COMB.seq:\*

32: /cgn2\_6/ptodata/1/pna/US097B COMB.seq:\*

33: /cgn2\_6/ptodata/1/pna/US097C COMB.seq:\*

34: /cgn2\_6/ptodata/1/pna/US098A COMB.seq:\*

35: /cgn2\_6/ptodata/1/pna/US098B COMB.seq:\*

36: /cgn2\_6/ptodata/1/pna/US098C COMB.seq:\*

37: /cgn2\_6/ptodata/1/pna/US098D COMB.seq:\*

38: /cgn2\_6/ptodata/1/pna/US099A COMB.seq:\*

39: /cgn2\_6/ptodata/1/pna/US099B COMB.seq:\*

40: /cgn2\_6/ptodata/1/pna/US099C COMB.seq:\*

41: /cgn2\_6/ptodata/1/pna/US099D COMB.seq:\*

42: /cgn2\_6/ptodata/1/pna/US099E COMB.seq:\*

43: /cgn2\_6/ptodata/1/pna/US099F COMB.seq:\*

44: /cgn2\_6/ptodata/1/pna/US100A COMB.seq:\*

45: /cgn2\_6/ptodata/1/pna/US100B COMB.seq:\*

46: /cgn2\_6/ptodata/1/pna/US101A COMB.seq:\*

47: /cgn2\_6/ptodata/1/pna/US101B COMB.seq:\*

48: /cgn2\_6/ptodata/1/pna/US102A COMB.seq:\*

49: /cgn2\_6/ptodata/1/pna/US102B COMB.seq:\*

50: /cgn2\_6/ptodata/1/pna/US103A COMB.seq:\*

51: /cgn2\_6/ptodata/1/pna/US103B COMB.seq:\*

52: /cgn2\_6/ptodata/1/pna/US104A COMB.seq:\*

53: /cgn2\_6/ptodata/1/pna/US104B COMB.seq:\*

54: /cgn2\_6/ptodata/1/pna/US6000 COMB.seq:\*

55: /cgn2\_6/ptodata/1/pna/US6001 COMB.seq:\*

56: /cgn2\_6/ptodata/1/pna/US6002 COMB.seq:\*

57: /cgn2\_6/ptodata/1/pna/US6003 COMB.seq:\*

58: /cgn2\_6/ptodata/1/pna/US6004 COMB.seq:\*

59: /cgn2\_6/ptodata/1/pna/US6005 COMB.seq:\*

60: /cgn2\_6/ptodata/1/pna/US6006 COMB.seq:\*

61: /cgn2\_6/ptodata/1/pna/US6007 COMB.seq:\*

62: /cgn2\_6/ptodata/1/pna/US6008 COMB.seq:\*

63: /cgn2\_6/ptodata/1/pna/US6009 COMB.seq:\*

64: /cgn2\_6/ptodata/1/pna/US6010 COMB.seq:\*

65: /cgn2\_6/ptodata/1/pna/US6011 COMB.seq:\*

66: /cgn2\_6/ptodata/1/pna/US6012 COMB.seq:\*

67: /cgn2\_6/ptodata/1/pna/US6013 COMB.seq:\*

68: /cgn2\_6/ptodata/1/pna/US6014 COMB.seq:\*

69: /cgn2\_6/ptodata/1/pna/US6015 COMB.seq:\*

70: /cgn2\_6/ptodata/1/pna/US6016 COMB.seq:\*

71: /cgn2\_6/ptodata/1/pna/US6017 COMB.seq:\*

72: /cgn2\_6/ptodata/1/pna/US6018 COMB.seq:\*

73: /cgn2\_6/ptodata/1/pna/US6019 COMB.seq:\*

74: /cgn2\_6/ptodata/1/pna/US6020 COMB.seq:\*

75: /cgn2\_6/ptodata/1/pna/US6021 COMB.seq:\*

76: /cgn2\_6/ptodata/1/pna/US6022 COMB.seq:\*

77: /cgn2\_6/ptodata/1/pna/US6023A COMB.seq:\*

78: /cgn2\_6/ptodata/1/pna/US6023B COMB.seq:\*

79: /cgn2\_6/ptodata/1/pna/US6024 COMB.seq:\*

80: /cgn2\_6/ptodata/1/pna/US6025 COMB.seq:\*

81: /cgn2\_6/ptodata/1/pna/US6026 COMB.seq:\*

82: /cgn2\_6/ptodata/1/pna/US6027 COMB.seq:\*

83: /cgn2\_6/ptodata/1/pna/US6028 COMB.seq:\*

84: /cgn2\_6/ptodata/1/pna/US6029 COMB.seq:\*

85: /cgn2\_6/ptodata/1/pna/US6030 COMB.seq:\*

86: /cgn2\_6/ptodata/1/pna/US6031 COMB.seq:\*

87: /cgn2\_6/ptodata/1/pna/US6032 COMB.seq:\*

88: /cgn2\_6/ptodata/1/pna/US6033 COMB.seq:\*

89: /cgn2\_6/ptodata/1/pna/US6034 COMB.seq:\*

90: /cgn2\_6/ptodata/1/pna/US6035 COMB.seq:\*

91: /cgn2\_6/ptodata/1/pna/US6036 COMB.seq:\*

92: /cgn2\_6/ptodata/1/pna/US6037 COMB.seq:\*

93: /cgn2\_6/ptodata/1/pna/US6038 COMB.seq:\*

94: /cgn2\_6/ptodata/1/pna/US6039 COMB.seq:\*

95: /cgn2\_6/ptodata/1/pna/US6040 COMB.seq:\*

96: /cgn2\_6/ptodata/1/pna/US6041 COMB.seq:\*

97: /cgn2\_6/ptodata/1/pna/US6042 COMB.seq:\*

98: /cgn2\_6/ptodata/1/pna/US6043 COMB.seq:\*

99: /cgn2\_6/ptodata/1/pna/US6044 COMB.seq:\*

100: /cgn2\_6/ptodata/1/pna/US6045 COMB.seq:\*

101: /cgn2\_6/ptodata/1/pna/US6046 COMB.seq:\*

102: /cgn2\_6/ptodata/1/pna/US6047 COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query			Description
	No.	Score	Match Length DB ID	
1	18	100.0	18 19	US-09-331-204-2 Sequence 2, Appli
2	18	100.0	18 19	US-09-331-204A-5 Sequence 5, Appli
C 3	18	100.0	18 19	US-09-331-204A-20 Sequence 20, Appli
4	15.4	85.6	22 50	US-10-310-188-60578 Sequence 60578, A

C	5	14.4	80.0	16	50	US-10-303-778-3565	Sequence 3565, Ap
C	6	14.4	80.0	16	50	US-10-310-188-5892	Sequence 5892, Ap
C	7	14.4	80.0	17	1	PCT-US02-25943-61140	Sequence 61140, A
C	8	14.4	80.0	17	48	US-10-227-565-61140	Sequence 61140, A
	9	14.4	80.0	17	50	US-10-310-188-84932	Sequence 84932, A
C	10	14.4	80.0	17	51	US-10-367-832A-61140	Sequence 61140, A
	11	14.4	80.0	18	50	US-10-310-188-24767	Sequence 24767, A
	12	14.4	80.0	18	50	US-10-310-188-61077	Sequence 61077, A
	13	14.4	80.0	18	50	US-10-310-188-61084	Sequence 61084, A
	14	14.4	80.0	21	50	US-10-310-188-41819	Sequence 41819, A
	15	14.4	80.0	21	50	US-10-310-188-41829	Sequence 41829, A
	16	14.4	80.0	21	50	US-10-310-188-41830	Sequence 41830, A
	17	14.4	80.0	22	50	US-10-303-778-1410	Sequence 1410, Ap
	18	14.4	80.0	22	50	US-10-310-188-42169	Sequence 42169, A
	19	14	77.8	20	50	US-10-310-188-18119	Sequence 18119, A
	20	13.8	76.7	17	50	US-10-303-778-16780	Sequence 16780, A
C	21	13.8	76.7	18	6	US-08-170-096-11	Sequence 11, Appl
C	22	13.8	76.7	18	49	US-10-266-090-38012	Sequence 38012, A
C	23	13.8	76.7	19	1	PCT-US03-07273-12	Sequence 12, Appl
C	24	13.8	76.7	19	1	PCT-US03-07273-165	Sequence 165, Appl
C	25	13.8	76.7	19	2	PCT-US03-07273-12	Sequence 12, Appl
C	26	13.8	76.7	19	2	PCT-US03-07273-165	Sequence 165, Appl
C	27	13.8	76.7	21	6	US-08-170-096-10	Sequence 10, Appl
C	28	13.8	76.7	21	6	US-08-170-096-13	Sequence 13, Appl
C	29	13.8	76.7	21	28	US-09-657-472-1424	Sequence 1424, Ap
C	30	13.8	76.7	21	50	US-10-310-188-39028	Sequence 39028, A
	31	13.8	76.7	22	50	US-10-310-188-18209	Sequence 18209, A
	32	13.4	74.4	16	50	US-10-303-778-14517	Sequence 14517, A
C	33	13.4	74.4	17	50	US-10-303-778-1396	Sequence 1396, Ap
C	34	13.4	74.4	18	50	US-10-310-188-84403	Sequence 84403, A
C	35	13.4	74.4	19	50	US-10-310-188-5724	Sequence 5724, Ap
	36	13.4	74.4	20	1	PCT-US00-04340-82	Sequence 82, Appl
	37	13.4	74.4	20	1	PCT-US98-01260-298	Sequence 298, Appl
	38	13.4	74.4	20	2	PCT-US00-04340-82	Sequence 82, Appl
	39	13.4	74.4	20	2	PCT-US98-01260-298	Sequence 298, Appl
	40	13.4	74.4	20	22	US-09-507-209-82	Sequence 82, Appl
	41	13.4	74.4	20	22	US-09-511-446-298	Sequence 298, Appl
	42	13.4	74.4	20	49	US-10-266-090-45537	Sequence 45537, A
	43	13.4	74.4	20	50	US-10-303-778-5139	Sequence 5139, Ap
	44	13.4	74.4	20	50	US-10-310-188-86072	Sequence 86072, A
	45	13.4	74.4	21	50	US-10-310-188-18091	Sequence 18091, A

ALIGNMENTS

RESULT 1  
US-09-331-204-2  
; Sequence 2, Application US/09331204  
; GENERAL INFORMATION:  
; APPLICANT: Tam, Robert  
; TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN  
; FILE REFERENCE: ICNSequence  
; CURRENT FILING DATE: 1999-08-20  
; PRIOR APPLICATION NUMBER: PCT/US97/23927  
; PRIOR FILING DATE: 1997-12-19  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: An oligomer  
; OTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic  
; OTHER INFORMATION: acid. This term includes oligomers consisting of  
; OTHER INFORMATION: naturally occurring bases, sugars and intersugar  
US-09-331-204-2

Query Match 100.0%; Score 18; DB 19; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGAGGAGGGGCTGGAA 18  
| | | | | | | | | | | | | | | | | |  
Db 1 GGGAGGAGGGGCTGGAA 18  
| | | | | | | | | | | | | | | | | |  
RESULT 2  
US-09-331-204A-5  
; Sequence 5, Application US/09331204A  
; GENERAL INFORMATION:  
; APPLICANT: ICN Pharmaceuticals, Inc.  
; APPLICANT: Tam, Robert  
; TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Res  
; FILE REFERENCE: 216/013-US1  
; CURRENT APPLICATION NUMBER: US/09/331,204A  
; CURRENT FILING DATE: 1999-08-20  
; PRIOR APPLICATION NUMBER: PCT/US97/23927  
; PRIOR FILING DATE: 1997-12-19  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: synthetic construct  
US-09-331-204A-5  
Query Match 100.0%; Score 18; DB 19; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAGGAGGGGCTGGAA 18  
| | | | | | | | | | | | | | | | | |  
Db 1 GGGAGGAGGGGCTGGAA 18  
| | | | | | | | | | | | | | | | | |

RESULT 3  
US-09-331-204A-20/c  
; Sequence 20, Application US/09331204A  
; GENERAL INFORMATION:  
; APPLICANT: ICN Pharmaceuticals, Inc.  
; APPLICANT: Tam, Robert  
; TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Res  
; FILE REFERENCE: 216/013-US1  
; CURRENT APPLICATION NUMBER: US/09/331,204A  
; CURRENT FILING DATE: 1999-08-20  
; PRIOR APPLICATION NUMBER: PCT/US97/23927  
; PRIOR FILING DATE: 1997-12-19  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 20  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: synthetic construct  
US-09-331-204A-20

Query Match 100.0%; Score 18; DB 19; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAGGAGGGGCTGGAA 18  
| | | | | | | | | | | | | | | | | |  
Db 18 GGGAGGAGGGGCTGGAA 1

RESULT 4  
US-10-310-188-60578  
; Sequence 60578, Application US/10310188  
; GENERAL INFORMATION:  
; APPLICANT: RosettaGenomics  
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: 47487

; CURRENT APPLICATION NUMBER: US/10/310,188  
; CURRENT FILING DATE: 2002-12-19  
; NUMBER OF SEQ ID NOS: 86841  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 60578  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-310-188-60578

Query Match 85.6%; Score 15.4; DB 50; Length 22;  
Best Local Similarity 94.1%; Pred. No. 3.6e+04;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTGGA 17  
|||||  
Db 1 GGGGAGGCGGGGCTGGA 17  
|||||

RESULT 5

US-10-303-778-3565/c  
; Sequence 3565, Application US/10303778

; GENERAL INFORMATION:  
; APPLICANT: RosettaGenomics  
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL  
; FILE REFERENCE: 47416  
; CURRENT APPLICATION NUMBER: US/10/303,778  
; NUMBER OF SEQ ID NOS: 17608  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3565  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-303-778-3565

Query Match 80.0%; Score 14.4; DB 50; Length 16;  
Best Local Similarity 93.8%; Pred. No. 8.9e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGAGGGGCTGGAA 18  
|||||  
Db 16 GGAGGAGGGGCTGGCA 1  
|||||

RESULT 6

US-10-310-188-5892/c  
; Sequence 5892, Application US/10310188

; GENERAL INFORMATION:  
; APPLICANT: RosettaGenomics  
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE  
; FILE REFERENCE: 47487  
; CURRENT APPLICATION NUMBER: US/10/310,188  
; CURRENT FILING DATE: 2002-12-19  
; NUMBER OF SEQ ID NOS: 86841  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5892  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-310-188-5892

Query Match 80.0%; Score 14.4; DB 50; Length 16;  
Best Local Similarity 93.8%; Pred. No. 8.9e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGAGGGGCTGGAA 18  
|||||  
Db 16 GGAGGAGGGGCTGGCA 1  
|||||

RESULT 7  
PCT-US02-25943-61140/c  
; Sequence 61140, Application PC/TUS0225943

; GENERAL INFORMATION:  
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.  
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333  
; CURRENT APPLICATION NUMBER: PCT/US02/25943  
; CURRENT FILING DATE: 2002-08-27  
; NUMBER OF SEQ ID NOS: 64158  
; SOFTWARE: Proprietary  
; SEQ ID NO 61140  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.  
; FEATURE:  
; LOCATION: (5963161)...(5963177)  
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 6548  
PCT-US02-25943-61140

Query Match 80.0%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 8.9e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGAGGGGCTGGAA 18  
|||||  
Db 17 GGAGGAGGGGCTGGAA 2  
|||||

RESULT 8

US-10-227-565-61140/c  
; Sequence 61140, Application US/10227565

; GENERAL INFORMATION:  
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.  
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333  
; CURRENT APPLICATION NUMBER: US/10/227,565  
; CURRENT FILING DATE: 2002-08-26  
; NUMBER OF SEQ ID NOS: 64158  
; SOFTWARE: Proprietary  
; SEQ ID NO 61140  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.  
; FEATURE:  
; LOCATION: (5963161)...(5963177)  
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 6548  
US-10-227-565-61140

Query Match 80.0%; Score 14.4; DB 48; Length 17;  
Best Local Similarity 93.8%; Pred. No. 8.9e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGAGGGGCTGGAA 18  
|||||  
Db 17 GGAGGAGGGGCTGGAA 2  
|||||

RESULT 9

US-10-310-188-84932  
; Sequence 84932, Application US/10310188

; GENERAL INFORMATION:  
; APPLICANT: RosettaGenomics  
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE  
; FILE REFERENCE: 47487  
; CURRENT APPLICATION NUMBER: US/10/310,188  
; CURRENT FILING DATE: 2002-12-19  
; NUMBER OF SEQ ID NOS: 86841  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 84932  
; LENGTH: 17  
; TYPE: DNA

```

; ORGANISM: Homo sapiens
US-10-310-188-84932

Query Match      80.0%; Score 14.4; DB 50; Length 17;
Best Local Similarity 93.8%; Pred. No. 8.9e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTGG 16
    |||||
Db 2 GGGGAGGAGGGGCTGG 17

RESULT 10
US-10-367-832A-61140/C
; Sequence 61140, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 61140
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (5963161)...(5963177)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 65484
US-10-367-832A-61140

Query Match      80.0%; Score 14.4; DB 51; Length 17;
Best Local Similarity 93.8%; Pred. No. 8.9e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGAGGGGCTGGAA 18
    |||||
Db 17 GGAGGAGGGGCTGGAA 2

RESULT 11
US-10-310-188-24767
; Sequence 24767, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGemonics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24767
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-24767

Query Match      80.0%; Score 14.4; DB 50; Length 18;
Best Local Similarity 93.8%; Pred. No. 8.9e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTGG 16
    |||||
Db 1 GGGGAGGAGGGGCTGG 16

RESULT 12
US-10-310-188-61077
; Sequence 61077, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGemonics
```

```

; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61077
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-61077

Query Match      80.0%; Score 14.4; DB 50; Length 18;
Best Local Similarity 93.8%; Pred. No. 8.9e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTGG 16
    |||||
Db 1 GGGGAGGAGGGGCTGG 16

RESULT 13
US-10-310-188-61084
; Sequence 61084, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGemonics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61084
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-61084

Query Match      80.0%; Score 14.4; DB 50; Length 18;
Best Local Similarity 93.8%; Pred. No. 8.9e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTGG 16
    |||||
Db 1 GGGGAGGAGGGGCTGG 16

RESULT 14
US-10-310-188-41819
; Sequence 41819, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGemonics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41819
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-41819

Query Match      80.0%; Score 14.4; DB 50; Length 21;
Best Local Similarity 93.8%; Pred. No. 9e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTGG 16
    |||||
```



Db 1 GGGGAGGAGGGGCTGG 16

RESULT 15

US-10-310-188-41829

; Sequence 41829, Application US/10310188

; GENERAL INFORMATION:

; APPLICANT: RosettaGenomics

; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE

; TITLE OF INVENTION: USES THEREOF

; FILE REFERENCE: 47487

; CURRENT APPLICATION NUMBER: US/10/310,188

; CURRENT FILING DATE: 2002-12-19

; NUMBER OF SEQ ID NOS: 86841

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 41829

; LENGTH: 21

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-310-188-41829

Query Match 80.0%; Score 14.4; DB 50; Length 21;

Best Local Similarity 93.8%; Pred. No. 9e+04;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTGG 16

|||||

Db 3 GGGGAGGAGGGGCTGG 18

Search completed: October 27, 2003, 17:52:52

Job time : 2357.29 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 11:09:34 ; Search time 307.029 Seconds  
(without alignments)  
97.777 Million cell updates/sec

Title: US-09-331-204A-5

Perfect score: 18

Sequence: 1 gggaggaggctggaa 18

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2231628 seqs, 833900706 residues

Total number of hits satisfying chosen parameters: 264402

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents\_NA\_New:\*  
1: /cgn2\_6/ptodata/1/pna/PCT\_NEW\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq:\*  
7: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	15.4	85.6	22	1	PCT-US02-38216-60578
2	14.4	80.0	16	1	PCT-US02-38216-5892
3	14.4	80.0	17	1	PCT-US02-38216-84932
4	14.4	80.0	18	1	PCT-US02-38216-24767
5	14.4	80.0	18	1	PCT-US02-38216-61077
6	14.4	80.0	18	1	PCT-US02-38216-61084
7	14.4	80.0	21	1	PCT-US02-38216-41819
8	14.4	80.0	21	1	PCT-US02-38216-41829
9	14.4	80.0	21	1	PCT-US02-38216-41830
10	14.4	80.0	22	1	PCT-US02-38216-42169
11	14	77.8	20	1	PCT-US02-38216-18119
12	13.8	76.7	21	1	PCT-US02-38216-39028
13	13.8	76.7	22	1	PCT-US02-38216-18209
14	13.4	74.4	18	1	PCT-US02-38216-84403
15	13.4	74.4	19	1	PCT-US02-38216-5724
16	13.4	74.4	20	1	PCT-US02-38216-86072
17	13.4	74.4	21	1	PCT-US02-38216-18091
18	13.2	73.3	20	1	PCT-US02-38216-60622
19	13.2	73.3	20	1	PCT-US02-38216-60794
20	13.2	73.3	22	1	PCT-US02-38216-41728
21	13	72.2	17	1	PCT-US02-38216-60969
22	13	72.2	18	1	PCT-US02-38216-9439
23	13	72.2	18	1	PCT-US02-38216-17023
24	13	72.2	18	1	PCT-US02-38216-58464
25	13	72.2	19	1	PCT-US02-38216-61056
26	13	72.2	19	1	PCT-US02-38216-61129

27	13	72.2	20	1	PCT-US02-38216-60580	Sequence 60580, A
28	13	72.2	22	1	PCT-US02-38216-10450	Sequence 10450, A
c 29	12.8	71.1	17	1	PCT-US02-38216-5934	Sequence 5934, Ap
30	12.8	71.1	17	6	US-10-271-602B-105	Sequence 105, App
c 31	12.8	71.1	18	1	PCT-US02-38216-6031	Sequence 6031, Ap
c 32	12.8	71.1	18	1	PCT-US02-38216-6080	Sequence 6080, Ap
c 33	12.8	71.1	18	1	PCT-US02-38216-6352	Sequence 6352, Ap
c 34	12.8	71.1	18	1	PCT-US02-38216-6445	Sequence 6445, Ap
35	12.8	71.1	18	1	PCT-US02-38216-9770	Sequence 9770, Ap
36	12.8	71.1	18	1	PCT-US02-38216-39006	Sequence 39006, A
37	12.8	71.1	18	1	PCT-US02-38216-39123	Sequence 39123, A
c 38	12.8	71.1	19	1	PCT-US02-38216-32501	Sequence 32501, A
39	12.8	71.1	19	1	PCT-US02-38216-38922	Sequence 38922, A
40	12.8	71.1	19	1	PCT-US02-38216-41632	Sequence 41632, A
41	12.8	71.1	19	1	PCT-US02-38216-42189	Sequence 42189, A
42	12.8	71.1	19	1	PCT-US02-38216-58264	Sequence 58264, A
43	12.8	71.1	19	1	PCT-US02-38216-60897	Sequence 60897, A
44	12.8	71.1	20	1	PCT-US02-38216-41804	Sequence 41804, A
45	12.8	71.1	20	1	PCT-US02-38216-48851	Sequence 48851, A

ALIGNMENTS

RESULT 1  
PCT-US02-38216-60578  
; Sequence 60578, Application PC/TUS0238216  
; GENERAL INFORMATION:  
; APPLICANT: Rosetta Genomics LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
; TITLE OF INVENTION: GENES AND USES THEREOF  
; FILE REFERENCE: 55002  
; CURRENT APPLICATION NUMBER: PCT/US02/38216  
; CURRENT FILING DATE: 2002-11-12  
; NUMBER OF SEQ ID NOS: 86841  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 60578  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US02-38216-60578

Query Match 85.6%; Score 15.4; DB 1; Length 22;  
Best Local Similarity 94.1%; Pred. No. 4.4e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGAGGAGGGGCTGGA 17  
| | | | | | | | | | | | | | | | | | | |  
Db 1 GGGAGGAGGGGCTGGA 17

RESULT 2  
PCT-US02-38216-5892/c  
; Sequence 5892, Application PC/TUS0238216  
; GENERAL INFORMATION:  
; APPLICANT: Rosetta Genomics LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
; TITLE OF INVENTION: GENES AND USES THEREOF  
; FILE REFERENCE: 55002  
; CURRENT APPLICATION NUMBER: PCT/US02/38216  
; CURRENT FILING DATE: 2002-11-12  
; NUMBER OF SEQ ID NOS: 86841  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5892  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US02-38216-5892

Query Match 80.0%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 1.1e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGAGGGGCTGGAA 18  
| | | | | | | | | | | | | | | |  
Db 16 GGAGGAGGGGCTGGCA 1

RESULT 3  
PCT-US02-38216-84932  
; Sequence 84932, Application PC/TUS0238216  
; GENERAL INFORMATION:  
; APPLICANT: Rosetta Genomics LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
; TITLE OF INVENTION: GENES AND USES THEREOF  
; FILE REFERENCE: 55002  
; CURRENT APPLICATION NUMBER: PCT/US02/38216  
; CURRENT FILING DATE: 2002-11-12  
; NUMBER OF SEQ ID NOS: 86841  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 84932  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US02-38216-84932

Query Match 80.0%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1.1e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTGG 16  
| | | | | | | | | | | | | | | |  
Db 2 GGGGAGGAGGGGCTGG 17

RESULT 4  
PCT-US02-38216-24767  
; Sequence 24767, Application PC/TUS0238216  
; GENERAL INFORMATION:  
; APPLICANT: Rosetta Genomics LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
; TITLE OF INVENTION: GENES AND USES THEREOF  
; FILE REFERENCE: 55002  
; CURRENT APPLICATION NUMBER: PCT/US02/38216  
; CURRENT FILING DATE: 2002-11-12  
; NUMBER OF SEQ ID NOS: 86841  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 24767  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US02-38216-24767

Query Match 80.0%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 1.1e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTGG 16  
| | | | | | | | | | | | | | | |  
Db 1 GGGCAGGAGGGGCTGG 16

RESULT 5  
PCT-US02-38216-61077  
; Sequence 61077, Application PC/TUS0238216  
; GENERAL INFORMATION:  
; APPLICANT: Rosetta Genomics LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
; TITLE OF INVENTION: GENES AND USES THEREOF  
; FILE REFERENCE: 55002  
; CURRENT APPLICATION NUMBER: PCT/US02/38216  
; CURRENT FILING DATE: 2002-11-12  
; NUMBER OF SEQ ID NOS: 86841  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 61077  
; LENGTH: 18

; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US02-38216-61077

Query Match 80.0%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 1.1e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTGG 16  
| | | | | | | | | | | | | | | |  
Db 1 GGGGAGGAGGGGCTGG 16

RESULT 6  
PCT-US02-38216-61084  
; Sequence 61084, Application PC/TUS0238216  
; GENERAL INFORMATION:  
; APPLICANT: Rosetta Genomics LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
; TITLE OF INVENTION: GENES AND USES THEREOF  
; FILE REFERENCE: 55002  
; CURRENT APPLICATION NUMBER: PCT/US02/38216  
; CURRENT FILING DATE: 2002-11-12  
; NUMBER OF SEQ ID NOS: 86841  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 61084  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US02-38216-61084

Query Match 80.0%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 1.1e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTGG 16  
| | | | | | | | | | | | | | | |  
Db 1 GGGGAGGAGGGGCTGG 16

RESULT 7  
PCT-US02-38216-41819  
; Sequence 41819, Application PC/TUS0238216  
; GENERAL INFORMATION:  
; APPLICANT: Rosetta Genomics LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
; TITLE OF INVENTION: GENES AND USES THEREOF  
; FILE REFERENCE: 55002  
; CURRENT APPLICATION NUMBER: PCT/US02/38216  
; CURRENT FILING DATE: 2002-11-12  
; NUMBER OF SEQ ID NOS: 86841  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 41819  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US02-38216-41819

Query Match 80.0%; Score 14.4; DB 1; Length 21;  
Best Local Similarity 93.8%; Pred. No. 1.1e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTGG 16  
| | | | | | | | | | | | | | | |  
Db 1 GGGGAGGAGGGGCTGG 16

RESULT 8  
PCT-US02-38216-41829  
; Sequence 41829, Application PC/TUS0238216  
; GENERAL INFORMATION:  
; APPLICANT: Rosetta Genomics LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY

; TITLE OF INVENTION: GENES AND USES THEREOF  
; FILE REFERENCE: 55002  
; CURRENT APPLICATION NUMBER: PCT/US02/38216  
; CURRENT FILING DATE: 2002-11-12  
; NUMBER OF SEQ ID NOS: 86841  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 41829  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US02-38216-41829

Query Match 80.0%; Score 14.4; DB 1; Length 21;  
Best Local Similarity 93.8%; Pred. No. 1e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGAGGAGGGGCTGG 16  
| | | | | | | | | |  
Db 3 GGGAGGTGGGCTGG 18

RESULT 9  
PCT-US02-38216-41830

; Sequence 41830, Application PC/TUS0238216  
; GENERAL INFORMATION:  
; APPLICANT: Rosetta Genomics LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
; FILE REFERENCE: 55002  
; CURRENT APPLICATION NUMBER: PCT/US02/38216  
; CURRENT FILING DATE: 2002-11-12  
; NUMBER OF SEQ ID NOS: 86841  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 41830  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US02-38216-41830

Query Match 80.0%; Score 14.4; DB 1; Length 21;  
Best Local Similarity 93.8%; Pred. No. 1e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGAGGAGGGGCTGG 16  
| | | | | | | | | |  
Db 6 GGGTGGAGGGGCTGG 21

RESULT 10  
PCT-US02-38216-42169

; Sequence 42169, Application PC/TUS0238216  
; GENERAL INFORMATION:  
; APPLICANT: Rosetta Genomics LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
; FILE REFERENCE: 55002  
; CURRENT APPLICATION NUMBER: PCT/US02/38216  
; CURRENT FILING DATE: 2002-11-12  
; NUMBER OF SEQ ID NOS: 86841  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 42169  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US02-38216-42169

Query Match 80.0%; Score 14.4; DB 1; Length 22;  
Best Local Similarity 93.8%; Pred. No. 1e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGAGGAGGGGCTGG 16  
| | | | | | | | | |  
Db 6 GGGAGGAGGGGCTGG 21

RESULT 11  
PCT-US02-38216-18119

; Sequence 18119, Application PC/TUS0238216  
; GENERAL INFORMATION:  
; APPLICANT: Rosetta Genomics LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
; FILE REFERENCE: 55002  
; CURRENT APPLICATION NUMBER: PCT/US02/38216  
; CURRENT FILING DATE: 2002-11-12  
; NUMBER OF SEQ ID NOS: 86841  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 18119  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US02-38216-18119

Query Match 77.8%; Score 14; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGAGGAGGGGCTGG 16  
| | | | | | | | | |  
Db 1 GGAGGAGGGGCTGG 14

RESULT 12

PCT-US02-38216-39028  
; Sequence 39028, Application PC/TUS0238216  
; GENERAL INFORMATION:  
; APPLICANT: Rosetta Genomics LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
; FILE REFERENCE: 55002  
; CURRENT APPLICATION NUMBER: PCT/US02/38216  
; CURRENT FILING DATE: 2002-11-12  
; NUMBER OF SEQ ID NOS: 86841  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 39028  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US02-38216-39028

Query Match 76.7%; Score 13.8; DB 1; Length 21;  
Best Local Similarity 88.2%; Pred. No. 1.8e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGAGGAGGGGCTGGA 17  
| | | | | | | | | |  
Db 5 GAGGAGGAGGGGATGGA 21

RESULT 13

PCT-US02-38216-18209  
; Sequence 18209, Application PC/TUS0238216  
; GENERAL INFORMATION:  
; APPLICANT: Rosetta Genomics LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
; FILE REFERENCE: 55002  
; CURRENT APPLICATION NUMBER: PCT/US02/38216  
; CURRENT FILING DATE: 2002-11-12  
; NUMBER OF SEQ ID NOS: 86841  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 18209  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US02-38216-18209

Query Match 76.7%; Score 13.8; DB 1; Length 22;  
 Best Local Similarity 88.2%; Pred. No. 1.8e+04;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTGGA 17  
 |||||  
 Db 3 GGGGAGGAGGGGCTGGA 19

RESULT 14  
 PCT-US02-38216-84403/c  
 ; Sequence 84403, Application PC/TUS0238216  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosetta Genomics LTD  
 ; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
 ; TITLE OF INVENTION: GENES AND USES THEREOF  
 ; FILE REFERENCE: 55002  
 ; CURRENT APPLICATION NUMBER: PCT/US02/38216  
 ; CURRENT FILING DATE: 2002-11-12  
 ; NUMBER OF SEQ ID NOS: 86841  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 84403  
 ; LENGTH: 18  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 PCT-US02-38216-84403

Query Match 74.4%; Score 13.4; DB 1; Length 18;  
 Best Local Similarity 93.3%; Pred. No. 2.5e+04;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGAGGGGCTGGA 17  
 |||||  
 Db 18 GGCGGAGGGGCTGGA 4

RESULT 15  
 PCT-US02-38216-5724  
 ; Sequence 5724, Application PC/TUS0238216  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosetta Genomics LTD  
 ; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
 ; TITLE OF INVENTION: GENES AND USES THEREOF  
 ; FILE REFERENCE: 55002  
 ; CURRENT APPLICATION NUMBER: PCT/US02/38216  
 ; CURRENT FILING DATE: 2002-11-12  
 ; NUMBER OF SEQ ID NOS: 86841  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 5724  
 ; LENGTH: 19  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 PCT-US02-38216-5724

Query Match 74.4%; Score 13.4; DB 1; Length 19;  
 Best Local Similarity 93.3%; Pred. No. 2.5e+04;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGAGGGGCTGGA 17  
 |||||  
 Db 1 GGAGGAGGGGCTGGA 15

Search completed: October 27, 2003, 18:22:55  
 Job time : 307.029 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:29 ; Search time 438.8 Seconds  
(without alignments)  
1957.844 Million cell updates/sec

Title: US-09-331-204A-6  
Perfect score: 21  
Sequence: 1 ggggtggaggggggtggtggg 21

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 681044

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:

- 1: gb\_ba:\*
- 2: gb\_htg:\*
- 3: gb\_in:\*
- 4: gb\_cm:\*
- 5: gb\_ov:\*
- 6: gb\_pat:\*
- 7: gb\_ph:\*
- 8: gb\_pl:\*
- 9: gb\_pr:\*
- 10: gb\_ro:\*
- 11: gb\_sts:\*
- 12: gb\_sy:\*
- 13: gb\_un:\*
- 14: gb\_vi:\*
- 15: em\_ba:\*
- 16: em\_fun:\*
- 17: em\_hum:\*
- 18: em\_in:\*
- 19: em\_mu:\*
- 20: em\_om:\*
- 21: em\_or:\*
- 22: em\_ov:\*
- 23: em\_pat:\*
- 24: em\_ph:\*
- 25: em\_pl:\*
- 26: em\_ro:\*
- 27: em\_sts:\*
- 28: em\_un:\*
- 29: em\_vi:\*
- 30: em\_htg\_hum:\*
- 31: em\_htg\_inv:\*
- 32: em\_htg\_other:\*
- 33: em\_htg\_mus:\*
- 34: em\_htg\_pln:\*
- 35: em\_htg\_rod:\*
- 36: em\_htg\_mam:\*
- 37: em\_htg\_vrt:\*
- 38: em\_sy:\*
- 39: em\_htgo\_hum:\*
- 40: em\_htgo\_mus:\*
- 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	18	85.7	18	6	AX023402	AX023402 Sequence
2	18	85.7	18	6	AX023427	AX023427 Sequence
3	14.2	67.6	20	6	AR078333	AR078333 Sequence
4	14.2	67.6	20	6	AR173053	AR173053 Sequence
5	14.2	67.6	21	6	AX384817	AX384817 Sequence
6	14	66.7	18	6	AX705574	AX705574 Sequence
7	14	66.7	18	6	AX705576	AX705576 Sequence
8	13.6	64.8	20	6	AR148843	AR148843 Sequence
9	13.2	62.9	20	6	AR092032	AR092032 Sequence
10	13.2	62.9	20	6	AR112167	AR112167 Sequence
11	13.2	62.9	20	6	AR149209	AR149209 Sequence
12	13.2	62.9	20	6	AR297674	AR297674 Sequence
13	13	61.9	21	6	AR084522	AR084522 Sequence
14	13	61.9	21	6	AR084523	AR084523 Sequence
15	13	61.9	21	6	AR084559	AR084559 Sequence
16	13	61.9	21	6	AR084587	AR084587 Sequence
17	13	61.9	21	6	AX023407	AX023407 Sequence
18	13	61.9	21	6	I21020	I21020 Sequence 3
19	13	61.9	22	6	AR074228	AR074228 Sequence
20	13	61.9	22	6	AR074236	AR074236 Sequence
21	13	61.9	22	6	AR074302	AR074302 Sequence
22	13	61.9	22	6	AR074309	AR074309 Sequence
23	13	61.9	22	6	AX032590	AX032590 Sequence
24	13	61.9	22	6	AX032598	AX032598 Sequence
25	13	61.9	22	6	AX032664	AX032664 Sequence
26	13	61.9	22	6	AX032671	AX032671 Sequence
27	12.8	61.0	18	6	AR168831	AR168831 Sequence
28	12.8	61.0	18	6	AR200300	AR200300 Sequence
29	12.8	61.0	18	6	AR262431	AR262431 Sequence
30	12.8	61.0	18	6	AX233412	AX233412 Sequence
31	12.8	61.0	18	6	E04543	E04543 linker. 9/1
32	12.8	61.0	19	6	AX659401	AX659401 Sequence
33	12.8	61.0	20	6	AR015996	AR015996 Sequence
34	12.8	61.0	20	6	AR082037	AR082037 Sequence
35	12.8	61.0	20	6	AR126606	AR126606 Sequence
36	12.8	61.0	20	6	AR167146	AR167146 Sequence
37	12.8	61.0	20	6	AR167147	AR167147 Sequence
38	12.8	61.0	21	6	A20477	A20477 oligonucleo
39	12.8	61.0	21	6	A28676	A28676 dsRNA with
40	12.8	61.0	21	6	AR061827	AR061827 Sequence
41	12.8	61.0	21	6	AR252818	AR252818 Sequence
42	12.8	61.0	22	6	BD182437	BD182437 Human art
43	12.8	61.0	22	6	E38866	E38866 Chimeric an
44	12.8	61.0	22	6	E63496	E63496 Non-human a
45	12.6	60.0	19	6	AR128076	AR128076 Sequence

ALIGNMENTS

RESULT 1  
AX023402  
LOCUS AX023402 18 bp DNA linear PAT 15-SEP-2000  
DEFINITION Sequence 17 from Patent WO0014217.  
ACCESSION AX023402  
VERSION AX023402.1 GI:10183802  
KEYWORDS .  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE 1  
AUTHORS Lipford,G.B., Heeg,K. and Wagner,H.  
TITLE G-motif oligonucleotides and uses thereof  
JOURNAL Patent: WO 0014217-A 17 16-MAR-2000;  
LIPFORD GRAYSON B (DE) ; HEEG KLAUS (DE) ; WAGNER HERMANN (DE) ;

CPG IMMUNOPHARMACEUTICALS GMBH (DE)

FEATURES  
source  
1. .18  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="synthetic, no natural origin"  
BASE COUNT 1 a 0 c 13 g 4 t  
ORIGIN

Query Match 85.7%; Score 18; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.9e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGGAGGGGGTGGTGGG 21  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 TTGGAGGGGGTGGTGGG 18

RESULT 2  
AX023427/c  
LOCUS AX023427 18 bp DNA linear PAT 15-SEP-2000  
DEFINITION Sequence 42 from Patent WO0014217.  
ACCESSION AX023427  
VERSION AX023427.1 GI:10183827  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1  
AUTHORS Lipford,G.B., Heeg,K. and Wagner,H.  
TITLE G-motif oligonucleotides and uses thereof  
JOURNAL Patent: WO 0014217-A 42 16-MAR-2000;  
LIPFORD GRAYSON B (DE); HEEG KLAUS (DE); WAGNER HERMANN (DE);  
CPG IMMUNOPHARMACEUTICALS GMBH (DE)

FEATURES  
source  
1. .18  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="synthetic, no natural origin"  
BASE COUNT 4 a 13 c 0 g 1 t  
ORIGIN

Query Match 85.7%; Score 18; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.9e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGGAGGGGGTGGTGGG 21  
| | | | | | | | | | | | | | | | | | | | | |  
Db 18 TTGGAGGGGGTGGTGGG 1

RESULT 3  
AR078333  
LOCUS AR078333 20 bp DNA linear PAT 31-AUG-2000  
DEFINITION Sequence 2 from patent US 5962426.  
ACCESSION AR078333  
VERSION AR078333.1 GI:10005079  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)  
AUTHORS Glazer,P.M.  
TITLE Triple-helix forming oligonucleotides for targeted mutagenesis  
JOURNAL Patent: US 5962426-A 2 05-OCT-1999;  
FEATURES  
source  
1. .20  
/organism="unknown"  
BASE COUNT 3 a 0 c 15 g 2 t  
ORIGIN

Query Match 67.6%; Score 14.2; DB 6; Length 20;  
Best Local Similarity 84.2%; Pred. No. 2.3e+05;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 GGTGGAGGGGGTGGTGGG 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 2 GGAAGGGGGGGTGGTGGG 20

RESULT 4  
AR173053  
LOCUS AR173053 20 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 2 from patent US 6303376.  
ACCESSION AR173053  
VERSION AR173053.1 GI:17912544  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)  
AUTHORS Glazer,P.M.  
TITLE Methods of targeted mutagenesis using triple-helix forming oligonucleotides  
JOURNAL Patent: US 6303376-A 2 16-OCT-2001;  
FEATURES  
source  
1. .20  
/organism="unknown"  
BASE COUNT 3 a 0 c 15 g 2 t  
ORIGIN

Query Match 67.6%; Score 14.2; DB 6; Length 20;  
Best Local Similarity 84.2%; Pred. No. 2.3e+05;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 GGTGGAGGGGGTGGTGGG 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 2 GGAAGGGGGGGTGGTGGG 20

RESULT 5  
AX384817  
LOCUS AX384817 21 bp DNA linear PAT 19-MAR-2002  
DEFINITION Sequence 17 from Patent WO0210452.  
ACCESSION AX384817  
VERSION AX384817.1 GI:19577951  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1  
AUTHORS Chang,C.  
TITLE Methods and compositions for predicting prostate cancer  
JOURNAL Patent: WO 0210452-A 17 07-FEB-2002;  
University of Rochester (US)  
FEATURES  
source  
1. .21  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Sequence can be repeated one or more times"  
BASE COUNT 0 a 1 c 15 g 5 t  
ORIGIN

Query Match 67.6%; Score 14.2; DB 6; Length 21;  
Best Local Similarity 84.2%; Pred. No. 2.3e+05;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GGGTTGGAGGGGGTGGTGG 19  
| | | | | | | | | | | | | | | | | | | | | |  
Db 2 GTGTGGTGGGGGGTGGTGG 20

RESULT 6

AX705574  
LOCUS AX705574 18 bp DNA linear PAT 04-APR-2003  
DEFINITION Sequence 243 from Patent WO03014388.  
ACCESSION AX705574  
VERSION AX705574.1 GI:29562239  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 Distler,J., Model,F. and Taubert,H.  
AUTHORS Method and nucleic acids for the analysis of colon cancer  
TITLE Patent: WO 03014388-A 243 20-FEB-2003;  
JOURNAL Epigenomics AG (DE)  
FEATURES Location/Qualifiers  
source 1..18  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Detection oligonucleotide for p16"  
BASE COUNT 3 a 0 c 11 g 4 t  
ORIGIN  
Query Match 66.7%; Score 14; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGTTGGAGGGGGT 14  
Db 5 GGGTTGGAGGGGGT 18  
RESULT 7  
AX705576/c  
LOCUS AX705576 18 bp DNA linear PAT 04-APR-2003  
DEFINITION Sequence 245 from Patent WO03014388.  
ACCESSION AX705576  
VERSION AX705576.1 GI:29562241  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 Distler,J., Model,F. and Taubert,H.  
AUTHORS Method and nucleic acids for the analysis of colon cancer  
TITLE Patent: WO 03014388-A 245 20-FEB-2003;  
JOURNAL Epigenomics AG (DE)  
FEATURES Location/Qualifiers  
source 1..18  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Detection oligonucleotide for p16"  
BASE COUNT 4 a 11 c 0 g 3 t  
ORIGIN  
Query Match 66.7%; Score 14; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGTTGGAGGGGGT 14  
Db 14 GGGTTGGAGGGGGT 1  
RESULT 8  
ARI48843  
LOCUS ARI48843 20 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 204 from patent US 6225451.  
ACCESSION ARI48843  
VERSION ARI48843.1 GI:15112933  
KEYWORDS  
SOURCE Unknown.

ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Ballinger,D.G., Ding,W., Wagner,S. and Hess,M.A.  
TITLE Chromosome 11-linked coronary heart disease susceptibility gene  
CHD1  
JOURNAL Patent: US 6225451-A 204 01-MAY-2001;  
FEATURES Location/Qualifiers  
source 1..20  
/organism="unknown"  
BASE COUNT 0 a 1 c 17 g 2 t  
ORIGIN  
Query Match 64.8%; Score 13.6; DB 6; Length 20;  
Best Local Similarity 80.0%; Pred. No. 4e+05;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 GGGTTGGAGGGGGTGGTGGG 20  
Db 1 GGGTGGGGCGGGTGGGGGG 20  
RESULT 9  
AR092032/c  
LOCUS AR092032 20 bp DNA linear PAT 08-SEP-2000  
DEFINITION Sequence 56 from patent US 5998141.  
ACCESSION AR092032  
VERSION AR092032.1 GI:10018786  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Acton,S.Laurene.  
TITLE Intronic and polymorphic SR-BI nucleic acids and uses therefor  
JOURNAL Patent: US 5998141-A 56 07-DEC-1999;  
FEATURES Location/Qualifiers  
source 1..20  
/organism="unknown"  
BASE COUNT 4 a 13 c 1 g 2 t  
ORIGIN  
Query Match 62.9%; Score 13.2; DB 6; Length 20;  
Best Local Similarity 83.3%; Pred. No. 5.8e+05;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 3 GTTGGAGGGGGTGGTGGG 20  
Db 20 GTGGGCTGGGGTGGTGGG 3  
RESULT 10  
ARI12167/c  
LOCUS ARI12167 20 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 56 from patent US 6130041.  
ACCESSION ARI12167  
VERSION ARI12167.1 GI:14092067  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Acton,S.Laurene.  
TITLE Human intronic and polymorphic SR-BI nucleic acids and uses therefor  
JOURNAL Patent: US 6130041-A 56 10-OCT-2000;  
FEATURES Location/Qualifiers  
source 1..20  
/organism="unknown"  
BASE COUNT 4 a 13 c 1 g 2 t  
ORIGIN  
Query Match 62.9%; Score 13.2; DB 6; Length 20;



Best Local Similarity 83.3%; Pred. No. 5.8e+05;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GTTGGAGGGGGTGGTGGG 20  
||| ||||| ||||| |||||  
Db 20 GTGGGCTGGGTGGTGGG 3

RESULT 11  
AR149209/c  
LOCUS AR149209 20 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 56 from patent US 6228581.  
ACCESSION AR149209  
VERSION AR149209.1 GI:15113800  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Acton, S.L. and Ordovas, J.M.  
TITLE Human intronic and polymorphic SR-BI nucleic acids and uses  
therefor  
JOURNAL Patent: US 6228581-A 56 08-MAY-2001;  
FEATURES Location/Qualifiers  
source  
1. .20  
/organism="unknown"  
BASE COUNT 4 a 13 c 1 g 2 t  
ORIGIN

Query Match 62.9%; Score 13.2; DB 6; Length 20;  
Best Local Similarity 83.3%; Pred. No. 5.8e+05;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GTTGGAGGGGGTGGTGGG 20  
||| ||||| ||||| |||||  
Db 20 GTGGGCTGGGTGGTGGG 3

RESULT 12  
AR297674/c  
LOCUS AR297674 20 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 9409 from patent US 6537751.  
ACCESSION AR297674  
VERSION AR297674.1 GI:31684958  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Cohen, D.; Chumakov, I. and Blumenfeld, M.  
TITLE Biallelic markers for use in constructing a high density  
disequilibrium map of the human genome  
JOURNAL Patent: US 6537751-A 9409 25-MAR-2003;  
FEATURES Location/Qualifiers  
source  
1. .20  
/organism="unknown"  
BASE COUNT 4 a 11 c 0 g 5 t  
ORIGIN

Query Match 62.9%; Score 13.2; DB 6; Length 20;  
Best Local Similarity 83.3%; Pred. No. 5.8e+05;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTTGGAGGGGGTGGTG 18  
| ||||| ||||| |||||  
Db 20 GAGTTGGAGGGGGGAGATG 3

RESULT 13  
AR084522/c  
LOCUS AR084522 21 bp DNA linear PAT 01-SEP-2000  
DEFINITION Sequence 11 from patent US 5981185.  
ACCESSION AR084522

VERSION AR084522.1 GI:10011293  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Matson, R.S., Coassin, P.J., Rampal, J.B. and Caskey, C.Thomas.  
TITLE Oligonucleotide repeat arrays  
JOURNAL Patent: US 5981185-A 11 09-NOV-1999;  
FEATURES Location/Qualifiers  
source  
1. .21  
/organism="unknown"  
BASE COUNT 0 a 21 c 0 g 0 t  
ORIGIN

Query Match 61.9%; Score 13; DB 6; Length 21;  
Best Local Similarity 76.2%; Pred. No. 6.9e+05;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGTTGGAGGGGGTGGTGGG 21  
||| ||||| ||||| |||||  
Db 21 GGGGGGGGGGGGGGGGGGG 1

RESULT 14  
AR084523  
LOCUS AR084523 21 bp DNA linear PAT 01-SEP-2000  
DEFINITION Sequence 12 from patent US 5981185.  
ACCESSION AR084523  
VERSION AR084523.1 GI:10011294  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Matson, R.S., Coassin, P.J., Rampal, J.B. and Caskey, C.Thomas.  
TITLE Oligonucleotide repeat arrays  
JOURNAL Patent: US 5981185-A 12 09-NOV-1999;  
FEATURES Location/Qualifiers  
source  
1. .21  
/organism="unknown"  
BASE COUNT 0 a 0 c 21 g 0 t  
ORIGIN

Query Match 61.9%; Score 13; DB 6; Length 21;  
Best Local Similarity 76.2%; Pred. No. 6.9e+05;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGTTGGAGGGGGTGGTGGG 21  
||| ||||| ||||| |||||  
Db 1 GGGGGGGGGGGGGGGGGGG 21

RESULT 15  
AR084559/c  
LOCUS AR084559 21 bp DNA linear PAT 01-SEP-2000  
DEFINITION Sequence 48 from patent US 5981185.  
ACCESSION AR084559  
VERSION AR084559.1 GI:10011330  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Matson, R.S., Coassin, P.J., Rampal, J.B. and Caskey, C.Thomas.  
TITLE Oligonucleotide repeat arrays  
JOURNAL Patent: US 5981185-A 48 09-NOV-1999;  
FEATURES Location/Qualifiers  
source  
1. .21  
/organism="unknown"  
BASE COUNT 7 a 14 c 0 g 0 t  
ORIGIN

Query Match 61.9%; Score 13; DB 6; Length 21;  
Best Local Similarity 76.2%; Pred. No. 6.9e+05;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GCGTTGGAGCGGTTGGTGGGG 21  
| | | | | | | | | | | | | | | | | | |  
Db 21 GTGGTGGTGGTGGTGGTGGTG 1

Search completed: October 27, 2003, 11:09:25  
Job time : 439.8 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:29 ; Search time 189 Seconds  
(without alignments)  
299.938 Million cell updates/sec

Title: US-09-331-204A-6

Perfect score: 21

Sequence: 1 ggggttgagggtgtgtgtggg 21

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 1643890

Minimum DB seq length: 0

Maximum DB seq length: 22

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_19Jun03.\*

- 1: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.\*
- 2: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.\*
- 3: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.\*
- 4: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.\*
- 5: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.\*
- 6: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.\*
- 7: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.\*
- 8: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.\*
- 9: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.\*
- 10: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.\*
- 11: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.\*
- 12: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.\*
- 13: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.\*
- 14: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.\*
- 15: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.\*
- 16: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.\*
- 17: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.\*
- 18: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.\*
- 19: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.\*
- 20: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.\*
- 21: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.\*
- 22: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.\*
- 23: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.\*
- 24: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.\*
- 25: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	21	17 AAT36197	Triplex forming ol
2	21	100.0	21	20 AAX90329	CD28 inhibiting ph
3	21	100.0	21	20 AAX90291	CD28 inhibition ol
4	18	85.7	18	17 AAT36196	Triplex forming ol
5	18	85.7	18	20 AAX90328	CD28 inhibiting ph
6	18	85.7	18	20 AAX90290	CD28 inhibition ol
7	18	85.7	18	21 AAZ99625	Nucleotide sequenc
8	18	85.7	18	21 AAZ99650	Nucleotide sequenc

9	16.4	78.1	18	17 AAT36243	CD28 expression in
10	16.4	78.1	18	20 AAX90336	CD28 inhibiting ph
11	14.8	70.5	18	17 AAT36242	CD28 expression in
12	14.8	70.5	18	17 AAT36244	CD28 expression in
13	14.8	70.5	18	20 AAX90335	CD28 inhibiting ph
14	14.8	70.5	18	20 AAX90337	CD28 inhibiting ph
15	14.2	67.6	20	16 AAQ81074	supF gene triplex
16	14.2	67.6	20	18 AAT70012	Triplex-forming ol
17	14.2	67.6	20	18 AAT47061	Oligonucleotide AG
18	14.2	67.6	21	24 AAD30438	Human androgen rec
19	13.6	64.8	20	20 AAZ27025	Apolipoprotein CII
20	13.6	64.8	22	22 AAF16593	Gastric acid produ
21	13.4	63.8	15	24 AAD25952	ASO probe #5 to de
22	13.4	63.8	20	24 ABK89176	Human jA2F1/jjA21
23	13.2	62.9	20	20 AAX24525	Human SR-BI gene e
24	13.2	62.9	20	20 AAX24617	Human SR-BI gene e
25	13.2	62.9	20	21 AAZ75053	Human biallelic ma
26	13.2	62.9	21	17 AAT35046	Triplex-forming ol
27	13.2	62.9	22	20 AAZ22690	StAR (5' sense) pr
28	13	61.9	15	24 ABL39459	Human ETPB allele-
29	13	61.9	21	14 AAQ50950	Synthetic oligonuc
30	13	61.9	21	21 AAZ99630	Protypic blocking
31	13	61.9	21	24 ABK99296	Hepatitis C virus
32	13	61.9	22	15 AAQ61991	Guanine quartet co
33	13	61.9	22	15 AAQ61998	Guanine quartet co
34	13	61.9	22	15 AAQ61895	HSV replication in
35	13	61.9	22	15 AAQ61903	Peptide nucleic ac
36	13	61.9	22	16 AAQ97987	CD28 expression in
37	12.8	61.0	16	17 AAT36247	CD28 inhibiting ph
38	12.8	61.0	16	20 AAX90340	Human tissue kalli
39	12.8	61.0	17	20 AAV55680	Hammerhead ribozym
40	12.8	61.0	17	21 AAF01954	Human tissue kalli
41	12.8	61.0	17	24 AAL43484	CD28 expression in
42	12.8	61.0	18	17 AAT36245	CD28 expression in
43	12.8	61.0	18	18 AAT51673	Viral integrase in
44	12.8	61.0	18	19 AAX79255	Oligonucleotide #4
45	12.8	61.0	18	20 AAX90338	CD28 inhibiting ph

ALIGNMENTS

RESULT 1

AAT36197

ID AAT36197 standard; DNA; 21 BP.

XX AAT36197;

XX 25-MAR-2003 (updated)

DT 15-APR-1997 (first entry)

XX Triplex forming oligo targetting CD28 5'-UTR (nt 58-78).

XX Reduction; T cell; CD28; gene expression; treatment; immune system;  
KW disorder; graft versus host disease; septic shock; viral disease;  
KW psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;  
KW multiple sclerosis; uveitis; rheumatoid arthritis; 5'-UTR;  
KW systemic lupus erythematosus; inflammatory bowel disease;  
KW triplex forming; oligonucleotide; 5'-untranslated region; ss

OS Synthetic.

XX WO9624380-A1.

XX 15-AUG-1996.

XX 05-FEB-1996; 96WO-US01507.

XX 09-FEB-1995; 95US-0387041.

XX 18-SEP-1995; 95US-0529878.

XX 09-FEB-1995; 95US-0387041.

XX 18-SEP-1995; 95US-0529878.

PA (ICNC ) ICN PHARM INC.  
XX PI Tam RC;  
XX WPI; 1996-384228/38.  
XX Oligo:nucleotide which reduces CD28 gene expression in T cells -  
PT for treating immune system diseases, e.g. graft vs. host disease,  
PT septic shock, psoriasis, etc.  
XX Claim 10; Page 54; 77pp; English.  
XX The present oligonucleotide reduces T cell CD28 gene expression,  
CC useful in the treatment of CD28 mediated diseases, particularly  
CC immune system disorders, e.g. graft versus host disease, septic  
CC shock, viral disease, psoriasis, type I diabetes mellitus,  
CC thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid  
CC arthritis, systemic lupus erythematosus, inflammatory bowel  
CC disease, etc.. Reducing CD28 expression may reduce the effects of  
CC antigenic stimulation of CD28 positive T cells, with a consequent  
CC reduction in cytokine release.  
CC (Updated on 25-MAR-2003 to correct PR field.)  
XX Sequence 21 BP; 1 A; 0 C; 16 G; 4 T; 0 other;  
SQ Query Match 100.0%; Score 21; DB 17; Length 21;  
Best Local Similarity 100.0%; Pred. No. 56;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGTTGAGGGGGTGGTGGGG 21  
Db 1 GGGTTGAGGGGGTGGTGGGG 21  
RESULT 2  
AAX90329  
ID AAX90329 standard; DNA; 21 BP.  
XX AAX90329;  
XX 24-SEP-1999 (first entry)  
XX CD28 inhibiting phosphorothioate oligonucleotide RT04S.  
XX CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;  
KW immune system mediated disease; gamma-interferon; IL-8;  
KW phosphorothioate; ss.  
XX Synthetic.  
XX US5932556-A.  
XX 03-AUG-1999.  
XX 18-SEP-1995; 95US-0529878.  
XX 18-SEP-1995; 95US-0529878.  
XX (TAMR/) TAM R C.  
XX Tam RC;  
XX WPI; 1999-443609/37.  
XX Treatment of immune system-mediated diseases by inhibiting  
PT expression of CD28, IL-2, gamma-interferon or IL-8  
PS Example; Column 21; 45pp; English.  
XX The present invention describes a method for inhibiting the expression  
CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method  
CC comprises subcutaneous administration of an oligonucleotide (OGN).  
CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the

CC method. The OGNs are used for the treatment of immune system-mediated  
CC diseases. The present sequence represents a CD28 inhibiting  
CC phosphorothioate oligonucleotide used in the exemplification of the  
CC present invention.  
XX Sequence 21 BP; 1 A; 0 C; 16 G; 4 T; 0 other;  
SQ Query Match 100.0%; Score 21; DB 20; Length 21;  
Best Local Similarity 100.0%; Pred. No. 56;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGTTGAGGGGGTGGTGGGG 21  
Db 1 GGGTTGAGGGGGTGGTGGGG 21  
RESULT 3  
AAX90291  
ID AAX90291 standard; DNA; 21 BP.  
XX AAX90291;  
AC AAX90291;  
XX 24-SEP-1999 (first entry)  
XX CD28 inhibition oligonucleotide RT04.  
XX CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;  
KW immune system mediated disease; gamma-interferon; IL-8; ss.  
XX Synthetic.  
XX US5932556-A.  
XX 03-AUG-1999.  
XX 18-SEP-1995; 95US-0529878.  
XX 18-SEP-1995; 95US-0529878.  
XX (TAMR/) TAM R C.  
XX Tam RC;  
XX WPI; 1999-443609/37.  
XX Treatment of immune system-mediated diseases by inhibiting  
PT expression of CD28, IL-2, gamma-interferon or IL-8  
PS Claim 6; Column 29; 45pp; English.  
XX The present invention describes a method for inhibiting the expression  
CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method  
CC comprises subcutaneous administration of an oligonucleotide (OGN).  
CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the  
CC method. The OGNs are used for the treatment of immune system-mediated  
CC diseases.  
XX Sequence 21 BP; 1 A; 0 C; 16 G; 4 T; 0 other;  
SQ Query Match 100.0%; Score 21; DB 20; Length 21;  
Best Local Similarity 100.0%; Pred. No. 56;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGTTGAGGGGGTGGTGGGG 21  
Db 1 GGGTTGAGGGGGTGGTGGGG 21  
RESULT 4  
AAT36196  
ID AAT36196 standard; DNA; 18 BP.  
XX AAT36196;  
AC AAT36196;

```
XX 25-MAR-2003 (updated)
DT 15-APR-1997 (first entry)
XX
XX Triplex forming oligo targetting CD28 5'-UTR (nt 58-75).
XX
XX Reduction; T cell; CD28; gene expression; treatment; immune system;
KW disorder; graft versus host disease; septic shock; viral disease;
KW psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;
KW multiple sclerosis; uveitis; rheumatoid arthritis; 5'-UTR;
KW systemic lupus erythematosus; inflammatory bowel disease;
KW triplex forming; oligonucleotide; 5'-untranslated region; ss
XX
OS Synthetic.
XX
XX WO9624380-A1.
PN
XX
XX 15-AUG-1996.
PD
XX
XX 05-FEB-1996; 96WO-US01507.
PF
XX
XX 09-FEB-1995; 95US-0387041.
PR
XX 18-SEP-1995; 95US-0529878.
PR
XX 09-FEB-1995; 95US-0387041.
PR
XX 18-SEP-1995; 95US-0529878.
PR
XX (ICNC ) ICN PHARM INC.
PA
XX
XX Tam RC;
PI
XX
XX WPI; 1996-384228/38.
DR
XX
XX Oligo:nucleotide which reduces CD28 gene expression in T cells -
PT for treating immune system diseases, e.g. graft vs. host disease,
PT septic shock, psoriasis, etc.
XX
XX Claim 9; Page 54; 77pp; English.
PS
XX
XX The present oligonucleotide reduces T cell CD28 gene expression,
CC useful in the treatment of CD28 mediated diseases, particularly
CC immune system disorders, e.g. graft versus host disease, septic
CC shock, viral disease, psoriasis, type I diabetes mellitus,
CC thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid
CC arthritis, systemic lupus erythematosus, inflammatory bowel
CC disease, etc.. Reducing CD28 expression may reduce the effects of
CC antigenic stimulation of CD28 positive T cells, with a consequent
CC reduction in cytokine release.
CC (Updated on 25-MAR-2003 to correct PR field.)
XX
XX Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;
SQ
Query Match 85.7%; Score 18; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 TTGAGGGGGTGGTGGGG 21
Db 1 TTGAGGGGGTGGTGGGG 18
RESULT 5
AAX90328
ID AAX90328 standard; DNA; 18 BP.
XX
XX AAX90328;
AC
XX
XX 24-SEP-1999 (first entry)
DT
XX
XX CD28 inhibiting phosphorothioate oligonucleotide RT03S.
DE
XX
XX CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
KW immune system mediated disease; gamma-interferon; IL-8;
KW phosphorothioate; ss.
```

```
XX Synthetic.
OS
XX US5932556-A.
PN
XX 03-AUG-1999.
PD
XX
XX 18-SEP-1995; 95US-0529878.
PF
XX 18-SEP-1995; 95US-0529878.
PR
XX (TAMR/) TAM R C.
PA
XX
XX Tam RC;
PI
XX
XX WPI; 1999-443609/37.
PN
XX
XX Treatment of immune system-mediated diseases by inhibiting
PT expression of CD28, IL-2, gamma-interferon or IL-8
PT
XX
XX Example; Column 21; 45pp; English.
PS
XX
XX The present invention describes a method for inhibiting the expression
CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method
CC comprises subcutaneous administration of an oligonucleotide (OGN).
CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the
CC method. The OGNs are used for the treatment of immune system-mediated
CC diseases. The present sequence represents a CD28 inhibiting
CC phosphorothioate oligonucleotide used in the exemplification of the
CC present invention.
XX
XX Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;
SQ
Query Match 85.7%; Score 18; DB 20; Length 18;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 TTGAGGGGGTGGTGGGG 21
Db 1 TTGAGGGGGTGGTGGGG 18
RESULT 6
AAX90290
ID AAX90290 standard; DNA; 18 BP.
XX
XX AAX90290;
AC
XX
XX 24-SEP-1999 (first entry)
DT
XX
XX CD28 inhibition oligonucleotide RT03.
DE
XX
XX CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
KW immune system mediated disease; gamma-interferon; IL-8; ss.
KW
XX
XX Synthetic.
OS
XX US5932556-A.
PN
XX
XX 03-AUG-1999.
PD
XX
XX 18-SEP-1995; 95US-0529878.
PF
XX 18-SEP-1995; 95US-0529878.
PR
XX (TAMR/) TAM R C.
PA
XX
XX Tam RC;
PI
XX
XX WPI; 1999-443609/37.
PN
XX
XX Treatment of immune system-mediated diseases by inhibiting
PT expression of CD28, IL-2, gamma-interferon or IL-8
PT
```

XX Claim 5; Column 29; 45pp; English.

XX The present invention describes a method for inhibiting the expression

CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method

CC comprises subcutaneous administration of an oligonucleotide (OGN).

CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the

CC method. The OGNs are used for the treatment of immune system-mediated

CC diseases.

XX Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;

SQ Query Match 85.7%; Score 18; DB 20; Length 18;

Best Local Similarity 100.0%; Pred. No. 7e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGGAGGGGGTGGTGGGG 21

Db 1 TTGGAGGGGGTGGTGGGG 18

RESULT 7

AAX99625

ID AAX99625 standard; DNA; 18 BP.

XX AAX99625;

AC AAX99625;

XX 12-JUL-2000 (first entry)

DT 12-JUL-2000 (first entry)

XX Nucleotide sequence of G-motif oligonucleotide GR1.

DE G-motif oligonucleotide; vaccine; Toxoplasmosis; viral infection;

XX antigen presenting cell activation; natural killer cell; septic shock;

KW cytotoxic T-lymphocyte; inflammation; autoimmune disease;

KW rheumatoid arthritis; Crohn's disease; sarcoidosis; multiple sclerosis;

KW Kawasaki syndrome; graft-versus-host disease; transplant rejection;

KW helper T cell response i-mediated disease; Lyme arthritis;

KW Streptococcal induced arthritis; chronic inflammatory bowel disease;

KW psoriasis vulgaris; experimental allergic encephalomyelitis;

KW insulin-dependent diabetes mellitus; bacterial infection;

KW parasitic infection; Leishmaniasis; spontaneous abortion; tumour; ss.

XX Synthetic.

OS WO200014217-A2.

XX 16-MAR-2000.

PD 03-SEP-1999; 99WO-EP06502.

XX 03-SEP-1998; 98EP-0116652.

PR (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.

XX Wagner H, Lipford GB, Heeg K;

PI WPI; 2000-256970/22.

DR Compositions comprising G-motif oligonucleotides useful for treating

XX e.g. septic shock, rheumatoid arthritis, diabetes and human

PT immunodeficiency virus infections -

XX Example 14; Page 32; 75pp; English.

PS The present sequence represents a G-motif oligonucleotide of the

XX invention. The specification describes compositions comprising G-motif

CC oligonucleotides. The G-motif oligonucleotides inhibit activation of

CC antigen presenting cells by inhibiting the uptake of DNA by a cell, by

CC stimulating natural killer cells, or by co-stimulating cytotoxic

CC T-lymphocytes. The G-motif oligonucleotides may be used for the

CC productions of vaccines for treating septic shock, inflammation,

CC autoimmune diseases (e.g. rheumatoid arthritis, Crohn's disease,

CC sarcoidosis, multiple sclerosis, Kawasaki syndrome, graft-versus-host

CC disease and transplant rejection), helper T cell response i-mediated

CC diseases (e.g. Streptococcal induced arthritis, Lyme arthritis, chronic

CC inflammatory bowel disease, psoriasis vulgaris, experimental allergic

CC encephalomyelitis, and insulin-dependent diabetes mellitus), bacterial

CC infections, parasitic infections (e.g. Leishmaniasis or Toxoplasmosis),

CC viral infections (e.g. Cytomegalovirus and human immunodeficiency virus

CC (HIV)-infections), spontaneous abortions and tumours. They may also be

CC used to induce proliferation of bone marrow cells, especially macrophage

CC precursor cells.

XX Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;

SQ Query Match 85.7%; Score 18; DB 21; Length 18;

Best Local Similarity 100.0%; Pred. No. 7e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGGAGGGGGTGGTGGGG 21

Db 1 TTGGAGGGGGTGGTGGGG 18

RESULT 8

AAX99650/c

ID AAX99650 standard; DNA; 18 BP.

XX AAX99650;

AC AAX99650;

XX 12-JUL-2000 (first entry)

DT 12-JUL-2000 (first entry)

XX Nucleotide sequence of non-G-motif oligonucleotide GRFicomp.

DE G-motif oligonucleotide; vaccine; Toxoplasmosis; viral infection;

XX antigen presenting cell activation; natural killer cell; septic shock;

KW cytotoxic T-lymphocyte; inflammation; autoimmune disease;

KW rheumatoid arthritis; Crohn's disease; sarcoidosis; multiple sclerosis;

KW Kawasaki syndrome; graft-versus-host disease; transplant rejection;

KW helper T cell response i-mediated disease; Lyme arthritis;

KW Streptococcal induced arthritis; chronic inflammatory bowel disease;

KW psoriasis vulgaris; experimental allergic encephalomyelitis;

KW insulin-dependent diabetes mellitus; bacterial infection;

KW parasitic infection; Leishmaniasis; spontaneous abortion; tumour; ss.

XX Synthetic.

OS WO200014217-A2.

XX 16-MAR-2000.

PD 03-SEP-1999; 99WO-EP06502.

XX 03-SEP-1998; 98EP-0116652.

PR (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.

XX Wagner H, Lipford GB, Heeg K;

PI WPI; 2000-256970/22.

DR Compositions comprising G-motif oligonucleotides useful for treating

XX e.g. septic shock, rheumatoid arthritis, diabetes and human

PT immunodeficiency virus infections -

XX Example 14; Page 32; 75pp; English.

PS The present sequence represents a non-G-motif oligonucleotide of the

XX invention. The specification describes compositions comprising G-motif

CC oligonucleotides. The G-motif oligonucleotides inhibit activation of

CC antigen presenting cells by inhibiting the uptake of DNA by a cell, by

CC stimulating natural killer cells, or by co-stimulating cytotoxic

CC T-lymphocytes. The G-motif oligonucleotides may be used for the

CC productions of vaccines for treating septic shock, inflammation,

CC autoimmune diseases (e.g. rheumatoid arthritis, Crohn's disease,

CC sarcoidosis, multiple sclerosis, Kawasaki syndrome, graft-versus-host

CC disease and transplant rejection), helper T cell response 1-mediated  
CC diseases (e.g. Streptococcal induced arthritis, Lyme arthritis, chronic  
CC inflammatory bowel disease, psoriasis vulgaris, experimental allergic  
CC encephalomyelitis, and insulin-dependent diabetes mellitus), bacterial  
CC infections, parasitic infections (e.g. Leishmaniasis or Toxoplasmosis),  
CC viral infections (e.g. Cytomegalovirus and human immunodeficiency virus  
CC (HIV)-infections), spontaneous abortions and tumours. They may also be  
CC used to induce proliferation of bone marrow cells, especially macrophage  
CC precursor cells.  
XX  
SQ Sequence 18 BP; 4 A; 13 C; 0 G; 1 T; 0 other;  
  
Query Match 85.7%; Score 18; DB 21; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 TTGGAGGGGGTGGTGGGG 21  
Db 18 TTGGAGGGGGTGGTGGGG 1  
  
RESULT 9  
AAT36243  
ID AAT36243 standard; DNA; 18 BP.  
XX  
AC AAT36243;  
XX  
DT 25-MAR-2003 (updated)  
DT 16-APR-1997 (first entry)  
XX  
DE CD28 expression inhibiting oligonucleotide, RT09s.  
XX  
KW Reduction; T cell; CD28; gene expression; treatment; immune system;  
KW disorder; graft versus host disease; septic shock; viral disease;  
KW psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;  
KW multiple sclerosis; uveitis; rheumatoid arthritis; interleukin 2;  
KW systemic lupus erythematosus; inflammatory bowel disease;  
KW IL-2; production; antisense; inhibition; ss  
XX  
OS Synthetic.  
XX  
PN WO9624380-A1.  
XX  
PD 15-AUG-1996.  
XX  
PF 05-FEB-1996; 96WO-US01507.  
XX  
PR 09-FEB-1995; 95US-0387041.  
PR 18-SEP-1995; 95US-0529878.  
PR 09-FEB-1995; 95US-0387041.  
PR 18-SEP-1995; 95US-0529878.  
XX  
PA (ICNC ) ICN PHARM INC.  
XX  
PI Tam RC;  
XX  
DR WPI; 1996-384228/38.  
XX  
PT Oligonucleotide which reduces CD28 gene expression in T cells -  
PT for treating immune system diseases, e.g. graft vs. host disease,  
PT septic shock, psoriasis, etc.  
XX  
PS Example 2; Page 45; 77pp; English.  
XX  
CC The present oligonucleotide reduces CD28 dependent interleukin-2  
CC (IL-2) production and T cell CD28 gene expression, useful in the  
CC treatment of CD28 mediated diseases, particularly immune system  
CC disorders, e.g. graft versus host disease, septic shock, viral  
CC disease, psoriasis, type I diabetes mellitus, thyroiditis,  
CC sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis,  
CC systemic lupus erythematosus, inflammatory bowel disease, etc..  
CC Reducing CD28 expression may reduce the effects of antigenic  
CC stimulation of CD28 positive T cells, with a consequent reduction

CC in cytokine release.  
CC (Updated on 25-MAR-2003 to correct PR field.)  
XX Sequence 18 BP; 2 A; 0 C; 13 G; 3 T; 0 other;  
SQ  
Query Match 78.1%; Score 16.4; DB 17; Length 18;  
Best Local Similarity 94.4%; Pred. No. 2.7e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 4 TTGAGGGGGTGGTGGGG 21  
Db 1 TTGAGGGGGAGGTGGGG 18  
  
RESULT 10  
AAX90336  
ID AAX90336 standard; DNA; 18 BP.  
XX  
AC AAX90336;  
XX  
DT 24-SEP-1999 (first entry)  
XX  
DE CD28 inhibiting phosphorothioate oligonucleotide RT09S.  
XX  
KW CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;  
KW immune system mediated disease; gamma-interferon; IL-8;  
KW phosphorothioate; ss.  
XX  
OS Synthetic.  
XX  
PN US5932556-A.  
XX  
PD 03-AUG-1999.  
XX  
PF 18-SEP-1995; 95US-0529878.  
XX  
PR 18-SEP-1995; 95US-0529878.  
XX  
PA (TAMR/) TAM R C.  
XX  
PI Tam RC;  
XX  
PN WPI; 1999-443609/37.  
XX  
PT Treatment of immune system-mediated diseases by inhibiting  
PT expression of CD28, IL-2, gamma-interferon or IL-8  
XX  
PS Example; Column 24; 45pp; English.  
XX  
CC The present invention describes a method for inhibiting the expression  
CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method  
CC comprises subcutaneous administration of an oligonucleotide (OGN).  
CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the  
CC method. The OGNs are used for the treatment of immune system-mediated  
CC diseases. The present sequence represents a CD28 inhibiting  
CC phosphorothioate oligonucleotide used in the exemplification of the  
CC present invention.  
XX  
SQ Sequence 18 BP; 2 A; 0 C; 13 G; 3 T; 0 other;  
  
Query Match 78.1%; Score 16.4; DB 20; Length 18;  
Best Local Similarity 94.4%; Pred. No. 2.7e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 4 TTGAGGGGGTGGTGGGG 21  
Db 1 TTGAGGGGGAGGTGGGG 18  
  
RESULT 11  
AAT36242  
ID AAT36242 standard; DNA; 18 BP.  
XX

AC AAT36242;  
XX  
DT 25-MAR-2003 (updated)  
DT 16-APR-1997 (first entry)  
XX  
DE CD28 expression inhibiting oligonucleotide, RT05s.  
XX  
KW Reduction; T cell; CD28; gene expression; treatment; immune system;  
KW disorder; graft versus host disease; septic shock; viral disease;  
KW psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;  
KW multiple sclerosis; uveitis; rheumatoid arthritis; interleukin 2;  
KW systemic lupus erythematosus; inflammatory bowel disease;  
KW IL-2; production; antisense; inhibition; ss  
XX  
OS Synthetic.  
XX  
PN WO9624380-A1.  
XX  
PD 15-AUG-1996.  
XX  
PF 05-FEB-1996; 95WO-US01507.  
XX  
PR 09-FEB-1995; 95US-0387041.  
PR 18-SEP-1995; 95US-0529878.  
PR 09-FEB-1995; 95US-0387041.  
PR 18-SEP-1995; 95US-0529878.  
XX  
PA (ICNC ) ICN PHARM INC.  
XX  
PI Tam RC;  
XX  
XX WPI; 1996-384228/38.  
DR  
XX Oligo:nucleotide which reduces CD28 gene expression in T cells -  
PT for treating immune system diseases, e.g. graft vs. host disease,  
PT septic shock, psoriasis, etc.  
XX  
PS Example 2; Page 45; 77pp; English.  
XX  
CC The present oligonucleotide reduces CD28 dependent interleukin-2  
CC (IL-2) production and T cell CD28 gene expression, useful in the  
CC treatment of CD28 mediated diseases, particularly immune system  
CC disorders, e.g. graft versus host disease, septic shock, viral  
CC disease, psoriasis, type I diabetes mellitus, thyroiditis,  
CC sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis,  
CC systemic lupus erythematosus, inflammatory bowel disease, etc..  
CC Reducing CD28 expression may reduce the effects of antigenic  
CC stimulation of CD28 positive T cells, with a consequent reduction  
CC in cytokine release.  
CC (Updated on 25-MAR-2003 to correct PR field.)  
XX  
SQ Sequence 18 BP; 3 A; 0 C; 13 G; 2 T; 0 other;  
Query Match 70.5%; Score 14.8; DB 17; Length 18;  
Best Local Similarity 88.9%; Pred. No. 1e+04;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 4 TTGGAGGGGGTGGTGGGG 21  
Db 1 TTGGAGGGGGGAGGAGGGG 18  
RESULT 12  
ID AAT36244  
XX AAT36244 standard; DNA; 18 BP.  
XX  
AC AAT36244;  
XX  
DT 25-MAR-2003 (updated)  
DT 16-APR-1997 (first entry)  
XX  
DE CD28 expression inhibiting oligonucleotide, RT10s.  
XX

KW Reduction; T cell; CD28; gene expression; treatment; immune system;  
KW disorder; graft versus host disease; septic shock; viral disease;  
KW psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;  
KW multiple sclerosis; uveitis; rheumatoid arthritis; interleukin 2;  
KW systemic lupus erythematosus; inflammatory bowel disease;  
KW IL-2; production; antisense; inhibition; ss  
XX  
OS Synthetic.  
XX  
PN WO9624380-A1.  
XX  
PD 15-AUG-1996.  
XX  
PF 05-FEB-1996; 95WO-US01507.  
XX  
PR 09-FEB-1995; 95US-0387041.  
PR 18-SEP-1995; 95US-0529878.  
PR 09-FEB-1995; 95US-0387041.  
PR 18-SEP-1995; 95US-0529878.  
XX  
PA (ICNC ) ICN PHARM INC.  
XX  
PI Tam RC;  
XX  
XX WPI; 1996-384228/38.  
DR  
XX Oligo:nucleotide which reduces CD28 gene expression in T cells -  
PT for treating immune system diseases, e.g. graft vs. host disease,  
PT septic shock, psoriasis, etc.  
XX  
PS Example 2; Page 45; 77pp; English.  
XX  
CC The present oligonucleotide reduces CD28 dependent interleukin-2  
CC (IL-2) production and T cell CD28 gene expression, useful in the  
CC treatment of CD28 mediated diseases, particularly immune system  
CC disorders, e.g. graft versus host disease, septic shock, viral  
CC disease, psoriasis, type I diabetes mellitus, thyroiditis,  
CC sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis,  
CC systemic lupus erythematosus, inflammatory bowel disease, etc..  
CC Reducing CD28 expression may reduce the effects of antigenic  
CC stimulation of CD28 positive T cells, with a consequent reduction  
CC in cytokine release.  
CC (Updated on 25-MAR-2003 to correct PR field.)  
XX  
SQ Sequence 18 BP; 1 A; 2 C; 11 G; 4 T; 0 other;  
Query Match 70.5%; Score 14.8; DB 17; Length 18;  
Best Local Similarity 88.9%; Pred. No. 1e+04;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 4 TTGGAGGGGGTGGTGGGG 21  
Db 1 TTGGAGGGGGTGGTGGCG 18  
RESULT 13  
ID AAX90335  
XX AAX90335 standard; DNA; 18 BP.  
XX  
AC AAX90335;  
XX  
DT 24-SEP-1999 (first entry)  
XX  
DE CD28 inhibiting phosphorothioate oligonucleotide RT05S.  
XX  
KW CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;  
KW immune system mediated disease; gamma-interferon; IL-8;  
KW phosphorothioate; ss.  
XX  
OS Synthetic.  
XX  
PN US5932556-A.  
XX



```
PD 03-AUG-1999.
XX
PF 18-SEP-1995; 95US-0529878.
XX
PR 18-SEP-1995; 95US-0529878.
XX
PA (TAMR/) TAM R C.
XX
PI Tam RC;
XX
DR WPI; 1999-443609/37.
XX
PT Treatment of immune system-mediated diseases by inhibiting
PT expression of CD28, IL-2, gamma-interferon or IL-8
XX
PS Example; Column 24; 45pp; English.
XX
CC The present invention describes a method for inhibiting the expression
CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method
CC comprises subcutaneous administration of an oligonucleotide (OGN).
CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the
CC method. The OGNs are used for the treatment of immune system-mediated
CC diseases. The present sequence represents a CD28 inhibiting
CC phosphorothioate oligonucleotide used in the exemplification of the
CC present invention.
XX
SQ Sequence 18 BP; 3 A; 0 C; 13 G; 2 T; 0 other;

Query Match 70.5%; Score 14.8; DB 20; Length 18;
Best Local Similarity 88.9%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TTGGAGGGGGTGGTGGG 21
Db 1 TTGGAGGGGGAGGAGGGG 18

RESULT 14
AAX90337
ID AAX90337 standard; DNA; 18 BP.
XX
AC AAX90337;
XX
DT 24-SEP-1999 (first entry)
XX
DE CD28 inhibiting phosphorothioate oligonucleotide RT10S.
XX
KW CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
KW immune system mediated disease; gamma-interferon; IL-8;
KW phosphorothioate; ss.
XX
OS Synthetic.
XX
US5932556-A.
XX
PD 03-AUG-1999.
XX
PF 18-SEP-1995; 95US-0529878.
XX
PR 18-SEP-1995; 95US-0529878.
XX
PA (TAMR/) TAM R C.
XX
PI Tam RC;
XX
DR WPI; 1999-443609/37.
XX
PT Treatment of immune system-mediated diseases by inhibiting
PT expression of CD28, IL-2, gamma-interferon or IL-8
XX
PS Example; Column 24; 45pp; English.
XX
CC The present invention describes a method for inhibiting the expression

of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method
comprises subcutaneous administration of an oligonucleotide (OGN).
AAX90288 to AAX90291 represent specifically claimed OGNs for use in the
method. The OGNs are used for the treatment of immune system-mediated
diseases. The present sequence represents a CD28 inhibiting
phosphorothioate oligonucleotide used in the exemplification of the
present invention.

Sequence 18 BP; 3 A; 0 C; 13 G; 2 T; 0 other;

Query Match 70.5%; Score 14.8; DB 20; Length 18;
Best Local Similarity 88.9%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TTGGAGGGGGTGGTGGG 21
Db 1 TTGGAGGGGGAGGAGGGG 18

RESULT 15
AAQ81074
ID AAQ81074 standard; DNA; 20 BP.
XX
AC AAQ81074;
XX
DT 25-MAR-2003 (updated)
DT 22-SEP-1995 (first entry)
XX
DE supF gene triplex forming mutagenic oligonucleotide pso-AGT20.
XX
KW supF gene; triplex forming mutagenic oligonucleotide; pso-AGT20;
KW 4'hydroxymethyl-4,5',8-trimethylpsoralenated; site specific; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /note= "4'hydroxymethyl-4,5',
FT 8-trimethylpsoralenated"
XX
PN WO9501364-A1.
XX
PD 12-JAN-1995.
XX
PF 24-JUN-1994; 94WO-US07234.
XX
PR 25-JUN-1993; 93US-0083088.
XX
PA (UYVA ) UNIV YALE.
XX
PI Glazer PM, Havre PA;
XX
DR WPI; 1995-060943/08.
XX
PT New mutagenic oligonucleotide(s) - having a mutagen incorporated
PT in an oligonucleotide which forms a triplex, for site-directed
PT mutagenesis
XX
PS Example 5; Page 38; 72pp; English.
XX
CC AAQ81074 is the supF gene triplex forming mutagenic oligonucleotide
CC pso-AGT20. It forms a triplex (a triple stranded nucleic acid) with
CC a specific site on the supF genome, enabling the covalently bound
CC 4'hydroxymethyl-4,5',8-trimethylpsoralen group to produce a site
CC specific mutation.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 20 BP; 3 A; 0 C; 15 G; 2 T; 0 other;

Query Match 67.6%; Score 14.2; DB 16; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.7e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

Qy 2 GGTTCGAGGGGGTGGTGGG 20  
| | | | | | | | | |  
Db 2 GGAAGGGGGGGTGGTGGG 20

Search completed: October 27, 2003, 11:25:19  
Job time : 189 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:29 ; Search time 1845.4 Seconds  
(without alignments)  
276.576 Million cell updates/sec

Title: US-09-331-204A-6  
Perfect score: 21  
Sequence: 1 ggggttgaggggggtggtggggg 21

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 11152

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :	EST:*
1:	em_estba:*
2:	em_esthum:*
3:	em_estin:*
4:	em_estnu:*
5:	em_estov:*
6:	em_estpl:*
7:	em_estro:*
8:	em_htc:*
9:	gb_est1:*
10:	gb_est2:*
11:	gb_htc:*
12:	gb_est3:*
13:	gb_est4:*
14:	gb_est5:*
15:	em_estfun:*
16:	em_estom:*
17:	em_gss_hum:*
18:	em_gss_inv:*
19:	em_gss_pln:*
20:	em_gss_vrt:*
21:	em_gss_fun:*
22:	em_gss_mam:*
23:	em_gss_mus:*
24:	em_gss_pro:*
25:	em_gss_rod:*
26:	em_gss_phg:*
27:	em_gss_vrl:*
28:	gb_gssi:*
29:	gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
C 1	14.6	69.5	22	28	AZ645874 1M0511C07
C 2	14.6	69.5	22	28	AZ766712 1M0564A03
C 3	14.6	69.5	22	28	AZ871408 2M0184B16
C 4	13.6	64.8	20	28	AZ666896 1M0549A24

C 5	13.6	64.8	20	28	AZ969440 2M0242O12
C 6	13.6	64.8	21	28	AZ476392 1M0295F12
C 7	13.6	64.8	22	9	AA911600 od90d06.s
8	13.6	64.8	22	13	BQ585098 E011826-0
9	13.6	64.8	22	28	AZ331988 1M0060B11
C 10	13.6	64.8	22	28	AZ607348 1M0429D18
11	13.6	64.8	22	28	AZ868780 2M0180E12
12	13.2	62.9	21	28	AZ468862 1M0282O04
13	13	61.9	21	13	BQ590339 E012845-0
C 14	13	61.9	21	13	BQ591392 E012713-0
15	13	61.9	21	13	BQ591421 E012714-0
C 16	13	61.9	21	28	AZ307440 1M0009D06
C 17	13	61.9	21	28	AZ309910 1M0017O17
C 18	13	61.9	21	28	AZ325151 1M0047K24
19	13	61.9	21	28	AZ345376 1M0079G22
C 20	13	61.9	21	28	AZ345432 1M0080D07
C 21	13	61.9	21	28	AZ349570 1M0086D10
22	13	61.9	22	28	AZ374427 1M0127111
C 23	13	61.9	21	28	AZ375567 1M0129A06
C 24	13	61.9	21	28	AZ379925 1M0135F10
25	13	61.9	21	28	AZ404075 1M0172I10
C 26	13	61.9	21	28	AZ433710 1M0219P12
C 27	13	61.9	21	28	AZ441558 1M0233G22
C 28	13	61.9	21	28	AZ479786 1M0300A14
C 29	13	61.9	21	28	AZ486754 1M0315K06
C 30	13	61.9	21	28	AZ486758 1M0315M02
31	13	61.9	21	28	AZ627987 1M0476P03
C 32	13	61.9	21	28	AZ629261 1M0482A07
C 33	13	61.9	21	28	AZ648382 1M0517E23
C 34	13	61.9	21	28	AZ654886 1M0529O24
C 35	13	61.9	21	28	AZ655958 1M0531P12
C 36	13	61.9	21	28	AZ665155 1M0545L21
C 37	13	61.9	21	28	AZ762085 1M0556I13
38	13	61.9	21	28	AZ764510 1M0560A10
C 39	13	61.9	21	28	AZ764596 1M0561L04
C 40	13	61.9	21	28	AZ769435 1M0570E12
C 41	13	61.9	21	28	AZ775790 2M0008O19
C 42	13	61.9	21	28	AZ779114 2M0015J01
C 43	13	61.9	21	28	AZ782599 2M0023A15
C 44	13	61.9	21	28	AZ783943 2M0026P05
C 45	13	61.9	21	28	AZ784621 2M0027G24

ALIGNMENTS

RESULT 1  
AZ645874/c  
LOCUS  
DEFINITION  
AZ645874 Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0511C07 R, genomic survey sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AZ645874 22 bp DNA linear GSS 14-DEC-2000  
1M0511C07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0511C07 R, genomic survey sequence.  
AZ645874 GI:11775791  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,  
and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0511 row: C column: 07  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 22.  
Location/Qualifiers

FEATURES

source

1. .22  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0511C07"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

0 a 21 C 0 G 1 t  
BASE COUNT  
ORIGIN

Query Match 69.5%; Score 14.6; DB 28; Length 22;  
Best Local Similarity 81.0%; Pred. No. 3.1e+05;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGTTGAGCGGGTGTGGGG 21  
||| ||||| |||||  
Db 22 GGGGGGAGCGGGGGGGGGG 2

RESULT 2

AZ766712/c

LOCUS

DEFINITION

1M0564A03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0564A03 R, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 22)

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0564 row: A column: 03  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 22.  
Location/Qualifiers

FEATURES

source

1. .22  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0564A03"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

1 a 21 C 0 G 0 t  
BASE COUNT  
ORIGIN

Query Match 69.5%; Score 14.6; DB 28; Length 22;  
Best Local Similarity 81.0%; Pred. No. 3.1e+05;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGTTGAGCGGGTGTGGGG 21  
||| ||||| |||||  
Db 21 GGGGTGGGGGGGGGGGGG 1

RESULT 3

AZ871408/c

LOCUS

DEFINITION

2M0184E16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0184E16 F, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 22)

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0184 row: E column: 16  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 22.  
Location/Qualifiers

FEATURES  
source

1. .22  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0184E16"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 21 c 0 g 1 t  
ORIGIN

Query Match 69.5%; Score 14.6; DB 28; Length 22;  
Best Local Similarity 81.0%; Pred. No. 3.1e+05;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGTTGGAGGGGGTGGTGGGG 21  
||| ||||| ||||| |||||  
Db 21 GGGGGGAGGGGGGGGGGGGGG 1

RESULT 4  
AZ666896/c  
LOCUS  
DEFINITION  
1M0549A24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0549A24 F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS  
1 (bases 1 to 20)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

TITLE  
JOURNAL  
COMMENT  
Unpublished  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0549 row: A column: 24  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers

FEATURES  
source

1. .20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0549A24"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 1 a 19 c 0 g 0 t  
ORIGIN

Query Match 64.8%; Score 13.6; DB 28; Length 20;  
Best Local Similarity 80.0%; Pred. No. 6.2e+05;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGTGGAGGGGGTGGTGGGG 21  
||| ||||| ||||| |||||  
Db 20 GGTGGGGGGGGGGGGGGGG 1

RESULT 5  
AZ669440/c  
LOCUS  
DEFINITION  
2M0242012F Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
clone UUGC2M0242012 F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS  
1 (bases 1 to 20)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

TITLE  
JOURNAL  
COMMENT  
Unpublished  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0242 row: 0 column: 12  
Seq primer: CGTTGTAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 20.

FEATURES  
source

1. .20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0242012"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, TI-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC2M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (female) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 0 a 19 c 0 g 1 t  
ORIGIN

Query Match 64.8%; Score 13.6; DB 28; Length 20;  
Best Local Similarity 80.0%; Pred. No. 6.2e+05;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGTTCGAGCGGGTGGTGGG 21  
||| ||||| |||||  
Db 20 GGGGGAGGGGGGGGGGG 1

RESULT 6  
AZ476392/c

LOCUS  
DEFINITION  
1M0295F12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0295F12 F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AZ476392 21 bp DNA linear GSS 04-OCT-2000  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 21)

REFERENCE  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT  
Unpublished  
Contact: Robert B. Weiss  
University of Utah Genome Center

University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0295 row: F column: 12  
Seq primer: CGTTGTAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 21.

FEATURES  
source

1. .21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0295F12"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 0 a 20 c 0 g 1 t  
ORIGIN

Query Match 64.8%; Score 13.6; DB 28; Length 21;  
Best Local Similarity 80.0%; Pred. No. 6.2e+05;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGTTGGAGGGGGTGGTGGG 20  
||| ||||| |||||  
Db 20 GGGGGGAGGGGGGGGGGG 1

RESULT 7  
AA911600

LOCUS  
DEFINITION  
AA911600 22 bp mRNA linear EST 21-APR-1998  
od90d06.s1 NCI CGAP Br5 Homo sapiens cDNA clone IMAGE:1377515  
similar to TR:Q18444 Q18444 COSMID C34D4. ;contains PTR5.t3 TAR1  
repetitive element ;, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AA911600.1 GI:3050964  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 22)

REFERENCE  
AUTHORS  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

JOURNAL  
COMMENT  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Ilan Kirsch, M.D., Kristina A. Cole, M.D.,

Ph.D. student, Rodrigo F. Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: David B. Krimman, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
Insert Length: 255 Std Error: 0.00  
Seq primer: -40m13 fwd. ET from Amersham  
High quality sequence stop: 1.

FEATURES

source

1. .22  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1377515"  
/sex="female"  
/tissue\_type="infiltrating ductal carcinoma"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Br5"

/note="Organ: breast; Vector: pAMP10; mRNA made from infiltrating ductal carcinoma, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. "  
1 a 1 c 17 g 3 t

BASE COUNT  
ORIGIN

Query Match 64.8%; Score 13.6; DB 9; Length 22;  
Best Local Similarity 80.0%; Pred. No. 6.2e+05;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGTTGGAGGGGGTGGTGGG 20  
|||||  
Db 3 GGTTGGCGGGGATGGGGG 22

RESULT 8

BQ585098

LOCUS

DEFINITION

BQ585098 22 bp mRNA linear EST 06-DEC-2002

E011826-024-002-K08-SP6 MP1Z-ADIS-024-inflorescence Beta vulgaris

CDNA clone 024-002-K08 5-PRIME, mRNA sequence.

BQ585098 1 GI:26114680

EST.

KEYWORDS

SOURCE

ORGANISM

Beta vulgaris

Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 22)

Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.

and Radelof, U.

Construction of a 'unigene' cDNA clone set by oligonucleotide

fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

Contact: Weisshaar B

ADIS DNA core facility at MP1Z

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de

Insert Length: 22 Std Error: 0.00

Plate: 2 row: K column: 08

Seq primer: SP6; CATACGATTTAGGTGACACTATAG.

Location/Qualifiers

1. .22

/organism="Beta vulgaris"

/mol\_type="mRNA"

/cultivar="KWS2320 (double haploid, monogerm breeding line

FEATURES

source

1. .22  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUC1M0060B11"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.

BASE COUNT 0 a 0 c 21 g  
ORIGIN  
Query Match 64.8%; Score 13.6; DB 13; Length 22;  
Best Local Similarity 76.2%; Pred. No. 6.2e+05;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
Qy 1 GGTTGGAGGGGGTGGTGGG 21  
|||||  
Db 1 GGGGGGNGGGGGGGGGGGG 21  
RESULT 9  
AZ331988 22 bp DNA linear GSS 29-SEP-2000  
LOCUS  
DEFINITION  
1M0060B11F Mouse 10kb plasmid UUC1M library Mus musculus genomic  
clone UUC1M0060B11 F, genomic survey sequence.  
AZ331988 1 GI:10395213  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 22)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.  
and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0060 row: B column: 11  
Seq primer: CGTTGTAACACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 22.  
Location/Qualifiers  
1. .22  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUC1M0060B11"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.

BASE COUNT 0 a 0 c 21 g  
ORIGIN  
Query Match 64.8%; Score 13.6; DB 13; Length 22;  
Best Local Similarity 76.2%; Pred. No. 6.2e+05;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
Qy 1 GGTTGGAGGGGGTGGTGGG 21  
|||||  
Db 1 GGGGGGNGGGGGGGGGGGG 21

RESULT 9

AZ331988

LOCUS

DEFINITION

1M0060B11F Mouse 10kb plasmid UUC1M library Mus musculus genomic

clone UUC1M0060B11 F, genomic survey sequence.

AZ331988 1 GI:10395213

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 22)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,

M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.

and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0060 row: B column: 11

Seq primer: CGTTGTAACACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1. .22

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUC1M0060B11"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.



musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 1 a 0 c 21 g 0 t  
ORIGIN

Query Match 64.8%; Score 13.6; DB 28; Length 22;  
Best Local Similarity 80.0%; Pred. No. 6.2e+05;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGTTGGAGGGGGTGGTGGG 20  
||| ||||| ||||| |||||  
Db 3 GGGGGGAGGGGGGGGGGGG 22

RESULT 10  
AZ607348/c  
LOCUS  
DEFINITION IM0429D18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0429D18 R, genomic survey sequence.  
ACCESSION AZ607348  
VERSION AZ607348.1 GI:11729538  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0429 row: D column: 18  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 22.

FEATURES  
source  
1. .22  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0429D18"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 21 c 0 g 1 t  
ORIGIN

Query Match 64.8%; Score 13.6; DB 28; Length 22;  
Best Local Similarity 80.0%; Pred. No. 6.2e+05;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGTTGGAGGGGGTGGTGGG 20  
||| ||||| ||||| |||||  
Db 20 GGGGGGAGGGGGGGGGGGG 1

RESULT 11  
AZ868780  
LOCUS  
DEFINITION 2M0180E12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0180E12 R, genomic survey sequence.  
ACCESSION AZ868780  
VERSION AZ868780.1 GI:13072436  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0180 row: E column: 12  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 22.

FEATURES  
source  
1. .22  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0180E12"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"



/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 1 a 0 c 17 g 4 t  
ORIGIN  
Query Match 64.8%; Score 13.6; DB 28; Length 22;  
Best Local Similarity 80.0%; Pred. No. 6.2e+05;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 GGGTTGGAGGGGGTGGTGGG 20  
||||| | | | |  
Db 3 GGGTTGGGGGTAGGGGTGGG 22

RESULT 12  
AZ468862  
LOCUS  
DEFINITION  
1M0282004F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0282004 F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)

REFERENCE  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D.,Weiss,R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0282 row: 0 column: 04  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 21.

FEATURES  
source  
Location/Qualifiers  
1..21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0282004"  
/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 0 a 1 c 15 g 5 t  
ORIGIN  
Query Match 62.9%; Score 13.2; DB 28; Length 21;  
Best Local Similarity 83.3%; Pred. No. 8.3e+05;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 4 TTGGAGGGGGTGGTGGGG 21  
||||| | | | |  
Db 1 TTGGGGGGTGGGTGGGG 18

RESULT 13  
BQ590339  
LOCUS  
DEFINITION  
BQ590339 21 bp mRNA linear EST 06-DEC-2002  
E012845-024-019-H11-T7 MP1Z-ADIS-024-storage root Beta vulgaris  
cDNA clone 024-019-H11 3-PRIME, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Beta vulgaris  
Beta vulgaris

REFERENCE  
AUTHORS  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 21)  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.

TITLE  
Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)

JOURNAL  
COMMENT  
Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
Insert Length: 21 Std Error: 0.00  
Plate: 19 row: H column: 11  
Seq primer: T7; GTAATACGACTCACTATAGGC.

FEATURES  
source  
Location/Qualifiers  
1..21  
/organism="Beta vulgaris"  
/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding line  
)"

/db\_xref="GABI:189782"  
/db\_xref="taxon:161934"  
/clone="024-019-H11"  
/tissue type="storage root"  
/lab\_host="EMDH10B"

/clone lib="MPIZ-ADIS-024-storage root"  
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGGGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet project  
, local PI: Dr. Katharina Schneider, coordinator: Prof.  
Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

BASE COUNT 0 a 0 c 21 g 0 t  
ORIGIN

Query Match 61.9%; Score 13; DB 13; Length 21;  
Best Local Similarity 76.2%; Pred. No. 9.5e+05;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGTTGAGGGGGTGGTGGGG 21  
||| ||||| |||||  
Db 1 GGGGGGGGGGGGGGGGGGGG 21

RESULT 14  
BQ591392/c  
LOCUS  
DEFINITION BQ591392 21 bp mRNA linear EST 06-DEC-2002  
CDNA clone 024-017-014-T7 MPIZ-ADIS-024-storage root Beta vulgaris  
BQ591392  
ACCESSION BQ591392.1 GI:26120975  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 21)  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)

JOURNAL  
COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@piz-koeln.mpg.de  
Insert Length: 21 Std Error: 0.00  
Plate: 17 row: 0 column: 14  
Seq primer: T7; GTAATACGACTCACTATAGGCG.

FEATURES  
source  
1..21  
/organism="Beta vulgaris"  
/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding line  
)"  
/db\_xref="GABI:188731"  
/db\_xref="taxon:161934"  
/clone="024-017-014"  
/tissue\_type="storage root"  
/lab\_host="EMDH10B"  
/clone\_lib="MPIZ-ADIS-024-storage root"  
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGGGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet project  
, local PI: Dr. Katharina Schneider, coordinator: Prof.  
Christian Jung; Sequence submission managed by

RZPD/GABI-Primary database: http://gabi.rzpd.de"

BASE COUNT 0 a 21 c 0 g 0 t  
ORIGIN

Query Match 61.9%; Score 13; DB 13; Length 21;  
Best Local Similarity 76.2%; Pred. No. 9.5e+05;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGTTGAGGGGGTGGTGGGG 21  
||| ||||| |||||  
Db 21 GGGGGGGGGGGGGGGGGGGG 1

RESULT 15  
BQ591421

LOCUS  
DEFINITION BQ591421 21 bp mRNA linear EST 06-DEC-2002  
CDNA clone 024-017-P09-T7 MPIZ-ADIS-024-storage root Beta vulgaris  
BQ591421  
ACCESSION BQ591421.1 GI:26121004  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 21)  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)

JOURNAL

COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@piz-koeln.mpg.de  
Insert Length: 21 Std Error: 0.00  
Plate: 17 row: P column: 09  
Seq primer: T7; GTAATACGACTCACTATAGGCG.

FEATURES  
source  
1..21  
/organism="Beta vulgaris"  
/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding line  
)"  
/db\_xref="GABI:188694"  
/db\_xref="taxon:161934"  
/clone="024-017-P09"  
/tissue\_type="storage root"  
/lab\_host="EMDH10B"  
/clone\_lib="MPIZ-ADIS-024-storage root"  
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGGGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet project  
, local PI: Dr. Katharina Schneider, coordinator: Prof.  
Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

BASE COUNT 0 a 0 c 21 g 0 t  
ORIGIN

Query Match 61.9%; Score 13; DB 13; Length 21;  
Best Local Similarity 76.2%; Pred. No. 9.5e+05;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGTTGAGGGGGTGGTGGGG 21  
||| ||||| |||||

Db 1 GGGGGGGGGGGGGGGGGGG 21

Search completed: October 27, 2003, 13:59:26  
Job time : 1847.4 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.  
OM nucleic - nucleic search, using sw model  
Run on: October 27, 2003, 10:32:34 ; Search time 48.2 Seconds  
(without alignments)  
192.304 Million cell updates/sec  
Title: US-09-331-204A-6  
Perfect score: 21  
Sequence: 1 ggggttgagggggtggtgggg 21  
Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 376294

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:  
5: /cgn2\_6/ptodata/1/ina/pctus\_COMB.seq:  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	21	100.0	21	2	US-08-529-878B-4
2	21	100.0	21	2	US-08-529-878B-45
3	18	85.7	18	2	US-08-529-878B-3
4	18	85.7	18	2	US-08-529-878B-44
5	14.2	67.6	20	2	US-08-476-712-2
6	14.2	67.6	20	4	US-09-411-291-2
7	13.6	64.8	20	3	US-09-262-773-204
8	13.2	62.9	20	3	US-08-890-980-56
9	13.2	62.9	20	3	US-08-890-979-56
10	13.2	62.9	20	3	US-09-032-894-56
11	13.2	62.9	20	3	US-09-031-626-56
12	13.2	62.9	20	4	US-09-422-978-9409
13	13	61.9	21	1	US-07-873-915A-3
14	13	61.9	21	1	US-08-257-964-3
15	13	61.9	21	2	US-08-863-639A-11
16	13	61.9	21	2	US-08-863-639A-12
17	13	61.9	21	2	US-08-863-639A-48
18	13	61.9	21	2	US-08-863-639A-76
19	13	61.9	22	2	US-08-403-888A-36
20	13	61.9	22	2	US-08-403-888A-44
21	13	61.9	22	2	US-08-403-888A-110
22	13	61.9	22	2	US-08-403-888A-117
23	12.8	61.0	17	4	US-09-495-140-26
24	12.8	61.0	18	3	US-09-017-974-57
25	12.8	61.0	18	4	US-08-682-255A-57
26	12.8	61.0	18	4	US-09-429-130-57
27	12.8	61.0	20	1	US-08-167-113-16

28	12.8	61.0	20	2	US-08-886-161-16	Sequence 16, Appl
29	12.8	61.0	20	3	US-09-490-692-35	Sequence 35, Appl
30	12.8	61.0	20	3	US-09-194-478-7	Sequence 7, Appl
31	12.8	61.0	20	3	US-09-194-478-8	Sequence 8, Appl
32	12.8	61.0	21	2	US-08-632-575B-19	Sequence 19, Appl
33	12.8	61.0	21	4	US-09-199-542B-19	Sequence 19, Appl
34	12.6	60.0	19	3	US-08-855-825-17	Sequence 17, Appl
35	12.6	60.0	20	3	US-09-487-368A-175	Sequence 175, App
36	12.6	60.0	20	4	US-09-629-644A-175	Sequence 175, App
37	12.6	60.0	21	2	US-08-863-639A-36	Sequence 36, Appl
38	12.6	60.0	21	2	US-08-863-639A-50	Sequence 50, Appl
39	12.6	60.0	21	2	US-08-863-639A-73	Sequence 73, Appl
40	12.6	60.0	21	2	US-08-863-639A-88	Sequence 88, Appl
41	12.6	60.0	21	3	US-09-109-663-24	Sequence 24, Appl
42	12.6	60.0	22	3	US-08-927-219-64	Sequence 64, Appl
43	12.2	58.1	17	4	US-09-809-713-3	Sequence 3, Appl
44	12.2	58.1	18	1	US-08-013-801-4	Sequence 4, Appl
45	12.2	58.1	18	1	US-08-072-063-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1  
US-08-529-878B-4  
; Sequence 4, Application US/08529878B  
; Patent No. 5932556  
; GENERAL INFORMATION:  
; APPLICANT: Tam, Robert C.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
; TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Crockett & Fish  
; STREET: 3000 S. Augusta Court  
; CITY: La Habra  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 90631  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/529,878B  
; FILING DATE: 13-SEP-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fish, Robert D.  
; REGISTRATION NUMBER: 33,880  
; REFERENCE/DOCKET NUMBER: 213/003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 714-525-3433  
; TELEFAX: 714-525-3303  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 21 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
; US-08-529-878B-4

Query Match 100.0%; Score 21; DB 2; Length 21;  
Best Local Similarity 100.0%; Pred. No. 4.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTTGGAGGGGGTGGTGGG 21  
|||||  
Db 1 GGGTTGGAGGGGGTGGTGGG 21

RESULT 2  
US-08-529-878B-45  
; Sequence 45, Application US/08529878B  
; Patent No. 5932556  
; GENERAL INFORMATION:  
; APPLICANT: Tam, Robert C.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
; TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Crockett & Fish  
; STREET: 3000 S. Augusta Court  
; CITY: La Habra  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 90631  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/529,878B  
; FILING DATE: 13-SEP-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fish, Robert D.  
; REGISTRATION NUMBER: 33,880  
; REFERENCE/DOCKET NUMBER: 213/003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 714-525-3433  
; TELEFAX: 714-525-3303  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 45:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 21 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
US-08-529-878B-45

Query Match 100.0%; Score 21; DB 2; Length 21;  
Best Local Similarity 100.0%; Pred. No. 4.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTTGGAGGGGTGGTGGG 21  
|||||  
Db 1 GGGTTGGAGGGGTGGTGGG 21

RESULT 3  
US-08-529-878B-3  
; Sequence 3, Application US/08529878B  
; Patent No. 5932556  
; GENERAL INFORMATION:  
; APPLICANT: Tam, Robert C.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
; TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Crockett & Fish  
; STREET: 3000 S. Augusta Court  
; CITY: La Habra  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 90631  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/529,878B  
; FILING DATE: 13-SEP-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fish, Robert D.  
; REGISTRATION NUMBER: 33,880  
; REFERENCE/DOCKET NUMBER: 213/003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 714-525-3433  
; TELEFAX: 714-525-3303  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
US-08-529-878B-3

Query Match 85.7%; Score 18; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGGAGGGGTGGTGGG 21  
|||||  
Db 1 TTGGAGGGGTGGTGGG 18

RESULT 4  
US-08-529-878B-44  
; Sequence 44, Application US/08529878B  
; Patent No. 5932556  
; GENERAL INFORMATION:  
; APPLICANT: Tam, Robert C.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
; TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Crockett & Fish  
; STREET: 3000 S. Augusta Court  
; CITY: La Habra  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 90631  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/529,878B  
; FILING DATE: 13-SEP-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fish, Robert D.  
; REGISTRATION NUMBER: 33,880  
; REFERENCE/DOCKET NUMBER: 213/003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 714-525-3433  
; TELEFAX: 714-525-3303  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 44:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
US-08-529-878B-44

Query Match 85.7%; Score 18; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 58;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGGAGGGGGTGGTGGG 21  
|||  
Db 1 TTGGAGGGGGTGGTGGG 18  
|||

## RESULT 5

US-08-476-712-2  
; Sequence 2, Application US/08476712  
; Patent No. 5962426  
; GENERAL INFORMATION:  
; APPLICANT: Glazer, Peter, M.  
; TITLE OF INVENTION: Triple-Helix Forming Oligonucleotides for  
; TITLE OF INVENTION: Targeted Mutagenesis  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patrea L. Pabst  
; STREET: 2800 One Atlantic Center  
; CITY: Atlanta  
; STATE: GA  
; COUNTRY: USA  
; ZIP: 30309-3450  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/476,712  
; FILING DATE: 7-JUNE-1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pabst, Patrea L.  
; REGISTRATION NUMBER: 31,284  
; REFERENCE/DOCKET NUMBER: YU114  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404)-873-8794  
; TELEFAX: (404)-873-8795  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 bases  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-476-712-2

Query Match 67.6%; Score 14.2; DB 2; Length 20;  
Best Local Similarity 84.2%; Pred. No. 1.7e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGTGGAGGGGGTGGTGGG 20  
|||  
Db 2 GGAAGGGGGGGTGGTGGG 20  
|||

## RESULT 6

US-09-411-291-2  
; Sequence 2, Application US/09411291  
; Patent No. 6303376  
; GENERAL INFORMATION:  
; APPLICANT: Glazer, Peter, M.  
; TITLE OF INVENTION: Triple-Helix Forming Oligonucleotides for  
; Targeted Mutagenesis  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patrea L. Pabst  
; STREET: 2800 One Atlantic Center  
; CITY: Atlanta

STATE: GA  
COUNTRY: USA  
ZIP: 30309-3450  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/411,291  
FILING DATE: 04-Oct-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/476,712  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: YU114  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404)-873-8794  
TELEFAX: (404)-873-8795  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-411-291-2

Query Match 67.6%; Score 14.2; DB 4; Length 20;  
Best Local Similarity 84.2%; Pred. No. 1.7e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGTGGAGGGGGTGGTGGG 20  
|||  
Db 2 GGAAGGGGGGGTGGTGGG 20  
|||

## RESULT 7

US-09-262-773-204  
; Sequence 204, Application US/09262773  
; Patent No. 6225451  
; GENERAL INFORMATION:  
; APPLICANT: Ballinger, Dennis G.  
; APPLICANT: Ding, Wei  
; APPLICANT: Wagner, Susanne  
; APPLICANT: Hess, Mark A.  
; TITLE OF INVENTION: CHROMOSOME 11-LINKED CORONARY HEART DISEASE  
; TITLE OF INVENTION: SUSCEPTIBILITY GENE CHD1  
; FILE REFERENCE: Myriad 3  
; CURRENT APPLICATION NUMBER: US/09/262,773  
; CURRENT FILING DATE: 1999-03-04  
; NUMBER OF SEQ ID NOS: 210  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 204  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: DNA fragment  
US-09-262-773-204

Query Match 64.8%; Score 13.6; DB 3; Length 20;  
Best Local Similarity 80.0%; Pred. No. 2.8e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGTTCGAGGGGGTGGTGGG 20  
|||  
Db 1 GGTTCGAGGGGGTGGTGGG 20  
|||

## RESULT 8

US-08-890-980-56/c  
; Sequence 56, Application US/08890980  
; Patent No. 598141  
; GENERAL INFORMATION:  
; APPLICANT: Acton, Susan L.  
; TITLE OF INVENTION: SR-B1 NUCLEIC ACIDS AND USES THEREFOR  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
; STREET: One Post Office Square  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109-2170  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/890,980  
; FILING DATE: 10-JUL-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Arnold, Beth E.  
; REGISTRATION NUMBER: 35,430  
; REFERENCE/DOCKET NUMBER: MIA-005.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-832-1000  
; TELEFAX: 617-832-7000  
; INFORMATION FOR SEQ ID NO: 56:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "primer"  
US-08-890-980-56  
Query Match 62.9%; Score 13.2; DB 2; Length 20;  
Best Local Similarity 83.3%; Pred. No. 4e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 3 GTTGGAGGGGTGGTGGG 20  
Db 20 GTGGGCTGGGTGGTGGG 3  
RESULT 9  
US-08-890-979-56/c  
; Sequence 56, Application US/08890979  
; Patent No. 6030778  
; GENERAL INFORMATION:  
; APPLICANT: Acton, Susan L.  
; APPLICANT: Ordovas, Jose M.  
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS  
; TITLE OF INVENTION: DISORDERS  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
; STREET: One Post Office Square  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109-2170  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/890,979

FILING DATE: 10-JUL-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: MIA-005.02  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-832-1000  
TELEFAX: 617-832-7000  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "primer"  
US-08-890-979-56  
Query Match 62.9%; Score 13.2; DB 3; Length 20;  
Best Local Similarity 83.3%; Pred. No. 4e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 3 GTTGGAGGGGTGGTGGG 20  
Db 20 GTGGGCTGGGTGGTGGG 3  
RESULT 10  
US-09-032-894-56/c  
; Sequence 56, Application US/09032894  
; Patent No. 6130041  
; GENERAL INFORMATION:  
; APPLICANT: Acton, Susan L.  
; TITLE OF INVENTION: SR-BI NUCLEIC ACIDS AND USES THEREFOR  
; FILE REFERENCE: MIA-005.03  
; CURRENT APPLICATION NUMBER: US/09/032,894  
; CURRENT FILING DATE: 1998-02-27  
; EARLIER APPLICATION NUMBER: 08/890,980  
; EARLIER FILING DATE: 1997-07-10  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 56  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Human  
US-09-032-894-56  
Query Match 62.9%; Score 13.2; DB 3; Length 20;  
Best Local Similarity 83.3%; Pred. No. 4e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 3 GTTGGAGGGGTGGTGGG 20  
Db 20 GTGGGCTGGGTGGTGGG 3  
RESULT 11  
US-09-031-626-56/c  
; Sequence 56, Application US/09031626  
; Patent No. 6228581  
; GENERAL INFORMATION:  
; APPLICANT: Acton, Susan L.  
; APPLICANT: Ordovas, Jose M.  
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS AND  
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS  
; FILE REFERENCE: MIA-005.04  
; CURRENT APPLICATION NUMBER: US/09/031,626  
; CURRENT FILING DATE: 1998-02-27  
; EARLIER APPLICATION NUMBER: 08/890,979  
; EARLIER FILING DATE: 1997-07-10  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn Ver. 2.0

```

; SEQ ID NO 56
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-031-626-56

Query Match
Best Local Similarity 62.9%; Score 13.2; DB 3; Length 20;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GTTGGAGGGGGTGGTGG 20
Db 20 GTGGCTGGGGTGGTGG 3

RESULT 12
US-09-422-978-9409/c
; Sequence 9409, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 9409
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20
; OTHER INFORMATION: downstream amplification primer 99-449 for SEQ 1544, in complement
US-09-422-978-9409

Query Match
Best Local Similarity 62.9%; Score 13.2; DB 4; Length 20;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTTGGAGGGGGTGGTG 18
Db 20 GAGTTGGAGGGGGAGATG 3

RESULT 13
US-07-873-915A-3
; Sequence 3, Application US/07873915A
; Patent No. 5348868
; GENERAL INFORMATION:
; APPLICANT: Reddy, Parameswara M.
; APPLICANT: Hanna, Naeem B.
; TITLE OF INVENTION: Methods and Reagents
; TITLE OF INVENTION: for Cleaving and
; TITLE OF INVENTION: Deprotecting
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Beckman Instruments, Inc.
; STREET: 2500 Harbor Boulevard
; CITY: Fullerton
; STATE: California
; COUNTRY: USA
; ZIP: 92634
; COMPUTER READABLE FORM:

```



SEQUENCE CHARACTERISTICS:

LENGTH: 21 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: no  
ANTI-SENSE: no  
US-08-257-964-3

Query Match 61.9%; Score 13; DB 1; Length 21;  
Best Local Similarity 76.2%; Pred. No. 4.8e+03;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GGGTTGGAGGGGTGTGGGG 21  
Db 1 GGGGGGGGGGGGGGGGGGG 21

RESULT 15

US-08-863-639A-11/c  
Sequence 11, Application US/08863639A  
Patent No. 5981185

GENERAL INFORMATION:

APPLICANT: Matson, Robert S.  
APPLICANT: Coassin, Peter J.  
APPLICANT: Rampal, Jang B.  
APPLICANT: Caskey, C. T.  
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS  
NUMBER OF SEQUENCES: 95  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Sheldon & Mak  
STREET: 225 South Lake Avenue, 9th Floor  
CITY: Pasadena  
STATE: CA  
COUNTRY: USA  
ZIP: 91101

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: Corel WordPerfect 8 version

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/863,639A  
FILING DATE: May 28, 1997  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Joseph E. Mueth  
REGISTRATION NUMBER: 20,532  
REFERENCE/DOCKET NUMBER: 11859-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (626) 796-4000  
TELEFAX: (626) 795-6321

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other nucleic acid  
US-08-863-639A-11

Query Match 61.9%; Score 13; DB 2; Length 21;  
Best Local Similarity 76.2%; Pred. No. 4.8e+03;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GGGTTGGAGGGGTGTGGGG 21  
Db 21 GGGGGGGGGGGGGGGGGGG 1

Search completed: October 27, 2003, 14:03:34  
Job time : 48.2 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 11:25:34 ; Search time 452.6 Seconds  
(without alignments)  
124.432 Million cell updates/sec

Title: US-09-331-204A-6  
Perfect score: 21  
Sequence: 1 ggggtggagggggtgtgtggg 21

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1792395 seqs, 1340900451 residues

Total number of hits satisfying chosen parameters: 408622

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	13.4	63.8	20	10	US-09-874-162A-22
C 2	13.2	62.9	20	11	US-09-779-152-56
C 3	13.2	62.9	20	14	US-10-023-610-56
C 4	13	61.9	17	11	US-09-740-332-2132
C 5	13	61.9	17	11	US-09-740-332-2133
C 6	13	61.9	17	11	US-09-740-332-2422
C 7	13	61.9	17	11	US-09-740-332-2423
C 8	13	61.9	17	12	US-09-817-879-2132
C 9	13	61.9	17	12	US-09-817-879-2133
C 10	13	61.9	17	12	US-09-817-879-2422
C 11	13	61.9	17	12	US-09-817-879-2423
C 12	13	61.9	21	9	US-09-828-034-31
C 13	12.8	61.0	17	12	US-10-059-877-26
C 14	12.8	61.0	17	12	US-10-303-109A-30
C 15	12.8	61.0	17	14	US-10-059-888-26
C 16	12.8	61.0	18	12	US-10-204-884-59

17	12.8	61.0	20	14	US-10-181-846-35	Sequence 35, Appl
C 18	12.8	61.0	22	11	US-09-988-115A-3	Sequence 3, Appli
C 19	12.8	61.0	22	11	US-09-988-115A-13	Sequence 13, Appl
C 20	12.8	61.0	22	11	US-09-988-115A-20	Sequence 20, Appl
C 21	12.8	61.0	22	11	US-09-988-115A-22	Sequence 22, Appl
C 22	12.6	60.0	20	9	US-09-854-883-175	Sequence 175, App
C 23	12.6	60.0	21	9	US-09-828-034-11	Sequence 11, Appl
C 24	12.6	60.0	21	9	US-09-828-034-30	Sequence 30, Appl
C 25	12.6	60.0	21	11	US-09-932-300-24	Sequence 24, Appl
C 26	12.6	60.0	21	12	US-10-083-246A-78	Sequence 78, Appl
C 27	12.6	60.0	21	12	US-10-184-085A-227	Sequence 227, App
C 28	12.4	59.0	20	12	US-10-032-585-5333	Sequence 5333, Ap
C 29	12.2	58.1	17	10	US-09-263-959-904	Sequence 904, App
C 30	12.2	58.1	17	11	US-09-818-875-295	Sequence 295, App
C 31	12.2	58.1	17	11	US-09-818-875-296	Sequence 296, App
C 32	12.2	58.1	18	10	US-09-969-373-1900	Sequence 1900, Ap
C 33	12.2	58.1	18	10	US-09-263-959-921	Sequence 921, App
C 34	12.2	58.1	18	14	US-10-196-460-4	Sequence 4, Appli
C 35	12.2	58.1	19	12	US-10-318-628-9	Sequence 9, Appli
C 36	12.2	58.1	20	9	US-09-854-883-174	Sequence 174, App
C 37	12.2	58.1	20	10	US-09-755-004-10	Sequence 10, Appl
C 38	12.2	58.1	20	12	US-09-767-421-36	Sequence 36, Appl
C 39	12.2	58.1	20	12	US-10-279-579A-47	Sequence 47, Appl
C 40	12.2	58.1	22	11	US-09-918-696-23	Sequence 23, Appl
C 41	12.2	58.1	22	11	US-09-918-696-24	Sequence 24, Appl
C 42	12.2	58.1	22	11	US-09-905-558C-14	Sequence 14, Appl
C 43	12	57.1	20	10	US-09-800-266A-133	Sequence 133, App
C 44	12	57.1	20	10	US-09-895-007A-133	Sequence 133, App
C 45	12	57.1	20	10	US-09-920-313-133	Sequence 133, App

ALIGNMENTS

RESULT 1  
US-09-874-162A-22/c  
; Sequence 22, Application US/09874162A  
; Patent No. US20020155452A1  
; GENERAL INFORMATION:  
; APPLICANT: Koontz, Jason  
; APPLICANT: Sklar, Jeffrey  
; TITLE OF INVENTION: FUSION OF JAZF1 AND JAZ1 GENES IN  
; TITLE OF INVENTION: ENDOMETRIAL STROMAL TUMORS  
; FILE REFERENCE: 05311-024001  
; CURRENT APPLICATION NUMBER: US/09/874,162A  
; PRIOR FILING DATE: 2001-06-04  
; PRIOR APPLICATION NUMBER: US 60/209,093  
; PRIOR FILING DATE: 2000-06-02  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 22  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: primer for PCR  
US-09-874-162A-22

Query Match 63.8%; Score 13.4; DB 10; Length 20;  
Best Local Similarity 93.3%; Pred. No. 2.3e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GGAGGGGGTGTGGG 20  
Db 19 GGAGGGGGTGTGGG 5

RESULT 2  
US-09-779-152-56/c  
; Sequence 56, Application US/09779152  
; Publication No. US20030044782A1  
; GENERAL INFORMATION:  
; APPLICANT: Acton, Susan L.

; APPLICANT: Ordovas, Jose M.  
; APPLICANT: McCarthy, Jeanette J.  
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS AND  
; TITLE OF INVENTION: RADIOVASCULAR DISORDERS  
; FILE REFERENCE: MNI-172CP2  
; CURRENT APPLICATION NUMBER: US/09/779,152  
; PRIOR FILING DATE: 2001-02-08  
; PRIOR APPLICATION NUMBER: 08/890,979  
; PRIOR FILING DATE: 1997-07-10  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 56  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Human  
US-09-779-152-56

Query Match 62.9%; Score 13.2; DB 11; Length 20;  
Best Local Similarity 83.3%; Pred. No. 2.7e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GTTGGAGGGGTGGTGGG 20  
||| |||||  
Db 20 GTGGGCTGGGTGGTGGG 3

RESULT 3  
US-10-023-610-56/c  
; Sequence 56, Application US/10023610  
; Publication No. US20030023059A1  
; GENERAL INFORMATION:  
; APPLICANT: Acton, Susan L.  
; TITLE OF INVENTION: SR-BI NUCLEIC ACIDS AND USES THEREFOR  
; FILE REFERENCE: MIA-005.03  
; CURRENT APPLICATION NUMBER: US/10/023,610  
; CURRENT FILING DATE: 2001-12-17  
; EARLIER APPLICATION NUMBER: 09/686,106  
; EARLIER FILING DATE: 2000-10-10  
; EARLIER APPLICATION NUMBER: 09/032,894  
; EARLIER FILING DATE: 1998-02-27  
; EARLIER APPLICATION NUMBER: 08/890,980  
; EARLIER FILING DATE: 1997-07-10  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 56  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Human  
US-10-023-610-56

Query Match 62.9%; Score 13.2; DB 14; Length 20;  
Best Local Similarity 83.3%; Pred. No. 2.7e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GTTGGAGGGGTGGTGGG 20  
||| |||||  
Db 20 GTGGGCTGGGTGGTGGG 3

RESULT 4  
US-09-740-332-2132/c  
; Sequence 2132, Application US/09740332  
; Publication No. US20030125270A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat  
; FILE REFERENCE: RPI 400/003  
; CURRENT APPLICATION NUMBER: US/09/740,332  
; CURRENT FILING DATE: 2001-03-26  
; NUMBER OF SEQ ID NOS: 9704  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2132

; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION:  
; OTHER INFORMATION: oligonucleotide substrate  
US-09-740-332-2132

Query Match 61.9%; Score 13; DB 11; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.3e+04;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGGGGTGGTGGG 21  
|||||  
Db 17 GGGGGTGGTGGG 5

RESULT 5  
US-09-740-332-2133/c  
; Sequence 2133, Application US/09740332  
; Publication No. US20030125270A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat  
; FILE REFERENCE: RPI 400/003  
; CURRENT APPLICATION NUMBER: US/09/740,332  
; CURRENT FILING DATE: 2001-03-26  
; NUMBER OF SEQ ID NOS: 9704  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2133  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION:  
; OTHER INFORMATION: oligonucleotide substrate  
US-09-740-332-2133

Query Match 61.9%; Score 13; DB 11; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.3e+04;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGGGGTGGTGGG 21  
|||||  
Db 14 GGGGGTGGTGGG 2

RESULT 6  
US-09-740-332-2422  
; Sequence 2422, Application US/09740332  
; Publication No. US20030125270A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat  
; FILE REFERENCE: RPI 400/003  
; CURRENT APPLICATION NUMBER: US/09/740,332  
; CURRENT FILING DATE: 2001-03-26  
; NUMBER OF SEQ ID NOS: 9704  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2422  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION:  
; OTHER INFORMATION: oligonucleotide substrate  
US-09-740-332-2422

Query Match 61.9%; Score 13; DB 11; Length 17;  
Best Local Similarity 84.6%; Pred. No. 3.3e+04;  
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
QY 9 GGGGGTGGTGGG 21  
| | | | | : | : | | |  
Db 5 GGGGGUGUGGGG 17  
  
RESULT 7  
US-09-740-332-2423  
; Sequence 2423, Application US/09740332  
; Publication No. US20030125270A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat  
; TITLE OF INVENTION: Hepatitis C Virus Infection  
; FILE REFERENCE: RPI 400/003  
; CURRENT APPLICATION NUMBER: US/09/740,332  
; CURRENT FILING DATE: 2001-03-26  
; NUMBER OF SEQ ID NOS: 9704  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2423  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION:  
; OTHER INFORMATION: oligonucleotide substrate  
US-09-740-332-2423

Query Match 61.9%; Score 13; DB 11; Length 17;  
Best Local Similarity 84.6%; Pred. No. 3.3e+04;  
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
QY 9 GGGGGTGGTGGG 21  
| | | | | : | : | | |  
Db 2 GGGGGUGUGGGG 14

RESULT 8  
US-09-817-879-2132/c  
; Sequence 2132, Application US/09817879  
; Publication No. US20030171311A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat  
; TITLE OF INVENTION: Hepatitis C Virus Infection  
; FILE REFERENCE: MBHB00-801-F  
; CURRENT APPLICATION NUMBER: US/09/817,879  
; CURRENT FILING DATE: 2001-03-26  
; NUMBER OF SEQ ID NOS: 9703  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2132  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION:  
; OTHER INFORMATION: oligonucleotide substrate  
US-09-817-879-2132

Query Match 61.9%; Score 13; DB 12; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.3e+04;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 9 GGGGGTGGTGGG 21  
| | | | | : | : | | |  
Db 17 GGGGGTGGTGGG 5

RESULT 9  
US-09-817-879-2133/c  
; Sequence 2133, Application US/09817879  
; Publication No. US20030171311A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat  
; TITLE OF INVENTION: Hepatitis C Virus Infection  
; FILE REFERENCE: MBHB00-801-F  
; CURRENT APPLICATION NUMBER: US/09/817,879  
; CURRENT FILING DATE: 2001-03-26  
; NUMBER OF SEQ ID NOS: 9703  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2133  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION:  
; OTHER INFORMATION: oligonucleotide substrate  
US-09-817-879-2133

Query Match 61.9%; Score 13; DB 12; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.3e+04;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 9 GGGGGTGGTGGG 21  
| | | | | : | : | | |  
Db 14 GGGGGTGGTGGG 2

RESULT 10  
US-09-817-879-2422  
; Sequence 2422, Application US/09817879  
; Publication No. US20030171311A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat  
; TITLE OF INVENTION: Hepatitis C Virus Infection  
; FILE REFERENCE: MBHB00-801-F  
; CURRENT APPLICATION NUMBER: US/09/817,879  
; CURRENT FILING DATE: 2001-03-26  
; NUMBER OF SEQ ID NOS: 9703  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2422  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION:  
; OTHER INFORMATION: oligonucleotide substrate  
US-09-817-879-2422

Query Match 61.9%; Score 13; DB 12; Length 17;  
Best Local Similarity 84.6%; Pred. No. 3.3e+04;  
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
QY 9 GGGGGTGGTGGG 21  
| | | | | : | : | | |  
Db 5 GGGGGUGUGGGG 17

RESULT 11  
US-09-817-879-2423  
; Sequence 2423, Application US/09817879  
; Publication No. US20030171311A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat  
; TITLE OF INVENTION: Hepatitis C Virus Infection  
; FILE REFERENCE: MBHB00-801-F

; CURRENT APPLICATION NUMBER: US/09/817,879  
; CURRENT FILING DATE: 2001-03-26  
; NUMBER OF SEQ ID NOS: 9703  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2423  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION:  
; OTHER INFORMATION: oligonucleotide substrate  
US-09-817-879-2423

Query Match 61.9%; Score 13; DB 12; Length 17;  
Best Local Similarity 84.6%; Pred. No. 3.3e+04;  
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGGGGTGGTGGG 21  
|||:|||||  
Db 2 GGGGUGUGGGG 14

## RESULT 12

US-09-828-034-31/c  
; Sequence 31, Application US/09828034  
; Patent No. US2002064771A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhong, Weidong  
; APPLICANT: Hong, Zhi  
; TITLE OF INVENTION: HCV REPLICASE COMPLEXES  
; FILE REFERENCE: IN01165  
; CURRENT APPLICATION NUMBER: US/09/828,034  
; CURRENT FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: U.S. 60/195,852  
; PRIOR FILING DATE: 2000-04-06  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 31  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA  
US-09-828-034-31

Query Match 61.9%; Score 13; DB 9; Length 21;  
Best Local Similarity 76.2%; Pred. No. 3.2e+04;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGTGGAGGGGGTGGGG 21  
|||:|||||  
Db 21 GTGGTGGTGGTGGTGGTG 1

## RESULT 13

US-10-059-877-26  
; Sequence 26, Application US/10059877  
; Publication No. US20030157490A1  
; GENERAL INFORMATION:  
; APPLICANT: CHAO, LEE  
; APPLICANT: CHAO, JULIE  
; APPLICANT: SONG, QING  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CORRELATING  
; TITLE OF INVENTION: TISSUE KALLIKREIN GENE PROMOTER POLYMORPHISMS WITH ESSENTIAL  
; FILE REFERENCE: 19113.0081U2  
; CURRENT APPLICATION NUMBER: US/10/059,877  
; CURRENT FILING DATE: 2002-01-29  
; PRIOR APPLICATION NUMBER: 09/495,140  
; PRIOR FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: 09/389,566

; PRIOR FILING DATE: 1999-09-03  
; PRIOR APPLICATION NUMBER: 08/856,141  
; PRIOR FILING DATE: 1997-05-14  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 26  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: /No. US20030157490A1e =  
; OTHER INFORMATION: synthetic construct  
US-10-059-877-26

Query Match 61.0%; Score 12.8; DB 12; Length 17;  
Best Local Similarity 87.5%; Pred. No. 4e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GGAGGGGGTGGTGGG 21  
|||:|||||  
Db 1 GGAGGGGGGGGGGG 16

## RESULT 14

US-10-303-109A-30/c  
; Sequence 30, Application US/10303109A  
; Publication No. US20030194726A1  
; GENERAL INFORMATION:  
; APPLICANT: BOLCHAKOVA, Elena  
; APPLICANT: ROZZELLE, James  
; TITLE OF INVENTION: Thermus Oshimai Nucleic Acid Polymerases  
; FILE REFERENCE: 4777US  
; CURRENT APPLICATION NUMBER: US/10/303,109A  
; CURRENT FILING DATE: 2002-11-22  
; PRIOR APPLICATION NUMBER: US 60/334,798  
; PRIOR FILING DATE: 2001-11-30  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 30  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Thermus oshimai  
US-10-303-109A-30

Query Match 61.0%; Score 12.8; DB 12; Length 17;  
Best Local Similarity 87.5%; Pred. No. 4e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 TGGAGGGGGTGGTGGG 20  
|||:|||||  
Db 16 TGGAGGTGGAGGTGGG 1

## RESULT 15

US-10-059-888-26  
; Sequence 26, Application US/10059888  
; Publication No. US20030025882A1  
; GENERAL INFORMATION:  
; APPLICANT: CHAO, LEE  
; APPLICANT: CHAO, JULIE  
; APPLICANT: SONG, QING  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CORRELATING  
; TITLE OF INVENTION: TISSUE KALLIKREIN GENE PROMOTER POLYMORPHISMS WITH ESSENTIAL  
; FILE REFERENCE: 19113.0081U2  
; CURRENT APPLICATION NUMBER: US/10/059,888  
; CURRENT FILING DATE: 2002-01-29  
; PRIOR APPLICATION NUMBER: 09/495,140  
; PRIOR FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: 09/389,566  
; PRIOR FILING DATE: 1999-09-03  
; PRIOR APPLICATION NUMBER: 08/856,141  
; PRIOR FILING DATE: 1997-05-14

```
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030025882A1e =
; OTHER INFORMATION: synthetic construct
US-10-059-888-26

Query Match      61.0%; Score 12.8; DB 14; Length 17;
Best Local Similarity 87.5%; Pred. No. 4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      6 GGAGGGGGTGGTGGG 21
        |||||
Db       1 GGAGGGGGGGGGGGG 16

Search completed: October 27, 2003, 19:00:53
Job time : 453.6 secs
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:35 ; Search time 2749 Seconds  
(without alignments)  
253.343 Million cell updates/sec

Title: US-09-331-204A-6  
Perfect score: 21  
Sequence: 1 999ttggagg999t99t999g 21

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 33363688 seqs, 16581889874 residues

Total number of hits satisfying chosen parameters: 2938060

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents\_NA\_Main:\*

1: /cgn2\_6/ptodata/1/pna/PCTUS COMB.seq.\*  
2: /cgn2\_6/ptodata/1/pna/PCTUS COMB.seq.\*  
3: /cgn2\_6/ptodata/1/pna/US06 COMB.seq.\*  
4: /cgn2\_6/ptodata/1/pna/US07 COMB.seq.\*  
5: /cgn2\_6/ptodata/1/pna/US08 COMB.seq.\*  
6: /cgn2\_6/ptodata/1/pna/US081 COMB.seq.\*  
7: /cgn2\_6/ptodata/1/pna/US082 COMB.seq.\*  
8: /cgn2\_6/ptodata/1/pna/US083 COMB.seq.\*  
9: /cgn2\_6/ptodata/1/pna/US084 COMB.seq.\*  
10: /cgn2\_6/ptodata/1/pna/US085 COMB.seq.\*  
11: /cgn2\_6/ptodata/1/pna/US086 COMB.seq.\*  
12: /cgn2\_6/ptodata/1/pna/US087 COMB.seq.\*  
13: /cgn2\_6/ptodata/1/pna/US088 COMB.seq.\*  
14: /cgn2\_6/ptodata/1/pna/US089 COMB.seq.\*  
15: /cgn2\_6/ptodata/1/pna/US090 COMB.seq.\*  
16: /cgn2\_6/ptodata/1/pna/US091 COMB.seq.\*  
17: /cgn2\_6/ptodata/1/pna/US092A COMB.seq.\*  
18: /cgn2\_6/ptodata/1/pna/US092B COMB.seq.\*  
19: /cgn2\_6/ptodata/1/pna/US093A COMB.seq.\*  
20: /cgn2\_6/ptodata/1/pna/US093B COMB.seq.\*  
21: /cgn2\_6/ptodata/1/pna/US094 COMB.seq.\*  
22: /cgn2\_6/ptodata/1/pna/US095A COMB.seq.\*  
23: /cgn2\_6/ptodata/1/pna/US095B COMB.seq.\*  
24: /cgn2\_6/ptodata/1/pna/US095C COMB.seq.\*  
25: /cgn2\_6/ptodata/1/pna/US095D COMB.seq.\*  
26: /cgn2\_6/ptodata/1/pna/US096A COMB.seq.\*  
27: /cgn2\_6/ptodata/1/pna/US096B COMB.seq.\*  
28: /cgn2\_6/ptodata/1/pna/US096C COMB.seq.\*  
29: /cgn2\_6/ptodata/1/pna/US096D COMB.seq.\*  
30: /cgn2\_6/ptodata/1/pna/US096E COMB.seq.\*  
31: /cgn2\_6/ptodata/1/pna/US097A COMB.seq.\*  
32: /cgn2\_6/ptodata/1/pna/US097B COMB.seq.\*  
33: /cgn2\_6/ptodata/1/pna/US097C COMB.seq.\*  
34: /cgn2\_6/ptodata/1/pna/US098A COMB.seq.\*  
35: /cgn2\_6/ptodata/1/pna/US098B COMB.seq.\*  
36: /cgn2\_6/ptodata/1/pna/US098C COMB.seq.\*  
37: /cgn2\_6/ptodata/1/pna/US098D COMB.seq.\*  
38: /cgn2\_6/ptodata/1/pna/US099A COMB.seq.\*  
39: /cgn2\_6/ptodata/1/pna/US099B COMB.seq.\*  
40: /cgn2\_6/ptodata/1/pna/US099C COMB.seq.\*  
41: /cgn2\_6/ptodata/1/pna/US099D COMB.seq.\*  
42: /cgn2\_6/ptodata/1/pna/US099E COMB.seq.\*  
43: /cgn2\_6/ptodata/1/pna/US099F COMB.seq.\*

44: /cgn2\_6/ptodata/1/pna/US100A COMB.seq.\*  
45: /cgn2\_6/ptodata/1/pna/US100B COMB.seq.\*  
46: /cgn2\_6/ptodata/1/pna/US101A COMB.seq.\*  
47: /cgn2\_6/ptodata/1/pna/US101B COMB.seq.\*  
48: /cgn2\_6/ptodata/1/pna/US102A COMB.seq.\*  
49: /cgn2\_6/ptodata/1/pna/US102B COMB.seq.\*  
50: /cgn2\_6/ptodata/1/pna/US103A COMB.seq.\*  
51: /cgn2\_6/ptodata/1/pna/US103B COMB.seq.\*  
52: /cgn2\_6/ptodata/1/pna/US104A COMB.seq.\*  
53: /cgn2\_6/ptodata/1/pna/US104B COMB.seq.\*  
54: /cgn2\_6/ptodata/1/pna/US6000 COMB.seq.\*  
55: /cgn2\_6/ptodata/1/pna/US6001 COMB.seq.\*  
56: /cgn2\_6/ptodata/1/pna/US6002 COMB.seq.\*  
57: /cgn2\_6/ptodata/1/pna/US6003 COMB.seq.\*  
58: /cgn2\_6/ptodata/1/pna/US6004 COMB.seq.\*  
59: /cgn2\_6/ptodata/1/pna/US6005 COMB.seq.\*  
60: /cgn2\_6/ptodata/1/pna/US6006 COMB.seq.\*  
61: /cgn2\_6/ptodata/1/pna/US6007 COMB.seq.\*  
62: /cgn2\_6/ptodata/1/pna/US6008 COMB.seq.\*  
63: /cgn2\_6/ptodata/1/pna/US6009 COMB.seq.\*  
64: /cgn2\_6/ptodata/1/pna/US6010 COMB.seq.\*  
65: /cgn2\_6/ptodata/1/pna/US6011 COMB.seq.\*  
66: /cgn2\_6/ptodata/1/pna/US6012 COMB.seq.\*  
67: /cgn2\_6/ptodata/1/pna/US6013 COMB.seq.\*  
68: /cgn2\_6/ptodata/1/pna/US6014 COMB.seq.\*  
69: /cgn2\_6/ptodata/1/pna/US6015 COMB.seq.\*  
70: /cgn2\_6/ptodata/1/pna/US6016 COMB.seq.\*  
71: /cgn2\_6/ptodata/1/pna/US6017 COMB.seq.\*  
72: /cgn2\_6/ptodata/1/pna/US6018 COMB.seq.\*  
73: /cgn2\_6/ptodata/1/pna/US6019 COMB.seq.\*  
74: /cgn2\_6/ptodata/1/pna/US6020 COMB.seq.\*  
75: /cgn2\_6/ptodata/1/pna/US6021 COMB.seq.\*  
76: /cgn2\_6/ptodata/1/pna/US6022 COMB.seq.\*  
77: /cgn2\_6/ptodata/1/pna/US6023A COMB.seq.\*  
78: /cgn2\_6/ptodata/1/pna/US6023B COMB.seq.\*  
79: /cgn2\_6/ptodata/1/pna/US6024 COMB.seq.\*  
80: /cgn2\_6/ptodata/1/pna/US6025 COMB.seq.\*  
81: /cgn2\_6/ptodata/1/pna/US6026 COMB.seq.\*  
82: /cgn2\_6/ptodata/1/pna/US6027 COMB.seq.\*  
83: /cgn2\_6/ptodata/1/pna/US6028 COMB.seq.\*  
84: /cgn2\_6/ptodata/1/pna/US6029 COMB.seq.\*  
85: /cgn2\_6/ptodata/1/pna/US6030 COMB.seq.\*  
86: /cgn2\_6/ptodata/1/pna/US6031 COMB.seq.\*  
87: /cgn2\_6/ptodata/1/pna/US6032 COMB.seq.\*  
88: /cgn2\_6/ptodata/1/pna/US6033 COMB.seq.\*  
89: /cgn2\_6/ptodata/1/pna/US6034 COMB.seq.\*  
90: /cgn2\_6/ptodata/1/pna/US6035 COMB.seq.\*  
91: /cgn2\_6/ptodata/1/pna/US6036 COMB.seq.\*  
92: /cgn2\_6/ptodata/1/pna/US6037 COMB.seq.\*  
93: /cgn2\_6/ptodata/1/pna/US6038 COMB.seq.\*  
94: /cgn2\_6/ptodata/1/pna/US6039 COMB.seq.\*  
95: /cgn2\_6/ptodata/1/pna/US6040 COMB.seq.\*  
96: /cgn2\_6/ptodata/1/pna/US6041 COMB.seq.\*  
97: /cgn2\_6/ptodata/1/pna/US6042 COMB.seq.\*  
98: /cgn2\_6/ptodata/1/pna/US6043 COMB.seq.\*  
99: /cgn2\_6/ptodata/1/pna/US6044 COMB.seq.\*  
100: /cgn2\_6/ptodata/1/pna/US6045 COMB.seq.\*  
101: /cgn2\_6/ptodata/1/pna/US6046 COMB.seq.\*  
102: /cgn2\_6/ptodata/1/pna/US6047 COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match %	Score	Length	ID	Description
1	21	100.0	21	8	US-08-387-041A-4 Sequence 4, Appli
2	21	100.0	21	19	US-09-331-204-6 Sequence 6, Appli
3	21	100.0	21	19	US-09-331-204A-6 Sequence 6, Appli
4	18	85.7	18	8	US-08-387-041A-3 Sequence 3, Appli

5 18 85.7 18 19 US-09-331-204-1  
6 18 85.7 18 19 US-09-331-204A-4  
7 18 85.7 18 33 US-09-786-436-17  
8 18 85.7 18 33 US-09-786-436-42  
9 16.4 78.1 18 19 US-09-331-204-5  
10 16.4 78.1 18 19 US-09-331-204A-8  
11 14.8 70.5 18 19 US-09-331-204A-7  
12 14.8 70.5 18 19 US-09-331-204A-9  
13 14.8 70.5 19 19 US-09-331-204-4  
14 14.8 70.5 22 50 US-10-303-778-3043  
15 14.6 69.5 21 50 US-10-310-188-41819  
16 14.6 69.5 22 5 US-08-013-418-17  
17 14.6 69.5 22 5 US-08-021-613-17  
18 14.6 69.5 22 6 US-08-172-676-17  
19 14.6 69.5 22 50 US-10-310-188-51871  
20 14.4 68.6 18 50 US-10-310-188-27376  
21 14.4 68.6 19 50 US-10-310-188-41647  
22 14.4 68.6 19 50 US-10-310-188-38943  
23 14.4 68.6 19 50 US-10-310-188-46976  
24 14.4 68.6 22 50 US-10-310-188-26689  
25 14.4 68.6 22 50 US-10-310-188-42141  
26 14.2 67.6 19 50 US-10-310-188-78687  
27 14.2 67.6 20 9 US-08-463-519-5  
28 14.2 67.6 21 50 US-10-310-188-51847  
29 14.2 67.6 21 50 US-10-310-188-55389  
30 14.2 67.6 22 9 US-08-472-801-186  
31 14.2 67.6 22 9 US-08-668-235-2660  
32 14.2 67.6 22 11 US-08-668-235-186  
33 14.2 67.6 22 11 US-08-668-235-2660  
34 14.2 67.6 22 47 US-10-160-499-186  
35 14.2 67.6 22 47 US-10-160-499-2660  
36 14.2 67.6 22 50 US-10-310-188-63940  
37 14 66.7 19 50 US-10-310-188-27360  
38 13.8 65.7 19 50 US-10-310-188-18278  
39 13.8 65.7 19 50 US-10-310-188-47426  
40 13.8 65.7 19 50 US-10-310-188-61865  
41 13.8 65.7 20 49 US-10-266-090-40745  
42 13.8 65.7 20 49 US-10-266-090-43563  
43 13.8 65.7 20 50 US-10-310-188-18418  
44 13.8 65.7 20 50 US-10-310-188-39237  
45 13.8 65.7 21 50 US-10-310-188-75562

ALIGNMENTS

RESULT 1  
US-08-387-041A-4  
; Sequence 4, Application US/08387041A  
; GENERAL INFORMATION:  
; APPLICANT: Tam, Robert C.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATION  
; TITLE OF INVENTION: OF CD28 EXPRESSION  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/387,041A  
; FILING DATE: 02-FEB-1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Halluin, Albert P.  
; REGISTRATION NUMBER: 25,227

Sequence 1, Appli  
Sequence 4, Appli  
Sequence 17, Appli  
Sequence 42, Appli  
Sequence 5, Appli  
Sequence 8, Appli  
Sequence 9, Appli  
Sequence 4, Appli  
Sequence 3043, Ap  
Sequence 41819, A  
Sequence 17, Appli  
Sequence 17, Appli  
Sequence 51871, A  
Sequence 27376, A  
Sequence 41647, A  
Sequence 38943, A  
Sequence 46976, A  
Sequence 26689, A  
Sequence 42141, A  
Sequence 78687, A  
Sequence 5, Appli  
Sequence 51847, A  
Sequence 55389, A  
Sequence 186, App  
Sequence 2660, Ap  
Sequence 186, App  
Sequence 2660, Ap  
Sequence 186, App  
Sequence 63940, A  
Sequence 27360, A  
Sequence 18278, A  
Sequence 47426, A  
Sequence 61865, A  
Sequence 40745, A  
Sequence 43563, A  
Sequence 18418, A  
Sequence 39237, A  
Sequence 75562, A

; REFERENCE/DOCKET NUMBER: 8250-011  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-854-3660  
; TELEFAX: 415-854-3694  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 21 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
US-08-387-041A-4

Query Match 100.0%; Score 21; DB 8; Length 21;  
Best Local Similarity 100.0%; Pred.No. 1.1e+03;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTTGGAGGGGGTGGTGGGG 21  
|||  
Db 1 GGGTTGGAGGGGGTGGTGGGG 21

RESULT 2  
US-09-331-204-6  
; Sequence 6, Application US/09331204  
; GENERAL INFORMATION:  
; APPLICANT: Tam, Robert  
; TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN  
; TITLE OF INVENTION: IMMUNE RESPONSE  
; FILE REFERENCE: ICNSequence  
; CURRENT APPLICATION NUMBER: US/09/331,204  
; CURRENT FILING DATE: 1999-08-20  
; PRIOR APPLICATION NUMBER: PCT/US97/23927  
; PRIOR FILING DATE: 1997-12-19  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: An oligomer  
; OTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic  
; OTHER INFORMATION: acid. This term includes oligomers consisting of  
; OTHER INFORMATION: naturally occurring bases, sugars and intersugar (  
US-09-331-204-6

Query Match 100.0%; Score 21; DB 19; Length 21;  
Best Local Similarity 100.0%; Pred.No. 1.1e+03;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTTGGAGGGGGTGGTGGGG 21  
|||  
Db 1 GGGTTGGAGGGGGTGGTGGGG 21

RESULT 3  
US-09-331-204A-6  
; Sequence 6, Application US/09331204A  
; GENERAL INFORMATION:  
; APPLICANT: ICN Pharmaceuticals, Inc.  
; TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Resi  
; FILE REFERENCE: 216/013-US1  
; CURRENT APPLICATION NUMBER: US/09/331,204A  
; CURRENT FILING DATE: 1999-08-20  
; PRIOR APPLICATION NUMBER: PCT/US97/23927  
; PRIOR FILING DATE: 1997-12-19  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 6  
; LENGTH: 21



```
/ TYPE: DNA
/ ORGANISM: synthetic construct
US-09-331-204A-6

Query Match      100.0%; Score 21; DB 19; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTTGAGGGGGTGGTGGG 21
      |||||
Db      1 GGGTTGAGGGGGTGGTGGG 21

RESULT 4
US-08-387-041A-3
; Sequence 3, Application US/08387041A
; GENERAL INFORMATION:
; APPLICANT: Tam, Robert C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATION
; TITLE OF INVENTION: OF CD28 EXPRESSION
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,041A
; FILING DATE: 02-FEB-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8250-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-387-041A-3

Query Match      85.7%; Score 18; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 TTGGAGGGGGTGGTGGG 21
      |||||
Db      1 TTGGAGGGGGTGGTGGG 18

RESULT 5
US-09-331-204-1
; Sequence 1, Application US/09331204
; GENERAL INFORMATION:
; APPLICANT: Tam, Robert
; TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN
; TITLE OF INVENTION: IMMUNE RESPONSE
; FILE REFERENCE: ICNSequence
; CURRENT APPLICATION NUMBER: US/09/331,204
; CURRENT FILING DATE: 1999-08-20
```

```
/ PRIOR APPLICATION NUMBER: PCT/US97/23927
/ PRIOR FILING DATE: 1997-12-19
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 18
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: An oligomer
/ OTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic
/ OTHER INFORMATION: acid including oligomers consisting of naturally
/ OTHER INFORMATION: occurring bases, sugars and intersugar
US-09-331-204-1

Query Match      85.7%; Score 18; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 TTGGAGGGGGTGGTGGG 21
      |||||
Db      1 TTGGAGGGGGTGGTGGG 18

RESULT 6
US-09-331-204A-4
; Sequence 4, Application US/09331204A
; GENERAL INFORMATION:
; APPLICANT: ICN Pharmaceuticals, Inc.
; APPLICANT: Tam, Robert
; TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Resp
; FILE REFERENCE: 216/013-US1
; CURRENT APPLICATION NUMBER: US/09/331,204A
; CURRENT FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: PCT/US97/23927
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 18
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-331-204A-4

Query Match      85.7%; Score 18; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 TTGGAGGGGGTGGTGGG 21
      |||||
Db      1 TTGGAGGGGGTGGTGGG 18

RESULT 7
US-09-786-436-17
; Sequence 17, Application US/09786436
; GENERAL INFORMATION:
; APPLICANT: Wagner, Hermann
; APPLICANT: Lipford, Grayson
; APPLICANT: Heeg, Klaus
; TITLE OF INVENTION: G-Motif Oligonucleotides and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: C1041/7010 (AWS)
; CURRENT APPLICATION NUMBER: US/09/786,436
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: PCT/EP99/06502
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-09-786-436-17

Query Match 85.7%; Score 18; DB 33; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TTGGAGGGGGTGGTGGG 21  
|||||  
Db 1 TTGGAGGGGGTGGTGGG 18

RESULT 8  
US-09-786-436-42/c  
; Sequence 42, Application US/09786436  
; GENERAL INFORMATION:  
; APPLICANT: Wagner, Hermann  
; APPLICANT: Lipford, Grayson  
; APPLICANT: Heeg, Klaus  
; TITLE OF INVENTION: G-Motif Oligonucleotides and Uses  
; FILE REFERENCE: C1041/7010 (AWS)  
; CURRENT APPLICATION NUMBER: US/09/786,436  
; PRIOR FILING DATE: 2001-03-02  
; PRIOR FILING DATE: 1999-09-03  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 42  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-09-786-436-42

Query Match 85.7%; Score 18; DB 33; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TTGGAGGGGGTGGTGGG 21  
|||||  
Db 18 TTGGAGGGGGTGGTGGG 1

RESULT 9  
US-09-331-204-5  
; Sequence 5, Application US/09331204  
; GENERAL INFORMATION:  
; APPLICANT: Tam, Robert  
; TITLE OF INVENTION: G-RICH OLIGO APAMERS AND METHODS OF MODULATING AN  
; FILE REFERENCE: ICNSequence  
; CURRENT APPLICATION NUMBER: US/09/331,204  
; CURRENT FILING DATE: 1999-08-20  
; PRIOR FILING DATE: 1997-12-19  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: An oligomer  
; OTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic  
; OTHER INFORMATION: acid. This term includes oligomers consisting of  
; OTHER INFORMATION: naturally occurring bases, sugars and intersugar (

Query Match 78.1%; Score 16.4; DB 19; Length 18;  
Best Local Similarity 94.4%; Pred. No. 4.5e+04;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 4 TTGGAGGGGGTGGTGGG 21  
|||||  
Db 1 TTGGAGGGGGAGGTGGG 18

RESULT 10  
US-09-331-204A-8  
; Sequence 8, Application US/09331204A  
; GENERAL INFORMATION:  
; APPLICANT: ICN Pharmaceuticals, Inc.  
; APPLICANT: Tam, Robert  
; TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Res  
; FILE REFERENCE: 216/013-US1  
; CURRENT APPLICATION NUMBER: US/09/331,204A  
; PRIOR FILING DATE: 1999-08-20  
; PRIOR FILING DATE: PCT/US97/23927  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 8  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: synthetic construct  
US-09-331-204A-8

Query Match 78.1%; Score 16.4; DB 19; Length 18;  
Best Local Similarity 94.4%; Pred. No. 4.5e+04;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TTGGAGGGGGTGGTGGG 21  
|||||  
Db 1 TTGGAGGGGGAGGTGGG 18

RESULT 11  
US-09-331-204A-7  
; Sequence 7, Application US/09331204A  
; GENERAL INFORMATION:  
; APPLICANT: ICN Pharmaceuticals, Inc.  
; APPLICANT: Tam, Robert  
; TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Res  
; FILE REFERENCE: 216/013-US1  
; CURRENT APPLICATION NUMBER: US/09/331,204A  
; CURRENT FILING DATE: 1999-08-20  
; PRIOR FILING DATE: PCT/US97/23927  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 7  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: synthetic construct  
US-09-331-204A-7

Query Match 70.5%; Score 14.8; DB 19; Length 18;  
Best Local Similarity 88.9%; Pred. No. 1.7e+05;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TTGGAGGGGGTGGTGGG 21  
|||||  
Db 1 TTGGAGGGGGAGGTGGG 18

RESULT 12  
US-09-331-204A-9  
; Sequence 9, Application US/09331204A  
; GENERAL INFORMATION:  
; APPLICANT: ICN Pharmaceuticals, Inc.  
; APPLICANT: Tam, Robert  
; TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Res  
; FILE REFERENCE: 216/013-US1

;/ CURRENT APPLICATION NUMBER: US/09/331,204A  
;/ CURRENT FILING DATE: 1999-08-20  
;/ PRIOR APPLICATION NUMBER: PCT/US97/23927  
;/ PRIOR FILING DATE: 1997-12-19  
;/ NUMBER OF SEQ ID NOS: 28  
;/ SOFTWARE: PatentIn version 3.0  
;/ SEQ ID NO 9  
;/ LENGTH: 18  
;/ TYPE: DNA  
;/ ORGANISM: synthetic construct  
US-09-331-204A-9

Query Match 70.5%; Score 14.8; DB 19; Length 18;  
Best Local Similarity 88.9%; Pred. No. 1.7e+05;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TTGGAGGGGGTGGTGGG 21  
|||||  
Db 1 TTGGAGCGGTGGTGGCG 18

RESULT 13  
US-09-331-204-4  
;/ Sequence 4, Application US/09331204  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Tam, Robert  
;/ TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN  
;/ FILE REFERENCE: ICNSequence  
;/ CURRENT APPLICATION NUMBER: US/09/331,204  
;/ CURRENT FILING DATE: 1999-08-20  
;/ PRIOR APPLICATION NUMBER: PCT/US97/23927  
;/ PRIOR FILING DATE: 1997-12-19  
;/ NUMBER OF SEQ ID NOS: 6  
;/ SOFTWARE: PatentIn Ver. 2.0  
;/ SEQ ID NO 4  
;/ LENGTH: 19  
;/ TYPE: DNA  
;/ ORGANISM: Artificial Sequence  
;/ FEATURE:  
;/ OTHER INFORMATION: Description of Artificial Sequence: An oligomer  
;/ OTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic  
;/ OTHER INFORMATION: acid. This term includes oligomers consisting of  
;/ OTHER INFORMATION: naturally occurring bases, sugars and intersugar (  
US-09-331-204-4

Query Match 70.5%; Score 14.8; DB 19; Length 19;  
Best Local Similarity 88.9%; Pred. No. 1.7e+05;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TTGGAGGGGGTGGTGGG 21  
|||||  
Db 1 TTGGAGGGGGAGGAGGGG 18

RESULT 14  
US-10-303-778-3043  
;/ Sequence 3043, Application US/10303778  
;/ GENERAL INFORMATION:  
;/ APPLICANT: RosettaGenomics  
;/ TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL  
;/ TITLE OF INVENTION: REGULATORY GENES AND USES THEREOF  
;/ FILE REFERENCE: 47416  
;/ CURRENT APPLICATION NUMBER: US/10/303,778  
;/ CURRENT FILING DATE: 2002-11-26  
;/ NUMBER OF SEQ ID NOS: 17608  
;/ SOFTWARE: PatentIn version 3.1  
;/ SEQ ID NO 3043  
;/ LENGTH: 22  
;/ TYPE: DNA  
;/ ORGANISM: Homo sapiens  
US-10-303-778-3043

Query Match 70.5%; Score 14.8; DB 50; Length 22;  
Best Local Similarity 88.9%; Pred. No. 1.6e+05;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GGGTTGGAGGGGGTGGTG 18  
|||||  
Db 5 GGGCTTGAGGGGGTGGTG 22

RESULT 15  
US-10-310-188-41819  
;/ Sequence 41819, Application US/10310188  
;/ GENERAL INFORMATION:  
;/ APPLICANT: RosettaGenomics  
;/ TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN  
;/ TITLE OF INVENTION: USES THEREOF  
;/ FILE REFERENCE: 47487  
;/ CURRENT APPLICATION NUMBER: US/10/310,188  
;/ CURRENT FILING DATE: 2002-12-19  
;/ NUMBER OF SEQ ID NOS: 86841  
;/ SOFTWARE: PatentIn version 3.1  
;/ SEQ ID NO 41819  
;/ LENGTH: 21  
;/ TYPE: DNA  
;/ ORGANISM: Homo sapiens  
US-10-310-188-41819

Query Match 69.5%; Score 14.6; DB 50; Length 21;  
Best Local Similarity 81.0%; Pred. No. 1.9e+05;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGTTGGAGGGGGTGGGG 21  
|||||  
Db 1 GGGAGGAGGGGGTGGGCGG 21

Search completed: October 27, 2003, 17:52:53  
Job time : 2750 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 11:09:34 ; Search time 358.2 Seconds  
(without alignments)  
97.777 Million cell updates/sec

Title: US-09-331-204A-6  
Perfect score: 21  
Sequence: 1 ggggttgagggggtgtgggg 21

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2231628 seqs, 833900706 residues

Total number of hits satisfying chosen parameters: 264402

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents\_NA\_New: \*  
1: /cgn2\_6/ptodata/1/pna/pct\_NEW\_COMB.seq: \*  
2: /cgn2\_6/ptodata/1/pna/US05\_NEW\_COMB.seq: \*  
3: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq: \*  
4: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq: \*  
5: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq: \*  
6: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq: \*  
7: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	14.6	69.5	21	1	PCT-US02-38216-41819 Sequence 41819, A
2	14.6	69.5	22	1	PCT-US02-38216-51871 Sequence 51871, A
3	14.4	68.6	18	1	PCT-US02-38216-27376 Sequence 27376, A
4	14.4	68.6	18	1	PCT-US02-38216-41647 Sequence 41647, A
5	14.4	68.6	19	1	PCT-US02-38216-38943 Sequence 38943, A
6	14.4	68.6	19	1	PCT-US02-38216-46976 Sequence 46976, A
7	14.4	68.6	22	1	PCT-US02-38216-26689 Sequence 26689, A
8	14.4	68.6	22	1	PCT-US02-38216-42141 Sequence 42141, A
9	14.2	67.6	19	1	PCT-US02-38216-78687 Sequence 78687, A
10	14.2	67.6	20	5	US-09-978-333B-2 Sequence 2, Appli
11	14.2	67.6	20	5	US-09-978-333C-2 Sequence 2, Appli
12	14.2	67.6	21	1	PCT-US02-38216-51847 Sequence 51847, A
13	14.2	67.6	21	1	PCT-US02-38216-55389 Sequence 55389, A
14	14.2	67.6	22	1	PCT-US02-38216-63940 Sequence 63940, A
15	14	66.7	19	1	PCT-US02-38216-27360 Sequence 27360, A
16	13.8	65.7	19	1	PCT-US02-38216-18278 Sequence 18278, A
17	13.8	65.7	19	1	PCT-US02-38216-47426 Sequence 47426, A
18	13.8	65.7	19	1	PCT-US02-38216-61865 Sequence 61865, A
19	13.8	65.7	20	1	PCT-US02-38216-18418 Sequence 18418, A
20	13.8	65.7	20	1	PCT-US02-38216-39237 Sequence 39237, A
21	13.8	65.7	21	1	PCT-US02-38216-75562 Sequence 75562, A
22	13.6	64.8	21	1	PCT-US02-38216-41967 Sequence 41967, A
23	13.6	64.8	21	1	PCT-US02-38216-72839 Sequence 72839, A
24	13.6	64.8	21	1	PCT-US02-38216-78761 Sequence 78761, A
25	13.6	64.8	21	1	PCT-US02-38216-84959 Sequence 84959, A
26	13.6	64.8	22	1	PCT-US02-38216-18413 Sequence 18413, A

27	13.6	64.8	22	1	PCT-US02-38216-39492 Sequence 39492, A
28	13.6	64.8	22	1	PCT-US02-38216-57248 Sequence 57248, A
29	13.4	63.8	18	1	PCT-US02-38216-10539 Sequence 10539, A
30	13.4	63.8	18	1	PCT-US02-38216-38927 Sequence 38927, A
31	13.4	63.8	19	1	PCT-US02-38216-53577 Sequence 53577, A
32	13.4	63.8	20	1	PCT-US02-38216-41804 Sequence 41804, A
33	13.4	63.8	21	1	PCT-US02-38216-55622 Sequence 55622, A
34	13.4	63.8	21	1	PCT-US02-38216-57364 Sequence 57364, A
35	13.4	63.8	22	1	PCT-US02-38216-10603 Sequence 10603, A
36	13.2	62.9	18	1	PCT-US02-38216-9731 Sequence 9731, Ap
37	13.2	62.9	18	1	PCT-US02-38216-29535 Sequence 29535, A
38	13.2	62.9	18	1	PCT-US02-38216-51842 Sequence 51842, A
39	13.2	62.9	18	1	PCT-US02-38216-51896 Sequence 51896, A
40	13.2	62.9	18	1	PCT-US02-38216-61077 Sequence 61077, A
41	13.2	62.9	18	1	PCT-US02-38216-86378 Sequence 86378, A
42	13.2	62.9	19	1	PCT-US02-38216-68852 Sequence 68852, A
43	13.2	62.9	19	1	PCT-US02-38216-69453 Sequence 69453, A
44	13.2	62.9	20	1	PCT-US02-38216-10564 Sequence 10564, A
45	13.2	62.9	21	1	PCT-US02-38216-26725 Sequence 26725, A

ALIGNMENTS

RESULT 1  
PCT-US02-38216-41819  
; Sequence 41819, Application PC/TUS0238216  
; GENERAL INFORMATION:  
; APPLICANT: Rosetta Genomics LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
; FILE REFERENCE: 55002  
; CURRENT APPLICATION NUMBER: PCT/US02/38216  
; CURRENT FILING DATE: 2002-11-12  
; NUMBER OF SEQ ID NOS: 86841  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 41819  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US02-38216-41819

Query Match 69.5%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 1.5e+04;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGTTCGAGGGGGTGGTGGG 21  
||| ||||| |||  
Db 1 GGGGAGGAGGGGGTGGGCGG 21

RESULT 2  
PCT-US02-38216-51871  
; Sequence 51871, Application PC/TUS0238216  
; GENERAL INFORMATION:  
; APPLICANT: Rosetta Genomics LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
; FILE REFERENCE: 55002  
; CURRENT APPLICATION NUMBER: PCT/US02/38216  
; CURRENT FILING DATE: 2002-11-12  
; NUMBER OF SEQ ID NOS: 86841  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 51871  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US02-38216-51871

Query Match 69.5%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 1.5e+04;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
QY 1 GGGTTGAGGGGGTGGTGGG 21
Db 1 GGGTGGGGTGGGGTGGG 21

RESULT 3
PCT-US02-38216-27376
; Sequence 27376, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27376
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-27376

Query Match
Best Local Similarity 68.6%; Score 14.4; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GTTGGAGGGGGTGGTG 18
Db 1 GGTGGAGGGGGTGGTG 16

RESULT 4
PCT-US02-38216-41647
; Sequence 41647, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 41647
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-41647

Query Match
Best Local Similarity 68.6%; Score 14.4; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GGAGGGGGTGGTGGG 21
Db 1 GGAGGGGGTGGAGGG 16

RESULT 5
PCT-US02-38216-38943
; Sequence 38943, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38943
; LENGTH: 19
```

```
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-38943

Query Match
Best Local Similarity 68.6%; Score 14.4; DB 1; Length 19;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GGAGGGGGTGGTGGG 21
Db 4 GGAGGGGGTGGCGGG 19

RESULT 6
PCT-US02-38216-46976
; Sequence 46976, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46976
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-46976

Query Match
Best Local Similarity 68.6%; Score 14.4; DB 1; Length 19;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GGAGGGGGTGGTGGG 21
Db 4 GGTGGGGGTGGTGGG 19

RESULT 7
PCT-US02-38216-26689/c
; Sequence 26689, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26689
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-26689

Query Match
Best Local Similarity 68.6%; Score 14.4; DB 1; Length 22;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TTGGAGGGGGTGGTG 19
Db 16 TTGGAGGAGGTGGTG 1

RESULT 8
PCT-US02-38216-42141
; Sequence 42141, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
```

; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 42141
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-42141

Query Match 68.6%; Score 14.4; DB 1; Length 22;
Best Local Similarity 93.8%; Pred. No. 1.8e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GGAGGGGGTGGTGGG 21
|||
Db 2 GGTGGGGTGGTGGG 17
|||

RESULT 9
PCT-US02-38216-78687
; Sequence 78687, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 78687
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-78687

Query Match 67.6%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGTGGAGGGGGTGGTGGG 20
|||
Db 1 GGGCGGTGGGGGTGGTGGG 19
|||

RESULT 10
US-09-978-333B-2
; Sequence 2, Application US/09978333B
; GENERAL INFORMATION:
; APPLICANT: Glazer, Peter M.
; TITLE OF INVENTION: Triple-Helix forming Oligonucleotides for Targeted Mutagenesis
; FILE REFERENCE: YU 132
; CURRENT APPLICATION NUMBER: US/09/978,333B
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 09/411,291
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: US 08/476,712
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide AG20
US-09-978-333B-2

Query Match 67.6%; Score 14.2; DB 5; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.1e+04;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 GGTGGAGGGGGTGGTGGG 20
|||
Db 2 GGAAGGGGGGGTGGTGGG 20
|||

RESULT 11
US-09-978-333C-2
; Sequence 2, Application US/09978333C
; GENERAL INFORMATION:
; APPLICANT: Glazer, Peter M.
; TITLE OF INVENTION: Triple-Helix Forming Oligonucleotides for Targeted Mutagenesis
; FILE REFERENCE: YU 132
; CURRENT APPLICATION NUMBER: US/09/978,333C
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 09/411,291
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: US 08/476,712
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide AG20
US-09-978-333C-2

Query Match 67.6%; Score 14.2; DB 5; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGTGGAGGGGGTGGTGGG 20
|||
Db 2 GGAAGGGGGGGTGGTGGG 20
|||

RESULT 12
PCT-US02-38216-51847
; Sequence 51847, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51847
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-51847

Query Match 67.6%; Score 14.2; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 2.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GTTGGAGGGGGTGGTGGG 21
|||
Db 2 GGTGGTGGGGGGTGGTGGG 20
|||

RESULT 13
PCT-US02-38216-55389/c
; Sequence 55389, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51847
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-51847

Search completed: October 27, 2003, 18:22:55  
Job time : 358.2 secs

FILE REFERENCE: 55002  
CURRENT APPLICATION NUMBER: PCT/US02/38216  
CURRENT FILING DATE: 2002-11-12  
NUMBER OF SEQ ID NOS: 86841  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 55389  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Homo sapiens  
PCT-US02-38216-55389

Query Match 67.6%; Score 14.2; DB 1; Length 21;  
Best Local Similarity 84.2%; Pred. No. 2.1e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTTGGAGGGGTGGTGG 19  
Db 20 GGGAAGGAGCGGTGGTGG 2

RESULT 14  
PCT-US02-38216-63940  
Sequence 63940, Application PC/TUS0238216  
GENERAL INFORMATION:  
APPLICANT: Rosetta Genomics LTD  
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
TITLE OF INVENTION: GENES AND USES THEREOF  
FILE REFERENCE: 55002  
CURRENT APPLICATION NUMBER: PCT/US02/38216  
CURRENT FILING DATE: 2002-11-12  
NUMBER OF SEQ ID NOS: 86841  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 63940  
LENGTH: 22  
TYPE: DNA  
ORGANISM: Homo sapiens  
PCT-US02-38216-63940

Query Match 67.6%; Score 14.2; DB 1; Length 22;  
Best Local Similarity 84.2%; Pred. No. 2.1e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GTTGGAGGGGTGGTGGG 21  
Db 1 GGTGGGGGGGTGGGGGG 19

RESULT 15  
PCT-US02-38216-27360  
Sequence 27360, Application PC/TUS0238216  
GENERAL INFORMATION:  
APPLICANT: Rosetta Genomics LTD  
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
TITLE OF INVENTION: GENES AND USES THEREOF  
FILE REFERENCE: 55002  
CURRENT APPLICATION NUMBER: PCT/US02/38216  
CURRENT FILING DATE: 2002-11-12  
NUMBER OF SEQ ID NOS: 86841  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 27360  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Homo sapiens  
PCT-US02-38216-27360

Query Match 66.7%; Score 14; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.5e+04;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGAGGGGGTGGTGG 19  
Db 5 GGAGGGGGTGGTGG 18

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: October 27, 2003, 10:32:29 ; Search time 376.114 Seconds  
(without alignments)  
1957.844 Million cell updates/sec

Title: US-09-331-204A-7  
Perfect score: 18  
Sequence: 1 ttggagggggaggagggg 18

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues  
Total number of hits satisfying chosen parameters: 681044

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:  
1: gb\_ba:  
2: gb\_htg:  
3: gb\_in:  
4: gb\_om:  
5: gb\_ov:  
6: gb\_pat:  
7: gb\_ph:  
8: gb\_pl:  
9: gb\_pr:  
10: gb\_ro:  
11: gb\_sts:  
12: gb\_sy:  
13: gb\_un:  
14: gb\_vi:  
15: em\_ba:  
16: em\_fun:  
17: em\_hum:  
18: em\_in:  
19: em\_mu:  
20: em\_om:  
21: em\_or:  
22: em\_ov:  
23: em\_pat:  
24: em\_ph:  
25: em\_pl:  
26: em\_ro:  
27: em\_sts:  
28: em\_un:  
29: em\_vi:  
30: em\_htg\_hum:  
31: em\_htg\_inv:  
32: em\_htg\_other:  
33: em\_htg\_mus:  
34: em\_htg\_pln:  
35: em\_htg\_rod:  
36: em\_htg\_mam:  
37: em\_htg\_vrt:  
38: em\_sy:  
39: em\_htgo\_hum:  
40: em\_htgo\_mus:  
41: em\_htgo\_other:

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	15.4	85.6	21	6	A31974	A31974 Synthetic H
2	15.4	85.6	21	6	AR131393	AR131393 Sequence
3	15.4	85.6	21	6	BD001798	BD001798 Immunogen
C 4	15	83.3	17	6	AX532425	AX532425 Sequence
C 5	15	83.3	17	6	AX532426	AX532426 Sequence
C 6	15	83.3	17	6	AX532427	AX532427 Sequence
C 7	14.8	82.2	18	6	AX023402	AX023402 Sequence
C 8	14.8	82.2	18	6	AX023427	AX023427 Sequence
C 9	14.4	80.0	17	6	AR029938	AR029938 Sequence
C 10	14	77.8	17	6	AX532424	AX532424 Sequence
C 11	14	77.8	17	6	AX532428	AX532428 Sequence
C 12	13.8	76.7	20	6	AR232303	AR232303 Sequence
C 13	13	72.2	17	6	AX214604	AX214604 Sequence
C 14	13	72.2	17	6	AX214605	AX214605 Sequence
C 15	13	72.2	17	6	AX215457	AX215457 Sequence
C 16	13	72.2	17	6	AX215458	AX215458 Sequence
C 17	13	72.2	17	6	AX215459	AX215459 Sequence
C 18	13	72.2	17	6	AX532423	AX532423 Sequence
C 19	13	72.2	17	6	AX532429	AX532429 Sequence
C 20	12.8	71.1	17	6	AX214603	AX214603 Sequence
C 21	12.8	71.1	17	6	AX215452	AX215452 Sequence
C 22	12.8	71.1	20	6	AR126724	AR126724 Sequence
C 23	12.8	71.1	20	6	AX033457	AX033457 Sequence
C 24	12.8	71.1	20	6	AX037370	AX037370 Sequence
C 25	12.8	71.1	20	6	AX241159	AX241159 Sequence
C 26	12.8	71.1	20	6	AX486754	AX486754 Sequence
C 27	12.8	71.1	20	6	AR072479	AR072479 Sequence
C 28	12.8	71.1	21	6	AR084552	AR084552 Sequence
C 29	12.8	71.1	21	6	AR084564	AR084564 Sequence
C 30	12.8	71.1	21	6	AR084570	AR084570 Sequence
C 31	12.8	71.1	21	6	AR084575	AR084575 Sequence
C 32	12.8	71.1	21	6	AR084581	AR084581 Sequence
C 33	12.8	71.1	21	6	AR084594	AR084594 Sequence
C 34	12.8	71.1	21	6	AR097224	AR097224 Sequence
C 35	12.8	71.1	21	6	AR097224	AR097224 Sequence
C 36	12.4	68.9	15	6	A12051	A12051 Oligonucleo
C 37	12.4	68.9	15	6	A12052	A12052 Oligonucleo
C 38	12.4	68.9	17	6	AX729881	AX729881 Sequence
C 39	12.4	68.9	17	6	AX739210	AX739210 Sequence
C 40	12.4	68.9	18	6	I07756	I07756 Sequence 12
C 41	12.4	68.9	21	6	AX154328	AX154328 Sequence
C 42	12.4	68.9	21	6	AX298242	AX298242 Sequence
C 43	12.4	68.9	22	6	AR116659	AR116659 Sequence
C 44	12.4	68.9	22	6	AR233018	AR233018 Sequence
C 45	12.4	68.9	22	6	AR237949	AR237949 Sequence

ALIGNMENTS

RESULT 1

A31974  
LOCUS A31974 Synthetic HIV-1/2 diagnosis primer.  
DEFINITION Synthetic HIV-1/2 diagnosis primer.  
ACCESSION A31974  
VERSION A31974.1 GI:1567257  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Moncany,M. and Montagnier,L.  
TITLE Nucleotide sequences of retroviral genomes of types HIV-1, HIV-2 and SIV, their uses for the amplification of these genomes and diagnosis in vitro of these viral infections

Pred. No. is the number of results predicted by chance to have a





AUTHORS Shannon,M.  
TITLE Human posh-like protein 1  
JOURNAL Patent: EP 1239051-A 1935 11-SEP-2002;  
Aeomica, Inc. (US)  
FEATURES Location/Qualifiers  
source  
1..17  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
BASE COUNT 1 a 12 c 0 g 4 t  
ORIGIN  
Query Match 83.3%; Score 15; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.2e+04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 GAGGGGAGGAGGGG 18  
Db 16 GAGGGGAGGAGGGG 2  
RESULT 6  
AX532427/c  
LOCUS AX532427 17 bp DNA linear PAT 22-NOV-2002  
DEFINITION Sequence 1936 from Patent EPI239051.  
ACCESSION AX532427  
VERSION AX532427.1 GI:25256629  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Shannon,M.  
TITLE Human posh-like protein 1  
JOURNAL Patent: EP 1239051-A 1936 11-SEP-2002;  
Aeomica, Inc. (US)  
FEATURES Location/Qualifiers  
source  
1..17  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
BASE COUNT 1 a 12 c 1 g 3 t  
ORIGIN  
Query Match 83.3%; Score 15; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.2e+04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGGGGAGGAGGGG 18  
Db 15 GAGGGGAGGAGGGG 1  
RESULT 7  
AX023402  
LOCUS AX023402 18 bp DNA linear PAT 15-SEP-2000  
DEFINITION Sequence 17 from Patent WO0014217.  
ACCESSION AX023402  
VERSION AX023402.1 GI:10183802  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1  
AUTHORS Lipford,G.B., Heeg,K. and Wagner,H.  
TITLE G-motif oligonucleotides and uses thereof  
JOURNAL Patent: WO 0014217-A 17 16-MAR-2000;  
LIPFORD GRAYSON B (DE) ; HEEG KLAUS (DE) ; WAGNER HERMANN (DE) ;  
CPG IMMUNOPHARMACEUTICALS GMBH (DE)  
FEATURES Location/Qualifiers  
source  
1..18  
/organism="synthetic construct"

/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="synthetic, no natural origin"  
BASE COUNT 1 a 0 c 13 g 4 t  
ORIGIN  
Query Match 82.2%; Score 14.8; DB 6; Length 18;  
Best Local Similarity 88.9%; Pred. No. 5e+04;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 TTGGAGGGGAGGAGGGG 18  
Db 1 TTGGAGGGGAGGAGGGG 18  
RESULT 8  
AX023427/c  
LOCUS AX023427 18 bp DNA linear PAT 15-SEP-2000  
DEFINITION Sequence 42 from Patent WO0014217.  
ACCESSION AX023427  
VERSION AX023427.1 GI:10183827  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE 1  
AUTHORS Lipford,G.B., Heeg,K. and Wagner,H.  
TITLE G-motif oligonucleotides and uses thereof  
JOURNAL Patent: WO 0014217-A 42 16-MAR-2000;  
LIPFORD GRAYSON B (DE) ; HEEG KLAUS (DE) ; WAGNER HERMANN (DE) ;  
CPG IMMUNOPHARMACEUTICALS GMBH (DE)  
FEATURES Location/Qualifiers  
source  
1..18  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="synthetic, no natural origin"  
BASE COUNT 4 a 13 c 0 g 1 t  
ORIGIN  
Query Match 82.2%; Score 14.8; DB 6; Length 18;  
Best Local Similarity 88.9%; Pred. No. 5e+04;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 TTGGAGGGGAGGAGGGG 18  
Db 18 TTGGAGGGGAGGAGGGG 1  
RESULT 9  
AR029938/c  
LOCUS AR029938 17 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 127 from patent US 5861244.  
ACCESSION AR029938  
VERSION AR029938.1 GI:5943152  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Wang,C.-G. and Hepburn,A.G.  
TITLE Genetic sequence assay using DNA triple strand formation  
JOURNAL Patent: US 5861244-A 127 19-JAN-1999;  
FEATURES Location/Qualifiers  
source  
1..17  
/organism="unknown"  
BASE COUNT 0 a 12 c 0 g 5 t  
ORIGIN  
Query Match 80.0%; Score 14.4; DB 6; Length 17;  
Best Local Similarity 93.8%; Pred. No. 7.4e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 3 GGAGGGGGAGGAGGGG 18
Db 16 GGAAGGGGAGGAGGGG 1

RESULT 10
AX532424/c
LOCUS AX532424 linear DNA 17 bp PAT 22-NOV-2002
DEFINITION Sequence 1933 from Patent EP1239051.
ACCESSION AX532424
VERSION AX532424.1 GI:25256623
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Shannon,M.
AUTHORS Human posh-like protein 1
TITLE Patent: EP 1239051-A 1933 11-SEP-2002;
JOURNAL Aeomica, Inc. (US)
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 1 a 11 c 1 g 4 t
ORIGIN

Query Match 77.8%; Score 14; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AGGGGGAGGAGGGG 18
Db 17 AGGGGGAGGAGGGG 4

RESULT 11
AX532428/c
LOCUS AX532428 linear DNA 17 bp PAT 22-NOV-2002
DEFINITION Sequence 1937 from Patent EP1239051.
ACCESSION AX532428
VERSION AX532428.1 GI:25256631
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Shannon,M.
AUTHORS Human posh-like protein 1
TITLE Patent: EP 1239051-A 1937 11-SEP-2002;
JOURNAL Aeomica, Inc. (US)
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 1 a 12 c 1 g 3 t
ORIGIN

Query Match 77.8%; Score 14; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGGGGGAGGAGGG 17
Db 14 GAGGGGGAGGAGGG 1

RESULT 12
AR232303
LOCUS AR232303 linear DNA 20 bp PAT 20-DEC-2002
DEFINITION Sequence 93 from patent US 6455307.
ACCESSION AR232303
VERSION AR232303.1 GI:27274295
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS McKay,R., Freier,S.M. and Wyatt,J.
TITLE Antisense modulation of casein kinase 2-alpha prime expression
JOURNAL Patent: US 6455307-A 93 24-SEP-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
BASE COUNT 6 a 1 c 12 g 1 t
ORIGIN

Query Match 76.7%; Score 13.8; DB 6; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.3e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGAGGGGAGGAGGGG 18
Db 2 TGGAGGAGGAGGAGGAG 18

RESULT 13
AX214604/c
LOCUS AX214604 linear mRNA 17 bp PAT 07-SEP-2001
DEFINITION Sequence 46 from Patent WO0159103.
ACCESSION AX214604
VERSION AX214604.1 GI:15524647
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Blatt,L., Mcswiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
PATENT: WO 0159103-A 46 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES Location/Qualifiers
source 1..17
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
BASE COUNT 0 a 13 c 1 g 3 t
ORIGIN

Query Match 72.2%; Score 13; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.9e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGGGGAGGAGGGG 18
Db 16 GGGGGAGGAGGGG 4

RESULT 14
AX214605/c
LOCUS AX214605 linear mRNA 17 bp PAT 07-SEP-2001
DEFINITION Sequence 47 from Patent WO0159103.
ACCESSION AX214605
VERSION AX214605.1 GI:15524648
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
```

```
AUTHORS      Blatt,L., Mcswiggen,J. and Chowrira,B.M.
TITLE        Method and reagent for the modulation and diagnosis of cd20 and
              nogo gene expression
JOURNAL      Patent: WO 0159103-A 47 16-AUG-2001;
              RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
              McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source       1..17
              /organism="synthetic construct"
              /mol_type="mRNA"
              /db_xref="taxon:32630"
              /note="Nucleic Acid"
BASE COUNT   0 a      13 c      2 g      2 t
ORIGIN
Query Match  72.2%; Score 13; DB 6; Length 17;
Best Local Similarity 100.0%; Pred.No. 2.9e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
,QY          6 GGGGGAGGAGGGG 18
              |||||
Db           13 GGGGGAGGAGGGG 1
RESULT 15
AX215457/c
LOCUS        AX215457              17 bp      mRNA      linear      PAT 07-SEP-2001
DEFINITION   Sequence 899 from Patent WO0159103.
ACCESSION    AX215457
VERSION      AX215457.1 GI:15525500
KEYWORDS     .
SOURCE       synthetic construct
ORGANISM     synthetic construct
              artificial sequences.
REFERENCE    1
AUTHORS      Blatt,L., Mcswiggen,J. and Chowrira,B.M.
TITLE        Method and reagent for the modulation and diagnosis of cd20 and
              nogo gene expression
JOURNAL      Patent: WO 0159103-A 899 16-AUG-2001;
              RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
              McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source       1..17
              /organism="synthetic construct"
              /mol_type="mRNA"
              /db_xref="taxon:32630"
              /note="Nucleic Acid"
BASE COUNT   0 a      14 c      0 g      3 t
ORIGIN
Query Match  72.2%; Score 13; DB 6; Length 17;
Best Local Similarity 100.0%; Pred.No. 2.9e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
,QY          6 GGGGGAGGAGGGG 18
              |||||
Db           17 GGGGGAGGAGGGG 5
Search completed: October 27, 2003, 11:09:26
Job time : 377.114 secs
```



/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1978032"  
/tissue\_type="tumor, 5 pooled (see description)"  
/lab\_host="DH10B"  
/clone\_lib="NCI\_CGAP\_Brn35"  
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: SalI;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.33 kb. Tumor types include:  
meningioma, oligodendroglioma, astrocytoma (grade II),  
medulloblastoma, astrocytoma (grade IV). Life Technologies  
catalog #: 11544-012"  
4 a 14 c 0 g 1 t

BASE COUNT  
ORIGIN

Query Match 76.7%; Score 13.8; DB 9; Length 19;  
Best Local Similarity 88.2%; Pred. No. 5.5e+05;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGAGGTGGG 17  
|||||  
Db 17 TTGGGGGGGAGGGGGG 1

RESULT 2  
AZ876923  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AZ876923 22 bp DNA linear GSS 21-FEB-2001  
2M0192D07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0192D07 F, genomic survey sequence.  
AZ876923  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 22)  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.,  
and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunne@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0192 row: D column: 07  
Seq primer: CGTTGTAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 22.  
Location/Qualifiers  
1. .22  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0192D07"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a

FEATURES  
source

1. .22  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1978032"  
/tissue\_type="tumor, 5 pooled (see description)"  
/lab\_host="DH10B"  
/clone\_lib="NCI\_CGAP\_Brn35"  
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: SalI;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.33 kb. Tumor types include:  
meningioma, oligodendroglioma, astrocytoma (grade II),  
medulloblastoma, astrocytoma (grade IV). Life Technologies  
catalog #: 11544-012"

0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT  
ORIGIN

Query Match 76.7%; Score 13.8; DB 28; Length 22;  
Best Local Similarity 88.2%; Pred. No. 5.4e+05;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGAGGTGGG 17  
|||||  
Db 2 TTGGAGGAGGAGGGGGG 18

RESULT 3  
AI582080/c  
LOCUS  
DEFINITION

AI582080 22 bp mRNA linear EST 06-APR-1999  
ar98b07.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone  
IMAGE:2173429 3' similar to SWI-FOR4 MOUSE Q05859 FORMIN 4 ; contains  
element MSR1 repetitive element ; mRNA sequence.  
AI582080  
AI582080.1 GI:4567977  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 22)  
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,  
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin  
J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,  
White, Y., Wylie, T., Waterston, R. and Wilson, R.  
WashU-NCI human EST Project  
Unpublished  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .22  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2173429"  
/sex="male"  
/dev\_stage="adult, age 25"  
/lab\_host="DH10B (phage resistant)"  
/clone\_lib="Barstead colon HPLRB7"  
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a  
modified polylinker; Site 1: EcoRI; Site 2: NotI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACGAATCTGAAGTGGAGCGCCGCTTTTTTTTTTTTTTTTTTT  
3']; double-stranded cDNA was ligated to Eco RI adaptors

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AI582080/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AI582080  
AI582080.1  
GI:4567977  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 22)  
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,  
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin  
J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,  
White, Y., Wylie, T., Waterston, R. and Wilson, R.  
WashU-NCI human EST Project  
Unpublished  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .22  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2173429"  
/sex="male"  
/dev\_stage="adult, age 25"  
/lab\_host="DH10B (phage resistant)"  
/clone\_lib="Barstead colon HPLRB7"  
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a  
modified polylinker; Site 1: EcoRI; Site 2: NotI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACGAATCTGAAGTGGAGCGCCGCTTTTTTTTTTTTTTTTTTT  
3']; double-stranded cDNA was ligated to Eco RI adaptors

AI582080  
AI582080.1  
GI:4567977  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 22)  
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,  
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin  
J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,  
White, Y., Wylie, T., Waterston, R. and Wilson, R.  
WashU-NCI human EST Project  
Unpublished  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .22  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2173429"  
/sex="male"  
/dev\_stage="adult, age 25"  
/lab\_host="DH10B (phage resistant)"  
/clone\_lib="Barstead colon HPLRB7"  
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a  
modified polylinker; Site 1: EcoRI; Site 2: NotI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACGAATCTGAAGTGGAGCGCCGCTTTTTTTTTTTTTTTTTTT  
3']; double-stranded cDNA was ligated to Eco RI adaptors

AI582080  
AI582080.1  
GI:4567977  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 22)  
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,  
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin  
J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,  
White, Y., Wylie, T., Waterston, R. and Wilson, R.  
WashU-NCI human EST Project  
Unpublished  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .22  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2173429"  
/sex="male"  
/dev\_stage="adult, age 25"  
/lab\_host="DH10B (phage resistant)"  
/clone\_lib="Barstead colon HPLRB7"  
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a  
modified polylinker; Site 1: EcoRI; Site 2: NotI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACGAATCTGAAGTGGAGCGCCGCTTTTTTTTTTTTTTTTTTT  
3']; double-stranded cDNA was ligated to Eco RI adaptors

AI582080  
AI582080.1  
GI:4567977  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 22)  
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,  
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin  
J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,  
White, Y., Wylie, T., Waterston, R. and Wilson, R.  
WashU-NCI human EST Project  
Unpublished  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .22  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2173429"  
/sex="male"  
/dev\_stage="adult, age 25"  
/lab\_host="DH10B (phage resistant)"  
/clone\_lib="Barstead colon HPLRB7"  
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a  
modified polylinker; Site 1: EcoRI; Site 2: NotI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACGAATCTGAAGTGGAGCGCCGCTTTTTTTTTTTTTTTTTTT  
3']; double-stranded cDNA was ligated to Eco RI adaptors

AI582080  
AI582080.1  
GI:4567977  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 22)  
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,  
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin  
J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,  
White, Y., Wylie, T., Waterston, R. and Wilson, R.  
WashU-NCI human EST Project  
Unpublished  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .22  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2173429"  
/sex="male"  
/dev\_stage="adult, age 25"  
/lab\_host="DH10B (phage resistant)"  
/clone\_lib="Barstead colon HPLRB7"  
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a  
modified polylinker; Site 1: EcoRI; Site 2: NotI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACGAATCTGAAGTGGAGCGCCGCTTTTTTTTTTTTTTTTTTT  
3']; double-stranded cDNA was ligated to Eco RI adaptors

AI582080  
AI582080.1  
GI:4567977  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 22)  
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,  
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin  
J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,  
White, Y., Wylie, T., Waterston, R. and Wilson, R.  
WashU-NCI human EST Project  
Unpublished  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .22  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2173429"  
/sex="male"  
/dev\_stage="adult, age 25"  
/lab\_host="DH10B (phage resistant)"  
/clone\_lib="Barstead colon HPLRB7"  
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a  
modified polylinker; Site 1: EcoRI; Site 2: NotI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACGAATCTGAAGTGGAGCGCCGCTTTTTTTTTTTTTTTTTTT  
3']; double-stranded cDNA was ligated to Eco RI adaptors

AI582080  
AI582080.1  
GI:4567977  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 22)  
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,  
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin  
J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,  
White, Y., Wylie, T., Waterston, R. and Wilson, R.  
WashU-NCI human EST Project  
Unpublished  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .22  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2173429"  
/sex="male"  
/dev\_stage="adult, age 25"  
/lab\_host="DH10B (phage resistant)"  
/clone\_lib="Barstead colon HPLRB7"  
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a  
modified polylinker; Site 1: EcoRI; Site 2: NotI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACGAATCTGAAGTGGAGCGCCGCTTTTTTTTTTTTTTTTTTT  
3']; double-stranded cDNA was ligated to Eco RI adaptors

AI582080  
AI582080.1  
GI:4567977  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 22)  
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,  
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin  
J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,  
White, Y., Wylie, T., Waterston, R. and Wilson, R.  
WashU-NCI human EST Project  
Unpublished  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .22  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2173429"  
/sex="male"  
/dev\_stage="adult, age 25"  
/lab\_host="DH10B (phage resistant)"  
/clone\_lib="Barstead colon HPLRB7"  
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a  
modified polylinker; Site 1: EcoRI; Site 2: NotI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACGAATCTGAAGTGGAGCGCCGCTTTTTTTTTTTTTTTTTTT  
3']; double-stranded cDNA was ligated to Eco RI adaptors

AI582080  
AI582080.1  
GI:4567977  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 22)  
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,  
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin  
J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,  
White, Y., Wylie, T., Waterston, R. and Wilson, R.  
WashU-NCI human EST Project  
Unpublished  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .22  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2173429"  
/sex="male"  
/dev\_stage="adult, age 25"  
/lab\_host="DH10B (phage resistant)"  
/clone\_lib="Barstead colon HPLRB7"  
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a  
modified polylinker; Site 1: EcoRI; Site 2: NotI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACGAATCTGAAGTGGAGCGCCGCTTTTTTTTTTTTTTTTTTT  
3']; double-stranded cDNA was ligated to Eco RI adaptors

AI582080  
AI582080.1  
GI:4567977  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 22)  
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,  
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin  
J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,  
White, Y., Wylie, T., Waterston, R. and Wilson, R.  
WashU-NCI human EST Project  
Unpublished  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .22  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2173429"  
/sex="male"  
/dev\_stage="adult, age 25"  
/lab\_host="DH10B (phage resistant)"  
/clone\_lib="Barstead colon HPLRB7"  
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a  
modified polylinker; Site 1: EcoRI; Site 2: NotI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACGAATCTGAAGTGGAGCGCCGCTTTTTTTTTTTTTTTTTTT  
3']; double-stranded cDNA was ligated to Eco RI adaptors

AI582080  
AI582080.1  
GI:4567977  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 22)  
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,  
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin  
J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,  
White, Y., Wylie, T., Waterston, R. and Wilson, R.  
WashU-NCI human EST Project  
Unpublished  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .22  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2173429"  
/sex="male"  
/dev\_stage="adult, age 25"  
/lab\_host="DH10B (phage resistant)"  
/clone\_lib="Barstead colon HPLRB7"  
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a  
modified polylinker; Site 1: EcoRI; Site 2: NotI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACGAATCTGAAGTGGAGCGCCGCTTTTTTTTTTTTTTTTTTT  
3']; double-stranded cDNA was ligated to Eco RI adaptors

AI582080  
AI582080.1  
GI:4567977  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 22)  
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,  
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin  
J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,  
White, Y., Wylie, T., Waterston, R. and Wilson, R.  
WashU-NCI human EST Project  
Unpublished  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .22  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2173429"  
/sex="male"  
/dev\_stage="adult, age 25"  
/lab\_host="DH10B (phage resistant)"  
/clone\_lib="Barstead colon HPLRB7"  
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a  
modified polylinker; Site 1: EcoRI; Site 2: NotI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACGAATCTGAAGTGGAGCGCCGCTTTTTTTTTTTTTTTTTTT  
3']; double-stranded cDNA was ligated to Eco RI adaptors

AI582080  
AI582080.1  
GI:4567977  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 22)  
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,  
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin  
J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,  
White, Y., Wylie, T., Waterston, R. and Wilson, R.  
WashU-NCI human EST Project  
Unpublished  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .22  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2173429"  
/sex="male"  
/dev\_stage="adult, age 25"  
/lab\_host="DH10B (phage resistant)"  
/clone\_lib="Barstead colon HPLRB7"  
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a  
modified polylinker; Site 1: EcoRI; Site 2: NotI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACGAATCTGAAGTGGAGCGCCGCTTTTTTTTTTTTTTTTTTT  
3']; double-stranded cDNA was ligated to Eco RI adaptors

AI582080  
AI582080.1  
GI:4567977  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 22)  
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,  
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin  
J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,  
White, Y., Wylie, T., Waterston, R. and Wilson, R.  
WashU-NCI human EST Project  
Unpublished  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .22  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2173429"  
/sex="male"  
/dev\_stage="adult, age 25"  
/lab\_host="DH10B (phage resistant)"  
/clone\_lib="Barstead colon HPLRB7"  
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a  
modified polylinker; Site 1: EcoRI; Site 2: NotI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACGAATCTGAAGTGGAGCGCCGCTTTTTTTTTTTTTTTTTTT  
3']; double-stranded cDNA was ligated to Eco RI adaptors

AI582080  
AI582080

[5' AATCACTAGTAAT 3' and 5' ATTACTAGTG 3'], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead."

BASE COUNT 1 a 16 c 0 g 3 t 2 others  
ORIGIN  
Query Match 74.4%; Score 13.4; DB 9; Length 22;  
Best Local Similarity 87.5%; Pred. No. 7.2e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGGAGGTGGG 18  
|||  
Db 18 GGNNGGGGAGGGGGG 3

RESULT 4  
AZ468862 21 bp DNA linear GSS 04-OCT-2000  
LOCUS  
DEFINITION IM0282004F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0282004 F, genomic survey sequence.

ACCESSION AZ468862  
VERSION  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0282 row: 0 column: 04  
Seq primer: CGTTGTAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 21.

Location/Qualifiers  
1. .21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0282004"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated

FEATURES  
source

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 1 c 15 g 5 t  
ORIGIN  
Query Match 73.3%; Score 13.2; DB 28; Length 21;  
Best Local Similarity 83.3%; Pred. No. 8.3e+05;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTGGAGGGGAGGTGGG 18  
|||  
Db 1 TTGGGGGTGGGTGGG 18

RESULT 5  
AZ345792

LOCUS  
DEFINITION AZ345792 19 bp DNA linear GSS 29-SEP-2000 IM0080G12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0080G12 R, genomic survey sequence.

ACCESSION AZ345792  
VERSION  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0080 row: G column: 12  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.

Location/Qualifiers  
1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0080G12"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT	1 a	1 c
ORIGIN		

Query Match 71.1%; Score 12.8; DB 28; Length 19;  
Best Local Similarity 87.5%; Pred. No. 1.1e+06;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGAGGGGAGGTGGG 18  
||| ||| ||| |||  
Db 2 GGGGGGGAGGGGGG 17

RESULT 6	AZ760597/c	AZ760597	19 bp	DNA	linear	GSS 16-FEB-2001
LOCUS						
DEFINITION		1M0554N21F	Mouse	10kb	plasmid UUGC1M	library Mus musculus genomic clone UUGC1M0554N21 F, genomic survey sequence.

ACCESSION AZ760597  
 VERSION AZ760597.1 GI:12868613  
 KEYWORDS GSS.

REFERENCE	ORGANISM	SOURCE	Occ.
1 (bases 1 to 19)	Mus musculus	Mus musculus (house mouse)	
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		

**AUTHORS**

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.

**TITLE**  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

Unpublished  
JOURNAL  
COMMENT  
Contact: Robert B. Weiss  
University of Utah  
University of Utah  
Rm. 308, Biomedical  
84112, USA  
20 S. 2030 E., SLC, UT

```

FEATURES
source
1. .19
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0554N21"
/sex="Male"

```

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

```

BASE COUNT
0 a 18 c 0 g 1 t

```

Query Match	71.1%;	Score 12.8;	DB 28;	Length 19;
Best Local Similarity	87.5%;	Pred. No. 1.1e+06;		
Matches 14;	Conservative	0;	Mismatches 2;	Indels 0;
				Gaps 0;

Qy 3 GGAGGGGAGGTGGG 18  
|||||  
Db 18 GGAGGGGGGGGGGG 3

RESULT 7					
AZ786308					
LOCUS	AZ786308	19 bp	DNA	linear	GSS 16-FEB-2001
DEFINITION	2M0031B17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0031B17 R. genomic survey sequence.				

ACCESSION	AZ786308
VERSION	AZ786308.1
	GI:12923936

KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE

**AUTHORS**

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A., and Wright, D., Weiss, R.

**TITLE**  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT

Unpublished  
manuscript

Contact: Robert B. Weiss  
University of Utah  
University of Utah  
University of Utah  
Rm. 308, Biomedical  
84112, USA

20 S. 2030 E., SLC, UT

```

FEATURES
source
1. .19
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0031B17"
/sex="Male"

```

/sex="Male"  
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel



electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 2 a 1 c 15 g 1 t  
ORIGIN  
Query Match 71.1%; Score 12.8; DB 28; Length 19;  
Best Local Similarity 87.5%; Pred. No. 1.1e+06;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 3 GGAGGGGGAGGTGGGG 18  
||| ||||| |||||  
Db 1 GGGCGGGGAGGTGGGG 16

RESULT 8  
AZ512326/c  
LOCUS  
DEFINITION  
AZ512326  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0357 row: 1 column: 18  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers  
1..20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0357118"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to

FEATURES  
source  
1..20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0357118"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 18 c 0 g 2 t  
ORIGIN  
Query Match 71.1%; Score 12.8; DB 28; Length 20;  
Best Local Similarity 87.5%; Pred. No. 1.1e+06;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 3 GGAGGGGGAGGTGGGG 18  
||| ||||| |||||  
Db 18 GGAGGGGGGGGGGGGG 3

RESULT 9  
AZ645269/c  
LOCUS  
DEFINITION  
AZ645269  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0510 row: B column: 10  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers  
1..20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0510B10"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The

FEATURES  
source  
1..20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0510B10"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 19 c 0 g 1 t

ORIGIN

Query Match 71.1%; Score 12.8; DB 28; Length 20;  
Best Local Similarity 87.5%; Pred. No. 1.1e+06;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGGAGGTGGGG 18

Db 17 GGAGGGGGGGGGGGG 2

RESULT 10

AZ659755/c

LOCUS

DEFINITION

1M0537F22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0537F22 F, genomic survey sequence.

AZ659755

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished

Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0537 row: F column: 22

Seq primer: CGTGTAAACGACGGCCAGT

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1. .20

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0537F22"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 18 c 0 g 2 t

ORIGIN

Query Match 71.1%; Score 12.8; DB 28; Length 20;  
Best Local Similarity 87.5%; Pred. No. 1.1e+06;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGGAGGTGGGG 18

Db 20 GGAGGGGGGGGGGGG 5

RESULT 11

AZ772707/c

LOCUS

DEFINITION

1M0583L18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0583L18 R, genomic survey sequence.

AZ772707

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished

Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0583 row: L column: 18

Seq primer: CACACAGGAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1. .20

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0583L18"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 19 c 0 g 1 t  
ORIGIN  
Query Match 71.1%; Score 12.8; DB 28; Length 20;  
Best Local Similarity 87.5%; Pred. No. 1.1e+06;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGGAGGTGGG 18  
|||  
Db 19 GGGGGGGAGGGGGG 4

RESULT 12  
AZ969440/c  
LOCUS  
DEFINITION  
2M0242012F Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
clone UUGC2M0242012 F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)

REFERENCE  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0242 row: 0 column: 12  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 20.

FEATURES  
source  
1..20  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0242012"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC2M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (female) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 19 c 0 g 1 t  
ORIGIN  
Query Match 71.1%; Score 12.8; DB 28; Length 20;  
Best Local Similarity 87.5%; Pred. No. 1.1e+06;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGGAGGTGGG 18  
|||  
Db 16 GGAGGGGGGGGGGG 1

RESULT 13  
AZ476392/c  
LOCUS

DEFINITION  
AZ476392  
1M0295F12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0295F12 F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)

REFERENCE  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0295 row: F column: 12  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 21.

FEATURES  
source  
1..21  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0295F12"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 20 c 0 g 1 t  
ORIGIN

Query Match 71.1%; Score 12.8; DB 28; Length 21;  
Best Local Similarity 87.5%; Pred. No. 1.1e+06;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGGAGGTGGGG 18  
||| ||||| |||||  
Db 21 GGGGGGGAGGGGGGG 6

RESULT 14  
AZ583408/c  
LOCUS  
DEFINITION  
1M0378N23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0378N23 F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

FEATURES  
source

1. .21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0378N23"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 20 c 0 g 1 t  
ORIGIN

Query Match 71.1%; Score 12.8; DB 28; Length 21;  
Best Local Similarity 87.5%; Pred. No. 1.1e+06;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGGAGGTGGGG 18  
||| ||||| |||||  
Db 18 GGAGGGGGGGGGGGGG 3

RESULT 15  
AZ653464/c  
LOCUS  
DEFINITION

1M0527G11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0527G11 F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

FEATURES  
source

1. .21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0527G11"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT            0 a       20 c       0 g       1 t  
ORIGIN

Query Match            71.1%;    Score 12.8;    DB 28;    Length 21;  
Best Local Similarity   87.5%;    Pred. No. 1.1e+06;  
Matches    14;    Conservative    0;    Mismatches    2;    Indels    0;    Gaps    0;

QY            3 GGAGGGGGGAGGTGGGG 18  
             |||||  
Db            20 GGGGGGGGAGGGGGG 5

Search completed: October 27, 2003, 13:59:28  
Job time : 1582.77 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:34 ; Search time 41.3143 Seconds  
(without alignments)  
192.304 Million cell updates/sec

Title: US-09-331-204A-8

Perfect score: 18

Sequence: 1 ttggagggggagggtgggg 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 376294

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_NA.\*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16.4	91.1	18	2	US-08-529-878B-3
2	16.4	91.1	18	2	US-08-529-878B-44
3	16.4	91.1	21	2	US-08-529-878B-4
4	16.4	91.1	21	2	US-08-529-878B-45
5	13.8	76.7	20	3	US-09-487-368A-174
6	13.8	76.7	20	4	US-09-629-644A-174
7	13.8	76.7	21	3	US-09-092-077-45
8	13.4	74.4	19	1	US-08-242-664-37
9	13.4	74.4	19	1	US-08-484-138-37
10	13.4	74.4	19	5	PCT-US95-06379-37
11	13.4	74.4	20	4	US-09-422-978-9409
12	12.8	71.1	17	2	US-08-173-489C-127
13	12.8	71.1	17	4	US-09-495-140-26
14	12.8	71.1	18	2	US-08-639-501-72
15	12.8	71.1	18	3	US-09-044-946-72
16	12.8	71.1	18	3	US-09-044-908-72
17	12.8	71.1	20	3	US-09-487-368A-175
18	12.8	71.1	20	4	US-09-056-285A-32
19	12.8	71.1	20	4	US-09-629-644A-175
20	12.8	71.1	21	2	US-08-632-575B-19
21	12.8	71.1	21	4	US-09-199-542B-19
22	12.2	67.8	19	1	US-08-486-913-2
23	12.2	67.8	19	2	US-08-486-535-2
24	12.2	67.8	19	2	US-08-300-484-2
25	12.2	67.8	19	3	US-08-486-885-2
26	12.2	67.8	19	3	US-08-486-536-2
27	12.2	67.8	19	5	PCT-US95-11234-2

28	12.2	67.8	20	1	US-08-486-913-3	Sequence 3, Appli
29	12.2	67.8	20	2	US-08-486-535-3	Sequence 3, Appli
30	12.2	67.8	20	2	US-08-300-484-3	Sequence 3, Appli
31	12.2	67.8	20	3	US-09-280-805-265	Sequence 265, App
32	12.2	67.8	20	3	US-08-486-885-3	Sequence 3, Appli
33	12.2	67.8	20	3	US-08-486-536-3	Sequence 3, Appli
34	12.2	67.8	20	4	US-09-780-173A-93	Sequence 93, Appli
35	12.2	66.7	15	1	PCT-US95-11234-3	Sequence 3, Appli
36	12.2	66.7	15	2	US-08-363-240A-117	Sequence 117, App
37	11.8	65.6	15	2	US-08-292-620A-348	Sequence 348, App
38	11.8	65.6	15	3	US-08-557-210A-1	Sequence 1, Appli
39	11.8	65.6	15	3	US-09-071-845-348	Sequence 348, App
40	11.8	65.6	16	2	US-08-856-141-22	Sequence 22, Appl
41	11.8	65.6	16	4	US-09-495-140-22	Sequence 22, Appl
42	11.8	65.6	18	3	US-09-106-038A-66	Sequence 66, Appl
43	11.8	65.6	20	1	US-08-487-141B-101	Sequence 101, App
44	11.8	65.6	20	2	US-08-927-561-101	Sequence 101, App
45	11.8	65.6	20	2	US-08-476-712-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-08-529-878B-3  
; Sequence 3, Application US/08529878B  
; Patent No. 5932556  
; GENERAL INFORMATION:  
; APPLICANT: Tam, Robert C.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
; TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Crockett & Fish  
; STREET: 3000 S. Augusta Court  
; CITY: La Habra  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 90631  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/529,878B  
; FILING DATE: 13-SEP-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fish, Robert D.  
; REGISTRATION NUMBER: 33,880  
; REFERENCE/DOCKET NUMBER: 213/003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 714-525-3433  
; TELEFAX: 714-525-3303  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
US-08-529-878B-3

Query Match 91.1%; Score 16.4; DB 2; Length 18;  
Best Local Similarity 94.4%; Pred. No. 1.6e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGAGGTGGGG 18  
|||||  
DB 1 TTGGAGGGGGGTGGTGGG 18

RESULT 2  
US-08-529-878B-44  
; Sequence 44, Application US/08529878B  
; Patent No. 5932556  
; GENERAL INFORMATION:  
; APPLICANT: Tam, Robert C.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
; TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Crockett & Fish  
; STREET: 3000 S. Augusta Court  
; CITY: La Habra  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 90631  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/529,878B  
; FILING DATE: 13-SEP-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fish, Robert D.  
; REGISTRATION NUMBER: 33,880  
; REFERENCE/DOCKET NUMBER: 213/003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 714-525-3433  
; TELEFAX: 714-525-3303  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 44:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
US-08-529-878B-44

Query Match 91.1%; Score 16.4; DB 2; Length 18;  
Best Local Similarity 94.4%; Pred. No. 1.6e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGGAGGGGAGGTGGG 18  
|||  
Db 1 TTGGAGGGGAGGTGGG 18

RESULT 3  
US-08-529-878B-44  
; Sequence 4, Application US/08529878B  
; Patent No. 5932556  
; GENERAL INFORMATION:  
; APPLICANT: Tam, Robert C.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
; TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Crockett & Fish  
; STREET: 3000 S. Augusta Court  
; CITY: La Habra  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 90631  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 6.1

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/529,878B  
; FILING DATE: 13-SEP-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fish, Robert D.  
; REGISTRATION NUMBER: 33,880  
; REFERENCE/DOCKET NUMBER: 213/003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 714-525-3433  
; TELEFAX: 714-525-3303  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 21 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
US-08-529-878B-4

Query Match 91.1%; Score 16.4; DB 2; Length 21;  
Best Local Similarity 94.4%; Pred. No. 1.6e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGGAGGGGAGGTGGG 18  
|||  
Db 4 TTGGAGGGGAGGTGGG 21

RESULT 4  
US-08-529-878B-45  
; Sequence 45, Application US/08529878B  
; Patent No. 5932556  
; GENERAL INFORMATION:  
; APPLICANT: Tam, Robert C.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
; TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Crockett & Fish  
; STREET: 3000 S. Augusta Court  
; CITY: La Habra  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 90631  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/529,878B  
; FILING DATE: 13-SEP-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fish, Robert D.  
; REGISTRATION NUMBER: 33,880  
; REFERENCE/DOCKET NUMBER: 213/003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 714-525-3433  
; TELEFAX: 714-525-3303  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 45:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 21 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
US-08-529-878B-45

Query Match 91.1%; Score 16.4; DB 2; Length 21;



Best Local Similarity 94.4%; Pred. No. 1.6e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 TTGAGGGGGGAGGTGGGG 18  
Db 4 TTGAGGGGGGAGGTGGGG 21

RESULT 5  
US-09-487-368A-174  
; Sequence 174, Application US/09487368A  
; Patent No. 6261840  
; GENERAL INFORMATION:  
; APPLICANT: Lex M. Cowser  
; APPLICANT: Jacqueline Wyatt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION  
; FILE REFERENCE: RTS-0093  
; CURRENT APPLICATION NUMBER: US/09/487,368A  
; CURRENT FILING DATE: 2000-01-18  
; NUMBER OF SEQ ID NOS: 240  
; SEQ ID NO 174  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-487-368A-174

Query Match 76.7%; Score 13.8; DB 3; Length 20;  
Best Local Similarity 88.2%; Pred. No. 1.7e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 TGGAGGGGGGAGGTGGGG 18  
Db 1 TGGCCGGGGGAGGTGGGG 17

RESULT 6  
US-09-629-644A-174  
; Sequence 174, Application US/09629644A  
; Patent No. 6492345  
; GENERAL INFORMATION:  
; APPLICANT: Lex M. Cowser  
; APPLICANT: Jacqueline Wyatt  
; APPLICANT: Susan M. Freier  
; APPLICANT: Brett P. Monia  
; APPLICANT: Madeline M. Butler  
; APPLICANT: Robert McKay  
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION  
; FILE REFERENCE: ISPH-0478  
; CURRENT APPLICATION NUMBER: US/09/629,644A  
; CURRENT FILING DATE: 2000-07-31  
; PRIOR APPLICATION NUMBER: US 09/487,368  
; PRIOR FILING DATE: 2000-01-18  
; NUMBER OF SEQ ID NOS: 242  
; SEQ ID NO 174  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-629-644A-174

Query Match 76.7%; Score 13.8; DB 4; Length 20;  
Best Local Similarity 88.2%; Pred. No. 1.7e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 TGGAGGGGGGAGGTGGGG 18  
Db 1 TGGCCGGGGGAGGTGGGG 17

RESULT 7

US-09-092-077-45  
; Sequence 45, Application US/09092077  
; Patent No. 6194142  
; GENERAL INFORMATION:  
; APPLICANT: Moncany, Maurice  
; APPLICANT: Montagnier, Luc  
; TITLE OF INVENTION: Nucleotide Sequences Derived From The  
; TITLE OF INVENTION: Genome Of Retroviruses Of The HIV-1, HIV-2 And SIV Type,  
; TITLE OF INVENTION: And Their Uses In Particular For The Amplification Of The  
; TITLE OF INVENTION: Genomes Of These Retroviruses And For The In Vitro Diagnosis  
; TITLE OF INVENTION: Of The Diseases Due To Those Viruses  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESSEE: Dunner  
; STREET: 1300 I Street, N.W., Suite 700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/092,077  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/472,928  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: US 08/160,465  
; FILING DATE: 02-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 8912371  
; FILING DATE: 20-SEP-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 8907354  
; FILING DATE: 06-FEB-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meyers, Kenneth J.  
; REGISTRATION NUMBER: 25,146  
; REFERENCE/DOCKET NUMBER: 02356.0062-02000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)408-4000  
; TELEFAX: (202)408-4400  
; INFORMATION FOR SEQ ID NO: 45:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 21 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-09-092-077-45  
Query Match 76.7%; Score 13.8; DB 3; Length 21;  
Best Local Similarity 88.2%; Pred. No. 1.7e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 TGGAGGGGGGAGGTGGGG 18  
Db 3 TGGAGGGGGGAGGTGGGG 19  
RESULT 8  
US-08-242-664-37  
; Sequence 37, Application US/08242664  
; Patent No. 5571937  
; GENERAL INFORMATION:  
; APPLICANT: Watanabe, Kyoichi A.  
; APPLICANT: Ren, Wu-Yun  
; APPLICANT: Weil, Roger



```

; TITLE OF INVENTION: Complementary DNA and Toxins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/242,664
; FILING DATE: May 12, 1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44683
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-977-9550
; TELEFAX: 212-664-0525
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-242-664-37

Query Match 74.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 2.5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGGGGAGGTGGG 17
Db 5 GGAGGAGGAGGTGGG 19

RESULT 9
US-08-484-138-37
; Sequence 37, Application US/08484138
; Patent No. 5652350
; GENERAL INFORMATION:
; APPLICANT: Watanabe, Kyoichi A.
; APPLICANT: Ren, Wu-Yun
; APPLICANT: Weil, Roger
; TITLE OF INVENTION: Complementary DNA and Toxins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44Mb
; COMPUTER: IBM PC
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,138
; FILING DATE: June 7, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44683-Z/JPW/MJG
```

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-977-9550
; TELEFAX: 212-664-0525
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-484-138-37

Query Match 74.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 2.5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGGGGAGGTGGG 17
Db 5 GGAGGAGGAGGTGGG 19

RESULT 10
PCT-US95-06379-37
; Sequence 37, Application PC/TUS9506379
; GENERAL INFORMATION:
; APPLICANT: Watanabe, Kyoichi A.
; APPLICANT: Ren, Wu-Yun
; APPLICANT: Weil, Roger
; TITLE OF INVENTION: Complementary DNA and Toxins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44Mb
; COMPUTER: IBM PC
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06379
; FILING DATE: May 13, 1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44683-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0526
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; PCT-US95-06379-37

Query Match 74.4%; Score 13.4; DB 5; Length 19;
Best Local Similarity 93.3%; Pred. No. 2.5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGGGGAGGTGGG 17
Db 5 GGAGGAGGAGGTGGG 19

RESULT 11
US-09-422-978-9409/c
```

; Sequence 9409, Application US/09422978  
; Patent No. 6537751  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Daniel  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Chumakov, Ilya  
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...  
; FILE REFERENCE: GENSET.020CPI  
; CURRENT APPLICATION NUMBER: US/09/422,978  
; CURRENT FILING DATE: 1999-10-20  
; EARLIER APPLICATION NUMBER: US 09/298,850  
; EARLIER FILING DATE: 1999-04-21  
; EARLIER APPLICATION NUMBER: US 60/109,732  
; EARLIER FILING DATE: 1998-11-23  
; EARLIER APPLICATION NUMBER: US 60/082,614  
; EARLIER FILING DATE: 1998-04-21  
; NUMBER OF SEQ ID NOS: 11796  
; SEQ ID NO 9409  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: primer\_bind  
; LOCATION: 1..20  
; OTHER INFORMATION: downstream amplification primer 99-449 for SEQ 1544, in complement  
US-09-422-978-9409

Query Match 74.4%; Score 13.4; DB 4; Length 20;  
Best Local Similarity 93.3%; Pred. No. 2.5e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGAGGTG 15  
Db 17 TTGGAGGGGGAGATG 3

RESULT 12  
US-08-173-489C-127/c  
; Sequence 127, Application US/08173489C  
; Patent No. 5861244  
; GENERAL INFORMATION:  
; APPLICANT: WANG, C. -G.  
; APPLICANT: HERBURN, A. G.  
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA  
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.  
; NUMBER OF SEQUENCES: 365  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,  
; STREET: 510 EAST 73RD STREET,  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10021.  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage  
; COMPUTER: IBM PC/XT/AT  
; OPERATING SYSTEM: MS-DOS version 6.2  
; SOFTWARE: Wordperfect Version 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/173,489C  
; FILING DATE: 22 DEC 1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/968,436  
; FILING DATE: 29 OCT 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Handelman, Joseph H.  
; REGISTRATION NUMBER: 26,179  
; REFERENCE/DOCKET NUMBER: U9518-6  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (attorney) (212) 708-1880  
; TELEFAX: (attorney) (212) 246-8959  
; INFORMATION FOR SEQ ID NO: 127:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double stranded  
; TOPOLOGY: linear  
; MOLECULE TYPE: genomic DNA  
; DESCRIPTION: alpha-1-globin gene (accession #  
; DESCRIPTION: V00491) nucleotides 827 to 843  
; HYPOTHETICAL: no  
; ANTI-SENSE: no  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; PUBLICATION INFORMATION:  
; AUTHORS: Michelson, A M, Orkin, S H.  
; TITLE: The 3' untranslated regions  
; TITLE: of the duplicated human alpha-globin genes are  
; TITLE: unexpectedly divergent  
; JOURNAL: Cell  
; VOLUME: 22  
; PAGES: 371-377  
; DATE: 1980  
; RELEVANT RESIDUES IN SEQ ID NO: 127 :FROM 1 TO 17  
US-08-173-489C-127

Query Match 71.1%; Score 12.8; DB 2; Length 17;  
Best Local Similarity 87.5%; Pred. No. 4.3e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGGAGGTGGG 18  
Db 16 GGAAGGGGAGGAGGG 1

RESULT 13  
US-09-495-140-26  
; Sequence 26, Application US/09495140  
; Patent No. 6376182  
; GENERAL INFORMATION:  
; APPLICANT: CHAO, LEE  
; APPLICANT: CHAO, JULIE  
; APPLICANT: SONG, QING  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CORRELATING  
; TITLE OF INVENTION: TISSUE KALLIKREIN GENE PROMOTER POLYMORPHISMS WITH TREATMENT  
; TITLE OF INVENTION: OF ESSENTIAL HYPERTENSION  
; FILE REFERENCE: 19113.0081  
; CURRENT APPLICATION NUMBER: US/09/495,140  
; CURRENT FILING DATE: 2000-01-31  
; EARLIER APPLICATION NUMBER: 09/389,566  
; EARLIER FILING DATE: 1999-09-03  
; EARLIER APPLICATION NUMBER: 08/856,141  
; EARLIER FILING DATE: 1997-05-14  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 26  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:/No. 6376182e =  
; OTHER INFORMATION: synthetic construct  
US-09-495-140-26

Query Match 71.1%; Score 12.8; DB 4; Length 17;  
Best Local Similarity 87.5%; Pred. No. 4.3e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGGAGGTGGG 18  
Db 1 GGAGGGGGGGGGGG 16

RESULT 14  
US-08-639-501-72

; Sequence 72, Application US/08639501  
; Patent No. 5837492  
; GENERAL INFORMATION:  
; APPLICANT: Tavtigian, Sean V.  
; APPLICANT: Kamb, Alexander  
; APPLICANT: Simard, Jacques  
; APPLICANT: Couch, Fergus  
; APPLICANT: Rommens, Johanna  
; APPLICANT: Weber, Barbara  
; TITLE OF INVENTION: Chromosome 13-Linked Breast Cancer  
; TITLE OF INVENTION: Susceptibility Gene  
; NUMBER OF SEQUENCES: 124  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
; STREET: 1201 New York Avenue N.W., Suite 1001  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 22204  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/639,501  
; FILING DATE: 29-APR-1996  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/585,391  
; FILING DATE: 11-JAN-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/576,559  
; FILING DATE: 21-DEC-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/575,359  
; FILING DATE: 20-DEC-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/573,779  
; FILING DATE: 18-DEC-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ihnen, Jeffrey L.  
; REGISTRATION NUMBER: 28,957  
; REFERENCE/DOCKET NUMBER: 24884-116802-04  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-962-4810  
; TELEFAX: 202-962-8300  
; INFORMATION FOR SEQ ID NO: 72:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; US-08-639-501-72

Query Match 71.1%; Score 12.8; DB 2; Length 18;  
Best Local Similarity 87.5%; Pred. No. 4.3e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 TTGGAGGGGAGGTGG 16  
|||||  
Db 1 TTGGAGAGGCAGGTGG 16

RESULT 15  
US-09-044-946-72  
; Sequence 72, Application US/09044946  
; Patent No. 5033857

; GENERAL INFORMATION:  
; APPLICANT: Tavtigian, Sean V.  
; APPLICANT: Kamb, Alexander  
; APPLICANT: Simard, Jacques  
; APPLICANT: Couch, Fergus  
; APPLICANT: Rommens, Johanna  
; APPLICANT: Weber, Barbara  
; TITLE OF INVENTION: Chromosome 13-Linked Breast Cancer  
; TITLE OF INVENTION: Susceptibility Gene  
; NUMBER OF SEQUENCES: 124  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
; STREET: 1201 New York Avenue N.W., Suite 1001  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 22204  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/044,946  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/639,501  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/576,559  
; FILING DATE: 21-DEC-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/575,359  
; FILING DATE: 20-DEC-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/573,779  
; FILING DATE: 18-DEC-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ihnen, Jeffrey L.  
; REGISTRATION NUMBER: 28,957  
; REFERENCE/DOCKET NUMBER: 24884-116802-04  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-962-4810  
; TELEFAX: 202-962-8300  
; INFORMATION FOR SEQ ID NO: 72:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; US-09-044-946-72

Query Match 71.1%; Score 12.8; DB 3; Length 18;  
Best Local Similarity 87.5%; Pred. No. 4.3e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 TTGGAGGGGAGGTGG 16  
|||||  
Db 1 TTGGAGAGGCAGGTGG 16

Search completed: October 27, 2003, 14:03:35  
Job time : 41.3143 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: October 27, 2003, 11:25:34 ; Search time 387.943 Seconds  
(without alignments)  
124.432 Million cell updates/sec

Title: US-09-331-204A-8  
Perfect score: 18  
Sequence: 1 ttggaggaggaggtggg 18  
Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1792395 seqs, 1340900451 residues

Total number of hits satisfying chosen parameters: 408622

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA: \*  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq: \*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq: \*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq: \*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq: \*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq: \*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq: \*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq: \*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq: \*  
9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq: \*  
10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq: \*  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq: \*  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq: \*  
13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq: \*  
14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq: \*  
15: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq: \*  
16: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq: \*  
17: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	14.4	80.0	17	12 US-10-303-109A-30	Sequence 30, Appl
C 2	13.8	76.7	20	9 US-09-854-883-174	Sequence 174, Appl
C 3	13.4	74.4	17	12 US-10-061-201-1934	Sequence 1934, Ap
C 4	13.4	74.4	17	12 US-10-061-201-1935	Sequence 1935, Ap
C 5	13.4	74.4	17	12 US-10-061-201-1936	Sequence 1936, Ap
C 6	13.4	74.4	19	14 US-10-010-920-67	Sequence 67, Appl
C 7	13.4	74.4	19	14 US-10-008-721-67	Sequence 67, Appl
C 8	13.2	73.3	21	9 US-09-828-034-28	Sequence 28, Appl
C 9	13	72.2	20	12 US-10-233-032A-22	Sequence 22, Appl
C 10	12.8	71.1	17	11 US-09-780-533A-45	Sequence 45, Appl
C 11	12.8	71.1	17	11 US-09-780-533A-894	Sequence 894, Appl
C 12	12.8	71.1	17	12 US-10-059-877-26	Sequence 26, Appl
C 13	12.8	71.1	17	14 US-10-059-888-26	Sequence 26, Appl
C 14	12.8	71.1	20	9 US-09-854-883-175	Sequence 175, Appl
C 15	12.8	71.1	20	11 US-09-952-464A-32	Sequence 32, Appl
C 16	12.8	71.1	20	13 US-10-060-301-34	Sequence 34, Appl

C 17	12.4	68.9	17	12 US-10-238-700-3257	Sequence 3257, Ap
C 18	12.4	68.9	17	12 US-10-061-201-1933	Sequence 1933, Ap
C 19	12.4	68.9	17	12 US-10-061-201-1937	Sequence 1937, Ap
C 20	12.4	68.9	21	11 US-09-382-860-181	Sequence 181, Appl
C 21	12.2	67.8	17	9 US-09-866-108-1256	Sequence 1256, Ap
C 22	12.2	67.8	17	11 US-09-930-423-1590	Sequence 1590, Ap
C 23	12.2	67.8	17	12 US-09-745-237A-1590	Sequence 1590, Ap
C 24	12.2	67.8	17	12 US-10-061-201-1956	Sequence 1956, Ap
C 25	12.2	67.8	20	9 US-09-752-983-265	Sequence 265, Appl
C 26	12.2	67.8	20	12 US-10-032-585-5333	Sequence 5333, Ap
C 27	12	66.7	16	11 US-09-864-636A-2570	Sequence 2570, Ap
C 28	12	66.7	16	12 US-10-084-839-2570	Sequence 2570, Ap
C 29	11.8	65.6	16	12 US-10-059-877-22	Sequence 22, Appl
C 30	11.8	65.6	16	14 US-10-059-888-22	Sequence 22, Appl
C 31	11.8	65.6	17	11 US-09-780-533A-893	Sequence 893, Appl
C 32	11.8	65.6	17	11 US-09-780-533A-895	Sequence 895, Appl
C 33	11.8	65.6	17	11 US-09-930-423-1591	Sequence 1591, Ap
C 34	11.8	65.6	17	11 US-09-740-332-1833	Sequence 1833, Ap
C 35	11.8	65.6	17	12 US-09-745-237A-1591	Sequence 1591, Ap
C 36	11.8	65.6	17	12 US-09-817-879-1833	Sequence 1833, Ap
C 37	11.8	65.6	18	14 US-10-265-689-40	Sequence 40, Appl
C 38	11.8	65.6	19	12 US-10-205-309-49	Sequence 49, Appl
C 39	11.8	65.6	19	12 US-10-205-309-374	Sequence 374, Appl
C 40	11.8	65.6	20	10 US-09-874-162A-22	Sequence 22, Appl
C 41	11.8	65.6	20	11 US-09-948-002-30	Sequence 30, Appl
C 42	11.8	65.6	20	12 US-10-024-369-5	Sequence 5, Appl
C 43	11.8	65.6	20	12 US-10-024-369-33	Sequence 33, Appl
C 44	11.8	65.6	21	11 US-09-932-300-10	Sequence 10, Appl
C 45	11.8	65.6	21	11 US-09-932-300-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1  
US-10-303-109A-30/c  
; Sequence 30, Application US/10303109A  
; Publication No. US20030194726A1  
; GENERAL INFORMATION:  
; APPLICANT: BOLCHAKOVA, Elena  
; APPLICANT: ROZZELLE, James  
; TITLE OF INVENTION: Thermus Oshimai Nucleic Acid Polymerases  
; FILE REFERENCE: 4777US  
; CURRENT APPLICATION NUMBER: US/10/303,109A  
; CURRENT FILING DATE: 2002-11-22  
; PRIOR APPLICATION NUMBER: US 60/334,798  
; PRIOR FILING DATE: 2001-11-30  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 30  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Thermus oshimai  
US-10-303-109A-30

Query Match 80.0%; Score 14.4; DB 12; Length 17;  
Best Local Similarity 93.8%; Pred. No. 6.9e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGGAGGGGGAGGTGGG 17  
| | | | | | | | | | | | | | | | | |  
Db 16 TGGAGGTGGAGGTGGG 1

RESULT 2  
US-09-854-883-174  
; Sequence 174, Application US/09854883  
; Patent No. US20020055479A1  
; GENERAL INFORMATION:  
; APPLICANT: Lex M. Cowser  
; APPLICANT: Jacqueline Wyatt  
; APPLICANT: Susan M. Freier  
; APPLICANT: Brett P. Monia

APPLICANT: Madeline M. Butler  
APPLICANT: Robert McKay  
TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION  
FILE REFERENCE: ISPH-0576  
CURRENT APPLICATION NUMBER: US/09/854,883  
CURRENT FILING DATE: 2001-05-14  
PRIOR APPLICATION NUMBER: US 09/629,644  
PRIOR FILING DATE: 2000-07-31  
PRIOR APPLICATION NUMBER: US 09/487,368  
PRIOR FILING DATE: 2000-01-18  
NUMBER OF SEQ ID NOS: 389  
SEQ ID NO 174  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-09-854-883-174

Query Match 76.7%; Score 13.8; DB 9; Length 20;  
Best Local Similarity 88.2%; Pred. No. 1.1e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGAGGGGGAGGTGGGG 18  
||| |||||  
Db 1 TGGCCGGGGAGGTGGGG 17

RESULT 3  
US-10-061-201-1934/c  
Sequence 1934, Application US/10061201  
Publication No. US20030166229A1  
GENERAL INFORMATION:  
APPLICANT: Shannon, Mark  
TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1  
FILE REFERENCE: PB0178  
CURRENT APPLICATION NUMBER: US/10/061,201  
CURRENT FILING DATE: 2002-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 09/864,761  
PRIOR FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/328,205  
PRIOR FILING DATE: 2001-10-10  
NUMBER OF SEQ ID NOS: 4162  
SOFTWARE: Aeomica Sequence Listing Engine  
SEQ ID NO 1934  
LENGTH: 17  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-061-201-1934

Query Match 74.4%; Score 13.4; DB 12; Length 17;  
Best Local Similarity 93.3%; Pred. No. 1.7e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAGGGGGAGGTGGGG 18  
|||||  
Db 17 GAGGGGGAGGTGGGG 3

RESULT 4  
US-10-061-201-1935/c  
Sequence 1935, Application US/10061201  
Publication No. US20030166229A1  
GENERAL INFORMATION:  
APPLICANT: Shannon, Mark  
TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1  
FILE REFERENCE: PB0178  
CURRENT APPLICATION NUMBER: US/10/061,201  
CURRENT FILING DATE: 2002-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 09/864,761  
PRIOR FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/328,205  
PRIOR FILING DATE: 2001-10-10  
NUMBER OF SEQ ID NOS: 4162  
SOFTWARE: Aeomica Sequence Listing Engine  
SEQ ID NO 1935  
LENGTH: 17  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-061-201-1935

Query Match 74.4%; Score 13.4; DB 12; Length 17;  
Best Local Similarity 93.3%; Pred. No. 1.7e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAGGGGGAGGTGGGG 18  
|||||  
Db 16 GAGGGGGAGGTGGGG 2

RESULT 5  
US-10-061-201-1936/c  
Sequence 1936, Application US/10061201  
Publication No. US20030166229A1  
GENERAL INFORMATION:  
APPLICANT: Shannon, Mark  
TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1  
FILE REFERENCE: PB0178  
CURRENT APPLICATION NUMBER: US/10/061,201  
CURRENT FILING DATE: 2002-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30

```

; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1936
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-061-201-1936

Query Match      74.4%; Score 13.4; DB 12; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.7e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 GAGGGGGAGGTGGG 18
Db      15 GAGGGGGAGGAGGG 1

RESULT 6
US-10-010-920-67
; Sequence 67, Application US/10010920
; Publication No. US20030027165A1
; GENERAL INFORMATION:
; APPLICANT: Saus, Juan
; TITLE OF INVENTION: Alternatively spliced polk nucleotide and amino acid sequences
; TITLE OF INVENTION: and methods for using
; FILE REFERENCE: 98,723-E3
; CURRENT APPLICATION NUMBER: US/10/010,920
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/254,649
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer ON-DHFR-F1
US-10-010-920-67

Query Match      74.4%; Score 13.4; DB 14; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.7e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 TGGAGGGGGAGGTGG 16
Db      5 TGGAGGAGGAGGTGG 19

RESULT 7
US-10-008-721-67
; Sequence 67, Application US/10008721
; Publication No. US20030082745A1
; GENERAL INFORMATION:
; APPLICANT: Saus, Juan
; TITLE OF INVENTION: TNF-Inducible Promoters and Methods for Using
; FILE REFERENCE: 98,723-E1
; CURRENT APPLICATION NUMBER: US/10/008,721
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/254,649
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; NAME/KEY: misc feature
; OTHER INFORMATION: Antisense PCR primer for CC3 promoter (spec Table IIia)
US-10-008-721-67
```

```

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer ON-DHFR-F1
US-10-008-721-67

Query Match      74.4%; Score 13.4; DB 14; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.7e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 TGGAGGGGGAGGTGG 16
Db      5 TGGAGGAGGAGGTGG 19

RESULT 8
US-09-828-034-28/c
; Sequence 28, Application US/09828034
; Patent No. US20020064771A1
; GENERAL INFORMATION:
; APPLICANT: Zhong, Weidong
; APPLICANT: Hong, Zhi
; APPLICANT: Ferrari, Eric
; TITLE OF INVENTION: HCV REPLICASE COMPLEXES
; FILE REFERENCE: IN01165
; CURRENT APPLICATION NUMBER: US/09/828,034
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: U.S. 60/195,852
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA
US-09-828-034-28

Query Match      73.3%; Score 13.2; DB 9; Length 21;
Best Local Similarity 83.3%; Pred. No. 1.9e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 TTGAGGGGGAGGTGGG 18
Db      20 TTGAGGAGGAGGAGGAG 3

RESULT 9
US-10-233-032A-22
; Sequence 22, Application US/10233032A
; Publication No. US20030157704A1
; GENERAL INFORMATION:
; APPLICANT: Poole, Jason
; APPLICANT: Roninson, Igor
; APPLICANT: Chang, Bey-Dih
; TITLE OF INVENTION: REAGENTS AND METHODS FOR IDENTIFYING AND MODULATING
; FILE REFERENCE: 01-1156-A
; CURRENT APPLICATION NUMBER: US/10/233,032A
; CURRENT FILING DATE: 2003-02-12
; PRIOR APPLICATION NUMBER: US 09/861,925
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/265,840
; PRIOR FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Antisense PCR primer for CC3 promoter (spec Table IIia)
US-10-233-032A-22
```

Query Match 72.2%; Score 13; DB 12; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e+04;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AGGGGGAGGTGGG 17  
|||||  
Db 1 AGGGGGAGGTGGG 13

RESULT 10  
US-09-780-533A-45/c  
; Sequence 45, Application US/09780533A  
; Publication No. US20030060611A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Chowrira, Bharat  
; APPLICANT: Haerberli, Pete  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene  
; FILE REFERENCE: MBH00,878-A (400/011)  
; CURRENT APPLICATION NUMBER: US/09/780,533A  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,797  
; PRIOR FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 6679  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 45  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-780-533A-45

Query Match 71.1%; Score 12.8; DB 11; Length 17;  
Best Local Similarity 87.5%; Pred. No. 2.9e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGAGGTGGG 18  
|||||  
Db 16 GGAGGGGAGGTGGG 1

RESULT 11  
US-09-780-533A-894/c  
; Sequence 894, Application US/09780533A  
; Publication No. US20030060611A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Chowrira, Bharat  
; APPLICANT: Haerberli, Pete  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene  
; FILE REFERENCE: MBH00,878-A (400/011)  
; CURRENT APPLICATION NUMBER: US/09/780,533A  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,797  
; PRIOR FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 6679  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 894  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-780-533A-894

Query Match 71.1%; Score 12.8; DB 11; Length 17;  
Best Local Similarity 87.5%; Pred. No. 2.9e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGAGGTGGG 18  
|||||

Db 17 GGAGGGGAGGTGGG 2  
  
RESULT 12  
US-10-059-877-26  
; Sequence 26, Application US/10059877  
; Publication No. US20030157490A1  
; GENERAL INFORMATION:  
; APPLICANT: CHAO, LEE  
; APPLICANT: CHAO, JULIE  
; APPLICANT: SONG, QING  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CORRELATING  
; TITLE OF INVENTION: TISSUE KALLIKREIN GENE PROMOTER POLYMORPHISMS WITH ESSENTIAL  
; TITLE OF INVENTION: HYPERTENSION  
; FILE REFERENCE: 19113.0081U2  
; CURRENT APPLICATION NUMBER: US/10/059,877  
; CURRENT FILING DATE: 2002-01-29  
; PRIOR APPLICATION NUMBER: 09/495,140  
; PRIOR FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: 09/389,566  
; PRIOR FILING DATE: 1999-09-03  
; PRIOR APPLICATION NUMBER: 08/856,141  
; PRIOR FILING DATE: 1997-05-14  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 26  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030157490A1e =  
; OTHER INFORMATION: synthetic construct  
US-10-059-877-26

Query Match 71.1%; Score 12.8; DB 12; Length 17;  
Best Local Similarity 87.5%; Pred. No. 2.9e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGAGGTGGG 18  
|||||  
Db 1 GGAGGGGAGGTGGG 16

RESULT 13  
US-10-059-888-26  
; Sequence 26, Application US/10059888  
; Publication No. US20030025882A1  
; GENERAL INFORMATION:  
; APPLICANT: CHAO, LEE  
; APPLICANT: CHAO, JULIE  
; APPLICANT: SONG, QING  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CORRELATING  
; TITLE OF INVENTION: TISSUE KALLIKREIN GENE PROMOTER POLYMORPHISMS WITH ESSENTIAL  
; TITLE OF INVENTION: HYPERTENSION  
; FILE REFERENCE: 19113.0081U2  
; CURRENT APPLICATION NUMBER: US/10/059,888  
; CURRENT FILING DATE: 2002-01-29  
; PRIOR APPLICATION NUMBER: 09/495,140  
; PRIOR FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: 09/389,566  
; PRIOR FILING DATE: 1999-09-03  
; PRIOR APPLICATION NUMBER: 08/856,141  
; PRIOR FILING DATE: 1997-05-14  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 26  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030025882A1e =  
; OTHER INFORMATION: synthetic construct  
US-10-059-888-26

```
Query Match      71.1%; Score 12.8; DB 14; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      3 GGAGGGGGGAGGTGGG 18
         |||||
Db      1 GGAGGGGGGGGGGGG 16
```

RESULT 14

```
US-09-854-883-175
; Sequence 175, Application US/09854883
; Patent No. US20020055479A1
```

GENERAL INFORMATION:

```
; APPLICANT: Lex M. Cowser
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier
; APPLICANT: Brett P. Monia
; APPLICANT: Madeline M. Butler
; APPLICANT: Robert McKay
```

TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION

```
; FILE REFERENCE: ISPH-0576
; CURRENT APPLICATION NUMBER: US/09/854,883
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/629,644
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/487,368
; PRIOR FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 389
; SEQ ID NO 175
```

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Antisense Oligonucleotide

US-09-854-883-175

```
Query Match      71.1%; Score 12.8; DB 9; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.8e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 TGGAGGGGGAGGTGGG 17
         |||
Db      5 TGGCCGGGGAGGTGGG 20
```

RESULT 15

```
US-09-952-464A-32/c
; Sequence 32, Application US/09952464A
; Publication No. US20030077587A1
```

GENERAL INFORMATION:

```
; APPLICANT: Stone, Edwin M.
; APPLICANT: Sheffield, Val C.
; APPLICANT: Alward, Wallace L.M.
; APPLICANT: Fingert, John
```

TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS

```
; FILE REFERENCE: 21087.0017U11
; CURRENT APPLICATION NUMBER: US/09/952,464A
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: 09/473,273
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 09/461,542
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: 09/366,952
; PRIOR FILING DATE: 1999-08-04
; PRIOR APPLICATION NUMBER: 09/056,285
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: 08/822,999
; PRIOR FILING DATE: 1997-03-21
; NUMBER OF SEQ ID NOS: 43
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
```

```
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; No. US20030077587A1e =
US-09-952-464A-32

Query Match      71.1%; Score 12.8; DB 11; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.8e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 TGGAGGGGGAGGTGGG 17
         |||||
Db      19 TGTAGGGGTAGGTGGG 4
```

Search completed: October 27, 2003, 19:00:53  
Job time : 387.943 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:35 ; Search time 2356.29 Seconds  
(without alignments)  
253.343 Million cell updates/sec

Title: US-09-331-204A-8  
Perfect score: 18  
Sequence: 1 ttggagggggagggtggg 18

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 33363688 seqs, 16581889874 residues 2938060  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents\_NA\_Main.\*  
1: /cgn2\_6/ptodata/1/pna/PCTUS\_COMB.seq.\*  
2: /cgn2\_6/ptodata/1/pna/PCTUS\_COMB.seq.old.\*  
3: /cgn2\_6/ptodata/1/pna/US06\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/pna/US07\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/pna/US08\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/pna/US081\_COMB.seq.\*  
7: /cgn2\_6/ptodata/1/pna/US082\_COMB.seq.\*  
8: /cgn2\_6/ptodata/1/pna/US083\_COMB.seq.\*  
9: /cgn2\_6/ptodata/1/pna/US084\_COMB.seq.\*  
10: /cgn2\_6/ptodata/1/pna/US085\_COMB.seq.\*  
11: /cgn2\_6/ptodata/1/pna/US086\_COMB.seq.\*  
12: /cgn2\_6/ptodata/1/pna/US087\_COMB.seq.\*  
13: /cgn2\_6/ptodata/1/pna/US088\_COMB.seq.\*  
14: /cgn2\_6/ptodata/1/pna/US089\_COMB.seq.\*  
15: /cgn2\_6/ptodata/1/pna/US090\_COMB.seq.\*  
16: /cgn2\_6/ptodata/1/pna/US091\_COMB.seq.\*  
17: /cgn2\_6/ptodata/1/pna/US092A\_COMB.seq.\*  
18: /cgn2\_6/ptodata/1/pna/US092B\_COMB.seq.\*  
19: /cgn2\_6/ptodata/1/pna/US093A\_COMB.seq.\*  
20: /cgn2\_6/ptodata/1/pna/US093B\_COMB.seq.\*  
21: /cgn2\_6/ptodata/1/pna/US094\_COMB.seq.\*  
22: /cgn2\_6/ptodata/1/pna/US095A\_COMB.seq.\*  
23: /cgn2\_6/ptodata/1/pna/US095B\_COMB.seq.\*  
24: /cgn2\_6/ptodata/1/pna/US095C\_COMB.seq.\*  
25: /cgn2\_6/ptodata/1/pna/US095D\_COMB.seq.\*  
26: /cgn2\_6/ptodata/1/pna/US096A\_COMB.seq.\*  
27: /cgn2\_6/ptodata/1/pna/US096B\_COMB.seq.\*  
28: /cgn2\_6/ptodata/1/pna/US096C\_COMB.seq.\*  
29: /cgn2\_6/ptodata/1/pna/US096D\_COMB.seq.\*  
30: /cgn2\_6/ptodata/1/pna/US096E\_COMB.seq.\*  
31: /cgn2\_6/ptodata/1/pna/US097A\_COMB.seq.\*  
32: /cgn2\_6/ptodata/1/pna/US097B\_COMB.seq.\*  
33: /cgn2\_6/ptodata/1/pna/US097C\_COMB.seq.\*  
34: /cgn2\_6/ptodata/1/pna/US098A\_COMB.seq.\*  
35: /cgn2\_6/ptodata/1/pna/US098B\_COMB.seq.\*  
36: /cgn2\_6/ptodata/1/pna/US098C\_COMB.seq.\*  
37: /cgn2\_6/ptodata/1/pna/US098D\_COMB.seq.\*  
38: /cgn2\_6/ptodata/1/pna/US099A\_COMB.seq.\*  
39: /cgn2\_6/ptodata/1/pna/US099B\_COMB.seq.\*  
40: /cgn2\_6/ptodata/1/pna/US099C\_COMB.seq.\*  
41: /cgn2\_6/ptodata/1/pna/US099D\_COMB.seq.\*  
42: /cgn2\_6/ptodata/1/pna/US099E\_COMB.seq.\*  
43: /cgn2\_6/ptodata/1/pna/US099F\_COMB.seq.\*

44: /cgn2\_6/ptodata/1/pna/US100A\_COMB.seq.\*  
45: /cgn2\_6/ptodata/1/pna/US100B\_COMB.seq.\*  
46: /cgn2\_6/ptodata/1/pna/US101A\_COMB.seq.\*  
47: /cgn2\_6/ptodata/1/pna/US101B\_COMB.seq.\*  
48: /cgn2\_6/ptodata/1/pna/US102A\_COMB.seq.\*  
49: /cgn2\_6/ptodata/1/pna/US102B\_COMB.seq.\*  
50: /cgn2\_6/ptodata/1/pna/US103A\_COMB.seq.\*  
51: /cgn2\_6/ptodata/1/pna/US103B\_COMB.seq.\*  
52: /cgn2\_6/ptodata/1/pna/US104A\_COMB.seq.\*  
53: /cgn2\_6/ptodata/1/pna/US104B\_COMB.seq.\*  
54: /cgn2\_6/ptodata/1/pna/US6000\_COMB.seq.\*  
55: /cgn2\_6/ptodata/1/pna/US6001\_COMB.seq.\*  
56: /cgn2\_6/ptodata/1/pna/US6002\_COMB.seq.\*  
57: /cgn2\_6/ptodata/1/pna/US6003\_COMB.seq.\*  
58: /cgn2\_6/ptodata/1/pna/US6004\_COMB.seq.\*  
59: /cgn2\_6/ptodata/1/pna/US6005\_COMB.seq.\*  
60: /cgn2\_6/ptodata/1/pna/US6006\_COMB.seq.\*  
61: /cgn2\_6/ptodata/1/pna/US6007\_COMB.seq.\*  
62: /cgn2\_6/ptodata/1/pna/US6008\_COMB.seq.\*  
63: /cgn2\_6/ptodata/1/pna/US6009\_COMB.seq.\*  
64: /cgn2\_6/ptodata/1/pna/US6010\_COMB.seq.\*  
65: /cgn2\_6/ptodata/1/pna/US6011\_COMB.seq.\*  
66: /cgn2\_6/ptodata/1/pna/US6012\_COMB.seq.\*  
67: /cgn2\_6/ptodata/1/pna/US6013\_COMB.seq.\*  
68: /cgn2\_6/ptodata/1/pna/US6014\_COMB.seq.\*  
69: /cgn2\_6/ptodata/1/pna/US6015\_COMB.seq.\*  
70: /cgn2\_6/ptodata/1/pna/US6016\_COMB.seq.\*  
71: /cgn2\_6/ptodata/1/pna/US6017\_COMB.seq.\*  
72: /cgn2\_6/ptodata/1/pna/US6018\_COMB.seq.\*  
73: /cgn2\_6/ptodata/1/pna/US6019\_COMB.seq.\*  
74: /cgn2\_6/ptodata/1/pna/US6020\_COMB.seq.\*  
75: /cgn2\_6/ptodata/1/pna/US6021\_COMB.seq.\*  
76: /cgn2\_6/ptodata/1/pna/US6022\_COMB.seq.\*  
77: /cgn2\_6/ptodata/1/pna/US6023A\_COMB.seq.\*  
78: /cgn2\_6/ptodata/1/pna/US6023B\_COMB.seq.\*  
79: /cgn2\_6/ptodata/1/pna/US6024\_COMB.seq.\*  
80: /cgn2\_6/ptodata/1/pna/US6025\_COMB.seq.\*  
81: /cgn2\_6/ptodata/1/pna/US6026\_COMB.seq.\*  
82: /cgn2\_6/ptodata/1/pna/US6027\_COMB.seq.\*  
83: /cgn2\_6/ptodata/1/pna/US6028\_COMB.seq.\*  
84: /cgn2\_6/ptodata/1/pna/US6029\_COMB.seq.\*  
85: /cgn2\_6/ptodata/1/pna/US6030\_COMB.seq.\*  
86: /cgn2\_6/ptodata/1/pna/US6031\_COMB.seq.\*  
87: /cgn2\_6/ptodata/1/pna/US6032\_COMB.seq.\*  
88: /cgn2\_6/ptodata/1/pna/US6033\_COMB.seq.\*  
89: /cgn2\_6/ptodata/1/pna/US6034\_COMB.seq.\*  
90: /cgn2\_6/ptodata/1/pna/US6035\_COMB.seq.\*  
91: /cgn2\_6/ptodata/1/pna/US6036\_COMB.seq.\*  
92: /cgn2\_6/ptodata/1/pna/US6037\_COMB.seq.\*  
93: /cgn2\_6/ptodata/1/pna/US6038\_COMB.seq.\*  
94: /cgn2\_6/ptodata/1/pna/US6039\_COMB.seq.\*  
95: /cgn2\_6/ptodata/1/pna/US6040\_COMB.seq.\*  
96: /cgn2\_6/ptodata/1/pna/US6041\_COMB.seq.\*  
97: /cgn2\_6/ptodata/1/pna/US6042\_COMB.seq.\*  
98: /cgn2\_6/ptodata/1/pna/US6043\_COMB.seq.\*  
99: /cgn2\_6/ptodata/1/pna/US6044\_COMB.seq.\*  
100: /cgn2\_6/ptodata/1/pna/US6045\_COMB.seq.\*  
101: /cgn2\_6/ptodata/1/pna/US6046\_COMB.seq.\*  
102: /cgn2\_6/ptodata/1/pna/US6047\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match %	Length	DB	ID	Description
1	18	100.0	18	19	US-09-331-204-5		Sequence 5, Appli
2	18	100.0	18	19	US-09-331-204A-8		Sequence 8, Appli
3	16.4	91.1	18	8	US-08-387-041A-3		Sequence 3, Appli
4	16.4	91.1	18	19	US-09-331-204-1		Sequence 1, Appli

5 16.4 91.1 18 19 US-09-331-204A-4  
6 16.4 91.1 18 19 US-09-331-204A-7  
7 16.4 91.1 18 33 US-09-786-436-17  
8 16.4 91.1 18 33 US-09-786-436-42  
9 16.4 91.1 19 19 US-09-331-204-4  
10 16.4 91.1 21 8 US-08-387-041A-4  
11 16.4 91.1 21 19 US-09-331-204-6  
12 16.4 91.1 21 19 US-09-331-204A-6  
13 15.4 85.6 19 50 US-10-310-188-47426  
14 15 83.3 18 50 US-10-310-188-38927  
15 14.8 82.2 22 42 US-09-979-666B-79  
16 14.4 80.0 17 1 PCT-US02-29102-30  
17 14.4 80.0 17 1 PCT-US02-37657-51  
18 14.4 80.0 17 1 PCT-US02-37764-30  
19 14.4 80.0 17 24 US-09-546-745A-1942  
20 14.4 80.0 17 50 US-10-302-817A-51  
21 14.4 80.0 17 50 US-10-303-109A-30  
22 14.4 80.0 22 50 US-10-310-188-47706  
23 14 77.8 19 50 US-10-303-778-14508  
24 13.8 76.7 17 29 US-09-670-607-147  
25 13.8 76.7 19 50 US-10-310-188-26651  
26 13.8 76.7 20 1 PCT-US01-00109-174  
27 13.8 76.7 20 1 PCT-US02-15301-174  
28 13.8 76.7 20 2 PCT-US01-00109-174  
29 13.8 76.7 20 35 US-09-854-883-174  
30 13.8 76.7 20 49 US-10-266-090-45656  
31 13.8 76.7 20 51 US-10-360-510-174  
32 13.8 76.7 21 9 US-08-472-928B-45  
33 13.8 76.7 21 29 US-09-670-105-45  
34 13.8 76.7 21 50 US-10-310-188-51847  
35 13.4 74.4 16 50 US-10-303-778-1282  
36 13.4 74.4 17 45 US-10-061-201-1934  
37 13.4 74.4 17 45 US-10-061-201-1935  
38 13.4 74.4 17 45 US-10-061-201-1936  
39 13.4 74.4 17 87 US-60-328-205-1934  
40 13.4 74.4 17 87 US-60-328-205-1935  
41 13.4 74.4 17 87 US-60-328-205-1936  
42 13.4 74.4 18 49 US-10-266-090-46765  
43 13.4 74.4 18 50 US-10-310-188-6227  
44 13.4 74.4 18 50 US-10-310-188-25860  
45 13.4 74.4 18 50 US-10-310-188-38977

Sequence 4, Appli  
Sequence 7, Appli  
Sequence 17, Appli  
Sequence 42, Appli  
Sequence 4, Appli  
Sequence 4, Appli  
Sequence 6, Appli  
Sequence 6, Appli  
Sequence 47426, A  
Sequence 38927, A  
Sequence 79, Appli  
Sequence 30, Appli  
Sequence 51, Appli  
Sequence 30, Appli  
Sequence 1942, Ap  
Sequence 51, Appli  
Sequence 30, Appli  
Sequence 30, Appli  
Sequence 47706, A  
Sequence 14508, A  
Sequence 147, App  
Sequence 26651, A  
Sequence 174, App  
Sequence 174, App  
Sequence 174, App  
Sequence 174, App  
Sequence 45656, A  
Sequence 174, App  
Sequence 45, Appli  
Sequence 51847, A  
Sequence 1282, Ap  
Sequence 1934, Ap  
Sequence 1935, Ap  
Sequence 1936, Ap  
Sequence 1934, Ap  
Sequence 1935, Ap  
Sequence 1936, Ap  
Sequence 46765, A  
Sequence 6227, Ap  
Sequence 25860, A  
Sequence 38977, A

ALIGNMENTS

RESULT 1  
US-09-331-204-5  
; Sequence 5, Application US/09331204  
; GENERAL INFORMATION:  
; APPLICANT: Tam, Robert  
; TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN  
; FILE REFERENCE: ICNSequence  
; CURRENT APPLICATION NUMBER: US/09/331,204  
; CURRENT FILING DATE: 1999-08-20  
; PRIOR APPLICATION NUMBER: PCT/US97/23927  
; PRIOR FILING DATE: 1997-12-19  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: An oligomer  
; OTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic  
; OTHER INFORMATION: acid. This term includes oligomers consisting of  
; OTHER INFORMATION: naturally occurring bases, sugars and intersugar (  
US-09-331-204-5

Query Match 100.0%; Score 18; DB 19; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.1e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGGAGGGGGAGGTGGGG 18  
| | | | | | | | | | | | | | | | | |  
Db 1 TTGGAGGGGGAGGTGGGG 18

RESULT 2

US-09-331-204A-8  
; Sequence 8, Application US/09331204A  
; GENERAL INFORMATION:  
; APPLICANT: ICN Pharmaceuticals, Inc.  
; APPLICANT: Tam, Robert  
; TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Res  
; FILE REFERENCE: 216/013-US1  
; CURRENT APPLICATION NUMBER: US/09/331,204A  
; CURRENT FILING DATE: 1999-08-20  
; PRIOR APPLICATION NUMBER: PCT/US97/23927  
; PRIOR FILING DATE: 1997-12-19  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 8  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: synthetic construct  
US-09-331-204A-8

Query Match 100.0%; Score 18; DB 19; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.1e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGAGGTGGGG 18  
| | | | | | | | | | | | | | | | | |  
Db 1 TTGGAGGGGGAGGTGGGG 18

RESULT 3

US-08-387-041A-3  
; Sequence 3, Application US/08387041A  
; GENERAL INFORMATION:  
; APPLICANT: Tam, Robert C.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATION  
; TITLE OF INVENTION: OF CD28 EXPRESSION  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/387,041A  
; FILING DATE: 02-FEB-1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Halluin, Albert P.  
; REGISTRATION NUMBER: 25,227  
; REFERENCE/DOCKET NUMBER: 8250-011  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-854-3660  
; TELEFAX: 415-854-3694  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown

TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
US-08-387-041A-3

Query Match 91.1%; Score 16.4; DB 8; Length 18;  
Best Local Similarity 94.4%; Pred. No. 2.1e+04;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGAGGGGGAGGTGGG 18  
|||||  
Db 1 TTGAGGGGGTGTGGG 18

## RESULT 4

US-09-331-204-1  
; Sequence 1, Application US/09331204  
; GENERAL INFORMATION:  
; APPLICANT: Tam, Robert  
; TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN  
; FILE REFERENCE: ICNSequence  
; CURRENT APPLICATION NUMBER: US/09/331,204  
; CURRENT FILING DATE: 1999-08-20  
; PRIOR APPLICATION NUMBER: PCT/US97/23927  
; PRIOR FILING DATE: 1997-12-19  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: An oligomer  
; OTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic  
; OTHER INFORMATION: acid including oligomers consisting of naturally  
; OTHER INFORMATION: occurring bases, sugars and intersugar  
US-09-331-204-1

Query Match 91.1%; Score 16.4; DB 19; Length 18;  
Best Local Similarity 94.4%; Pred. No. 2.1e+04;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGAGGGGGAGGTGGG 18  
|||||  
Db 1 TTGAGGGGGTGTGGG 18

## RESULT 5

US-09-331-204A-4  
; Sequence 4, Application US/09331204A  
; GENERAL INFORMATION:  
; APPLICANT: ICN Pharmaceuticals, Inc.  
; APPLICANT: Tam, Robert  
; TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Respo  
; FILE REFERENCE: 216/013-US1  
; CURRENT APPLICATION NUMBER: US/09/331,204A  
; CURRENT FILING DATE: 1999-08-20  
; PRIOR APPLICATION NUMBER: PCT/US97/23927  
; PRIOR FILING DATE: 1997-12-19  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: synthetic construct  
US-09-331-204A-4

Query Match 91.1%; Score 16.4; DB 19; Length 18;  
Best Local Similarity 94.4%; Pred. No. 2.1e+04;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGAGGGGGAGGTGGG 18  
|||||

Db 1 TTGAGGGGGTGTGGG 18

## RESULT 6

US-09-331-204A-7  
; Sequence 7, Application US/09331204A  
; GENERAL INFORMATION:  
; APPLICANT: ICN Pharmaceuticals, Inc.  
; APPLICANT: Tam, Robert  
; TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Resi  
; FILE REFERENCE: 216/013-US1  
; CURRENT APPLICATION NUMBER: US/09/331,204A  
; CURRENT FILING DATE: 1999-08-20  
; PRIOR APPLICATION NUMBER: PCT/US97/23927  
; PRIOR FILING DATE: 1997-12-19  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 7  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: synthetic construct  
US-09-331-204A-7

Query Match 91.1%; Score 16.4; DB 19; Length 18;  
Best Local Similarity 94.4%; Pred. No. 2.1e+04;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGAGGGGGAGGTGGG 18  
|||||  
Db 1 TTGAGGGGGAGGTGGG 18

## RESULT 7

US-09-786-436-17  
; Sequence 17, Application US/09786436  
; GENERAL INFORMATION:  
; APPLICANT: Wagner, Hermann  
; APPLICANT: Lipford, Grayson  
; APPLICANT: Heeg, Klaus  
; TITLE OF INVENTION: G-Motif Oligonucleotides and Uses  
; FILE REFERENCE: C1041/7010 (AWS)  
; CURRENT APPLICATION NUMBER: US/09/786,436  
; CURRENT FILING DATE: 2001-03-02  
; PRIOR APPLICATION NUMBER: PCT/EP99/06502  
; PRIOR FILING DATE: 1999-09-03  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 17  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-09-786-436-17

Query Match 91.1%; Score 16.4; DB 33; Length 18;  
Best Local Similarity 94.4%; Pred. No. 2.1e+04;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGAGGGGGAGGTGGG 18  
|||||  
Db 1 TTGAGGGGGTGTGGG 18

## RESULT 8

US-09-786-436-42/c  
; Sequence 42, Application US/09786436  
; GENERAL INFORMATION:  
; APPLICANT: Wagner, Hermann  
; APPLICANT: Lipford, Grayson  
; APPLICANT: Heeg, Klaus  
; TITLE OF INVENTION: G-Motif Oligonucleotides and Uses

```
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: C1041/7010 (AWS)
; CURRENT APPLICATION NUMBER: US/09/786,436
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: PCT/EP99/06502
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-09-786-436-42

Query Match          91.1%; Score 16.4; DB 33; Length 18;
Best Local Similarity 94.4%; Pred. No. 2.1e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 TTGAGGGGGAGGTGGGG 18
        |||||
Db      18 TTGAGGGGGGTGGTGGG 1

RESULT 9
US-09-331-204-4
; Sequence 4, Application US/09331204
; GENERAL INFORMATION:
; APPLICANT: Tam, Robert
; TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN
; FILE REFERENCE: ICNSequence
; CURRENT APPLICATION NUMBER: US/09/331,204
; CURRENT FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: PCT/US97/23927
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: An oligomer
; OTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic
; OTHER INFORMATION: acid. This term includes oligomers consisting of
; OTHER INFORMATION: naturally occurring bases, sugars and intersugar (
US-09-331-204-4

Query Match          91.1%; Score 16.4; DB 19; Length 19;
Best Local Similarity 94.4%; Pred. No. 2.1e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 TTGAGGGGGAGGTGGGG 18
        |||||
Db      1 TTGAGGGGGAGGAGGGG 18

RESULT 10
US-08-387-041A-4
; Sequence 4, Application US/08387041A
; GENERAL INFORMATION:
; APPLICANT: Tam, Robert C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATION
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
```

```
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,041A
; FILING DATE: 02-FEB-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8250-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-387-041A-4

Query Match          91.1%; Score 16.4; DB 8; Length 21;
Best Local Similarity 94.4%; Pred. No. 2.1e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 TTGAGGGGGAGGTGGGG 18
        |||||
Db      4 TTGAGGGGGGTGGTGGG 21

RESULT 11
US-09-331-204-6
; Sequence 6, Application US/09331204
; GENERAL INFORMATION:
; APPLICANT: Tam, Robert
; TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN
; TITLE OF INVENTION: IMMUNE RESPONSE
; FILE REFERENCE: ICNSequence
; CURRENT APPLICATION NUMBER: US/09/331,204
; CURRENT FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: PCT/US97/23927
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: An oligomer
; OTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic
; OTHER INFORMATION: acid. This term includes oligomers consisting of
; OTHER INFORMATION: naturally occurring bases, sugars and intersugar (
US-09-331-204-6

Query Match          91.1%; Score 16.4; DB 19; Length 21;
Best Local Similarity 94.4%; Pred. No. 2.1e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 TTGAGGGGGAGGTGGGG 18
        |||||
Db      4 TTGAGGGGGGTGGTGGG 21

RESULT 12
US-09-331-204A-6
; Sequence 6, Application US/09331204A
```

GENERAL INFORMATION:  
APPLICANT: ICN Pharmaceuticals, Inc.  
APPLICANT: Tam, Robert  
TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Response  
FILE REFERENCE: 216/013-US1  
CURRENT APPLICATION NUMBER: US/09/331,204A  
CURRENT FILING DATE: 1999-08-20  
PRIOR APPLICATION NUMBER: PCT/US97/23927  
PRIOR FILING DATE: 1997-12-19  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 6  
LENGTH: 21  
TYPE: DNA  
ORGANISM: synthetic construct  
US-09-331-204A-6

Query Match 91.1%; Score 16.4; DB 19; Length 21;  
Best Local Similarity 94.4%; Pred. No. 2.1e+04;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGAGGGGGAGGTGGG 18  
Db 4 TTGAGGGGGTGGTGGG 21

RESULT 13  
US-10-310-188-47426  
Sequence 47426, Application US/10310188  
GENERAL INFORMATION:  
APPLICANT: RosettaGenomics  
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE  
FILE REFERENCE: 47487  
CURRENT APPLICATION NUMBER: US/10/310,188  
CURRENT FILING DATE: 2002-12-19  
NUMBER OF SEQ ID NOS: 86841  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 47426  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-310-188-47426

Query Match 85.6%; Score 15.4; DB 50; Length 19;  
Best Local Similarity 94.1%; Pred. No. 4.9e+04;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGGAGGGGGAGGTGGG 18  
Db 3 TGGAGGGGGAGGAGGG 19

RESULT 14  
US-10-310-188-38927  
Sequence 38927, Application US/10310188  
GENERAL INFORMATION:  
APPLICANT: RosettaGenomics  
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE  
FILE REFERENCE: 47487  
CURRENT APPLICATION NUMBER: US/10/310,188  
CURRENT FILING DATE: 2002-12-19  
NUMBER OF SEQ ID NOS: 86841  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 38927  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-310-188-38927

Query Match 83.3%; Score 15; DB 50; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.9e+04;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 GGAGGGGGAGGTGGG 17  
Db 3 GGAGGGGGAGGTGGG 17

RESULT 15  
US-09-979-666B-79  
Sequence 79, Application US/09979666B  
GENERAL INFORMATION:  
APPLICANT: TACHAS, GEORGE  
TITLE OF INVENTION: INHIBITION OF GASTRIC ACID PRODUCTION AND/OR SECRETION  
FILE REFERENCE: 47-162  
CURRENT APPLICATION NUMBER: US/09/979,666B  
CURRENT FILING DATE: 2001-11-26  
NUMBER OF SEQ ID NOS: 143  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 79  
LENGTH: 22  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Combined DNA/RNA Molecule:  
OTHER INFORMATION: Synthetic antisense oligonucleotide, can be  
OTHER INFORMATION: RNA, DNA or chimera  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: antisense oligonucleotide, can be RNA, DNA  
OTHER INFORMATION: or chimera  
US-09-979-666B-79

Query Match 82.2%; Score 14.8; DB 42; Length 22;  
Best Local Similarity 81.2%; Pred. No. 8.3e+04;  
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGAGGGGGAGGTGGG 17  
Db 2 TGGMGGGGGGMGGKGG 17

Search completed: October 27, 2003, 17:52:54  
Job time : 2357.29 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 11:09:34 ; Search time 307.029 Seconds  
(without alignments)  
97.777 Million cell updates/sec

Title: US-09-331-204A-8  
Perfect score: 18  
Sequence: 1 ttggagggggaggtggg 18

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2231628 seqs, 833900706 residues

Total number of hits satisfying chosen parameters: 264402

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents NA New.\*

- 1: /cgn2\_6/ptodata/1/pna/PCT\_NEW\_COMB.seq.\*
- 2: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq.\*
- 7: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	15.4	85.6	19	1	PCT-US02-38216-47426
2	15	83.3	18	1	PCT-US02-38216-38927
3	14.4	80.0	21	1	PCT-US03-26780-1166
4	14.4	80.0	22	1	PCT-US02-38216-47706
5	13.8	76.7	19	1	PCT-US02-38216-26651
6	13.8	76.7	20	5	US-09-629-644A-174
7	13.8	76.7	21	1	PCT-US02-38216-51847
8	13.4	74.4	18	1	PCT-US02-38216-6227
9	13.4	74.4	18	1	PCT-US02-38216-25860
10	13.4	74.4	18	1	PCT-US02-38216-38977
11	13.4	74.4	21	1	PCT-US02-38216-51829
12	13.2	73.3	20	1	PCT-US02-38216-36515
13	13.2	73.3	22	1	PCT-US02-38216-18159
14	13	72.2	19	1	PCT-US02-38216-25810
15	13	72.2	19	1	PCT-US02-38216-64492
16	13	72.2	19	1	PCT-US02-38216-64684
17	13	72.2	21	1	PCT-US02-38216-41829
18	12.8	71.1	16	1	PCT-US02-38216-18366
19	12.8	71.1	16	1	PCT-US02-38216-39032
20	12.8	71.1	17	1	PCT-US02-38216-14773
21	12.8	71.1	17	1	PCT-US02-38216-14816
22	12.8	71.1	17	1	PCT-US02-38216-38911
23	12.8	71.1	18	1	PCT-US02-38216-6229
24	12.8	71.1	18	1	PCT-US02-38216-9731
25	12.8	71.1	18	1	PCT-US02-38216-18298
26	12.8	71.1	18	1	PCT-US02-38216-39006

27	12.8	71.1	18	1	PCT-US02-38216-39031	Sequence 39031, A
28	12.8	71.1	18	1	PCT-US02-38216-39102	Sequence 39102, A
29	12.8	71.1	18	1	PCT-US02-38216-41647	Sequence 41647, A
30	12.8	71.1	18	1	PCT-US02-38216-51842	Sequence 51842, A
31	12.8	71.1	18	1	PCT-US02-38216-58279	Sequence 58279, A
32	12.8	71.1	18	1	PCT-US02-38216-60182	Sequence 60182, A
33	12.8	71.1	18	1	PCT-US02-38216-61077	Sequence 61077, A
34	12.8	71.1	18	1	PCT-US02-38216-61101	Sequence 61101, A
35	12.8	71.1	18	1	PCT-US02-38216-72811	Sequence 72811, A
36	12.8	71.1	19	1	PCT-US02-38216-10778	Sequence 10778, A
37	12.8	71.1	19	1	PCT-US02-38216-18422	Sequence 18422, A
38	12.8	71.1	19	1	PCT-US02-38216-38912	Sequence 38912, A
39	12.8	71.1	19	1	PCT-US02-38216-38943	Sequence 38943, A
40	12.8	71.1	19	1	PCT-US02-38216-46976	Sequence 46976, A
41	12.8	71.1	20	1	PCT-US02-38216-14886	Sequence 14886, A
42	12.8	71.1	20	1	PCT-US02-38216-18227	Sequence 18227, A
43	12.8	71.1	20	1	PCT-US02-38216-18520	Sequence 18520, A
44	12.8	71.1	20	1	PCT-US02-38216-26672	Sequence 26672, A
45	12.8	71.1	20	1	PCT-US02-38216-41837	Sequence 41837, A

ALIGNMENTS

RESULT 1  
PCT-US02-38216-47426  
; Sequence 47426, Application PC/TUS0238216  
; GENERAL INFORMATION:  
; APPLICANT: Rosetta Genomics LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
; TITLE OF INVENTION: GENES AND USES THEREOF  
; FILE REFERENCE: 55002  
; CURRENT APPLICATION NUMBER: PCT/US02/38216  
; CURRENT FILING DATE: 2002-11-12  
; NUMBER OF SEQ ID NOS: 86841  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 47426  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US02-38216-47426

Query Match 85.6%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 5.9e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGGAGGGGAGGTGGG 18  
|||  
Db 3 TGGAGGGGAGGTGGG 19

RESULT 2  
PCT-US02-38216-38927  
; Sequence 38927, Application PC/TUS0238216  
; GENERAL INFORMATION:  
; APPLICANT: Rosetta Genomics LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
; TITLE OF INVENTION: GENES AND USES THEREOF  
; FILE REFERENCE: 55002  
; CURRENT APPLICATION NUMBER: PCT/US02/38216  
; CURRENT FILING DATE: 2002-11-12  
; NUMBER OF SEQ ID NOS: 86841  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 38927  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US02-38216-38927

Query Match 83.3%; Score 15; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 8.2e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGAGGGGGAGGTGGG 17  
| | | | | | | | | |  
Db 3 GGAGGGGGAGGTGGG 17

RESULT 3  
PCT-US03-26780-1166  
; Sequence 1166, Application PC/TUS0326780  
; GENERAL INFORMATION:  
; APPLICANT: FIVEPRIME THERAPEUTICS, INC.  
; TITLE OF INVENTION: HUMAN POLYPEPTIDES ENCODED BY POLYNUCLEOTIDES AND METHODS OF  
; FILE REFERENCE: 08940.0014-00304  
; CURRENT APPLICATION NUMBER: PCT/US03/26780  
; CURRENT FILING DATE: 2003-08-28  
; PRIOR APPLICATION NUMBER: 60/406,616  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: 60/406,579  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: 60/406,655  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: 60/406,642  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: 60/406,640  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: 60/406,588  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: 60/406,666  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: 60/406,653  
; PRIOR FILING DATE: 2002-08-29  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 3700  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1166  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US03-26780-1166

Query Match 80.0%; Score 14.4; DB 1; Length 21;  
Best Local Similarity 93.8%; Pred. No. 1.3e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGGGGAGGTGGG 18  
| | | | | | | | | |  
Db 1 GGAGGAGGAGGTGGG 16

RESULT 4  
PCT-US02-38216-47706  
; Sequence 47706, Application PC/TUS0238216  
; GENERAL INFORMATION:  
; APPLICANT: Rosetta Genomics LTD  
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
; FILE REFERENCE: 55002  
; CURRENT APPLICATION NUMBER: PCT/US02/38216  
; CURRENT FILING DATE: 2002-11-12  
; NUMBER OF SEQ ID NOS: 86841  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 47706  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US02-38216-47706

Query Match 80.0%; Score 14.4; DB 1; Length 22;  
Best Local Similarity 93.8%; Pred. No. 1.3e+04;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 3 GGAGGGGGAGGTGGG 18  
| | | | | | | | | |  
Db 1 GGAGGGGGAGGTGGG 16

RESULT 5  
PCT-US02-38216-26651/c  
; Sequence 26651, Application PC/TUS0238216  
; GENERAL INFORMATION:  
; APPLICANT: Rosetta Genomics LTD  
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
; FILE REFERENCE: 55002  
; CURRENT APPLICATION NUMBER: PCT/US02/38216  
; CURRENT FILING DATE: 2002-11-12  
; NUMBER OF SEQ ID NOS: 86841  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 26651  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US02-38216-26651

Query Match 76.7%; Score 13.8; DB 1; Length 19;  
Best Local Similarity 88.2%; Pred. No. 2.2e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGAGGGGGAGGTGGG 18  
| | | | | | | | | |  
Db 18 TGGAGGTGGAGGTGGAG 2

RESULT 6  
US-09-629-644A-174  
; Sequence 174, Application US/09629644A  
; GENERAL INFORMATION:  
; APPLICANT: Lex M. Cowser  
; APPLICANT: Jacqueline Wyatt  
; APPLICANT: Susan M. Freier  
; APPLICANT: Brett P. Monia  
; APPLICANT: Madeline M. Butler  
; APPLICANT: Robert McKay  
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION  
; FILE REFERENCE: ISPH-0478  
; CURRENT APPLICATION NUMBER: US/09/629,644A  
; CURRENT FILING DATE: 2000-07-31  
; PRIOR APPLICATION NUMBER: US 09/487,368  
; PRIOR FILING DATE: 2000-01-18  
; NUMBER OF SEQ ID NOS: 242  
; SEQ ID NO 174  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-629-644A-174

Query Match 76.7%; Score 13.8; DB 5; Length 20;  
Best Local Similarity 88.2%; Pred. No. 2.2e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGAGGGGGAGGTGGG 18  
| | | | | | | | | |  
Db 1 TGGCCGGGGAGGTGGG 17

RESULT 7  
PCT-US02-38216-51847  
; Sequence 51847, Application PC/TUS0238216  
; GENERAL INFORMATION:  
; APPLICANT: Rosetta Genomics LTD



; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51847
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-51847

Query Match 76.7%; Score 13.8; DB 1; Length 21;
Best Local Similarity 88.2%; Pred. No. 2.2e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGAGGGGAGGTGGG 18
||| ||||| |||||
DB 4 TGGTGGGGCGGTGGG 20

RESULT 8
PCT-US02-38216-6227/c
; Sequence 6227, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6227
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-6227

Query Match 74.4%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 3e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGGGAGGTGGG 17
||| ||||| |||||
DB 15 GGAGGGGAGGAGGG 1

RESULT 9
PCT-US02-38216-25860/c
; Sequence 25860, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25860
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-25860

Query Match 74.4%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 3e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGGGAGGTGGG 17
||| ||||| |||||

Db 18 GGTGGGGAGGTGGG 4
;
RESULT 10
PCT-US02-38216-38977
; Sequence 38977, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38977
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-38977

Query Match 74.4%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 3e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAGGGGAGGTGGG 18
||| ||||| |||||
DB 2 GAGGAGGAGGTGGG 16

RESULT 11
PCT-US02-38216-51829
; Sequence 51829, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51829
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-51829

Query Match 74.4%; Score 13.4; DB 1; Length 21;
Best Local Similarity 93.3%; Pred. No. 3e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAGGGGAGGTGGG 18
||| ||||| |||||
DB 6 GTGGGGAGGTGGG 20

RESULT 12
PCT-US02-38216-36515
; Sequence 36515, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36515
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens



```
PCT-US02-38216-36515
Query Match      73.3%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.6e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTGGAGGGGAGGTGGG 18
   ||||| ||||| |||||
Db 2 TTGGGAGTGAGGTGGG 19

RESULT 13
PCT-US02-38216-18159
; Sequence 18159, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18159
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-18159

Query Match      73.3%; Score 13.2; DB 1; Length 22;
Best Local Similarity 83.3%; Pred. No. 3.5e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTGGAGGGGAGGTGGG 18
   ||||| ||||| |||||
Db 1 TGGAGGGGGAGGAAGG 18

RESULT 14
PCT-US02-38216-25810/c
; Sequence 25810, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25810
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-25810

Query Match      72.2%; Score 13; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGGGAGGTGGG 18
   ||||| |||||
Db 14 GGGGAGGTGGG 2

RESULT 15
PCT-US02-38216-64492/c
; Sequence 64492, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
```

```
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 64492
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-64492

Query Match      72.2%; Score 13; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGGGAGGTGGG 18
   ||||| |||||
Db 18 GGGGAGGTGGG 6

Search completed: October 27, 2003, 18:22:55
Job time : 307.029 secs
```

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: October 27, 2003, 10:32:29 ; Search time 250.743 Seconds  
(without alignments)  
1957.844 Million cell updates/sec

Title: US-09-331-204A-13  
Perfect score: 12  
Sequence: 1 ggggtgtgtggg 12

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 681044

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:

- 1: gb\_ba:
- 2: gb\_htg:
- 3: gb\_in:
- 4: gb\_om:
- 5: gb\_ov:
- 6: gb\_pat:
- 7: gb\_ph:
- 8: gb\_pl:
- 9: gb\_pr:
- 10: gb\_ro:
- 11: gb\_sts:
- 12: gb\_sy:
- 13: gb\_un:
- 14: gb\_vi:
- 15: em\_ba:
- 16: em\_fun:
- 17: em\_hum:
- 18: em\_in:
- 19: em\_mu:
- 20: em\_om:
- 21: em\_or:
- 22: em\_ov:
- 23: em\_pat:
- 24: em\_ph:
- 25: em\_pl:
- 26: em\_ro:
- 27: em\_sts:
- 28: em\_un:
- 29: em\_vi:
- 30: em\_htg\_hum:
- 31: em\_htg\_inv:
- 32: em\_htg\_other:
- 33: em\_htg\_mus:
- 34: em\_htg\_pln:
- 35: em\_htg\_rod:
- 36: em\_htg\_mam:
- 37: em\_htg\_vrt:
- 38: em\_sy:
- 39: em\_htgo\_hum:
- 40: em\_htgo\_mus:
- 41: em\_htgo\_other:

Pred. No. is the number of results predicted by chance to have a

Result No.	Score	Query Match %	Length	DB	ID	Description
1	12	100.0	18	6	AX023402	AX023402 Sequence
C	2	12	100.0	18	AX023427	AX023427 Sequence
C	3	11	91.7	17	A25058	A25058 Nucleoprote
	4	11	91.7	17	AR168836	AR168836 Sequence
	5	11	91.7	17	AR168838	AR168838 Sequence
	6	11	91.7	17	AR168839	AR168839 Sequence
	7	11	91.7	17	AR200305	AR200305 Sequence
	8	11	91.7	17	AR200307	AR200307 Sequence
	9	11	91.7	17	AR200308	AR200308 Sequence
	10	11	91.7	17	AR262436	AR262436 Sequence
	11	11	91.7	17	AR262438	AR262438 Sequence
	12	11	91.7	17	AR262439	AR262439 Sequence
	13	11	91.7	17	AX284071	AX284071 Sequence
	14	11	91.7	20	AR078333	AR078333 Sequence
C	15	11	91.7	20	AR092032	AR092032 Sequence
C	16	11	91.7	20	AR112167	AR112167 Sequence
C	17	11	91.7	20	AR149209	AR149209 Sequence
	18	11	91.7	20	AR173053	AR173053 Sequence
	19	11	91.7	20	AX298761	AX298761 Sequence
	20	11	91.7	21	AR168785	AR168785 Sequence
	21	11	91.7	21	AR200254	AR200254 Sequence
	22	11	91.7	21	AR262386	AR262386 Sequence
	23	11	91.7	21	I27779	I27779 Sequence 11
	24	10.4	86.7	15	AX572880	AX572880 Sequence
C	25	10.4	86.7	15	I72532	I72532 Sequence 2
C	26	10.4	86.7	17	AX214607	AX214607 Sequence
C	27	10.4	86.7	17	AX215490	AX215490 Sequence
C	28	10.4	86.7	17	AX215491	AX215491 Sequence
C	29	10.4	86.7	17	AX215492	AX215492 Sequence
C	30	10.4	86.7	17	AX215493	AX215493 Sequence
	31	10.4	86.7	17	AX673765	AX673765 Sequence
C	32	10.4	86.7	17	AX728115	AX728115 Sequence
	33	10.4	86.7	18	A87857	A87857 Sequence 5
	34	10.4	86.7	18	A89824	A89824 Sequence 5
	35	10.4	86.7	18	AR002274	AR002274 Sequence
	36	10.4	86.7	18	AR053125	AR053125 Sequence
C	37	10.4	86.7	18	AX117823	AX117823 Sequence
	38	10.4	86.7	18	AX599746	AX599746 Sequence
	39	10.4	86.7	18	BD065370	BD065370 An antise
	40	10.4	86.7	20	AR313443	AR313443 Sequence
	41	10.4	86.7	20	AX418779	AX418779 Sequence
C	42	10.4	86.7	20	AX440601	AX440601 Sequence
	43	10.4	86.7	20	BD000527	BD000527 Method fo
C	44	10.4	86.7	20	E59330	E59330 Method for
C	45	10.4	86.7	21	A28676	A28676 dsRNA with

ALIGNMENTS

RESULT 1	AX023402	AX023402	18 bp	DNA	linear	PAT 15-SEP-2000
LOCUS	Sequence 17 from Patent WO0014217.					
DEFINITION	AX023402					
ACCESSION	AX023402.1	GI:10183802				
VERSION						
KEYWORDS	synthetic construct					
SOURCE	synthetic construct					
ORGANISM	artificial sequences.					
REFERENCE	1					
AUTHORS	Lipford, G.B., Heeg, K. and Wagner, H.					
TITLE	G-motif oligonucleotides and uses thereof					
JOURNAL	Patent: WO 0014217-A 17 16-MAR-2000;					
	LIPFORD GRAYSON B (DE); HEEG KLAUS (DE); WAGNER HERMANN (DE);					

```
CPG IMMUNOPHARMACEUTICALS GMBH (DE)
FEATURES
  source
    Location/Qualifiers
      1..18
      /organism="synthetic construct"
      /mol_type="genomic DNA"
      /db_xref="taxon:32630"
      /note="synthetic, no natural origin"
BASE COUNT      1 a      0 c      13 g      4 t
ORIGIN

Query Match      100.0%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 7e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGTGGTGGG 12
      |||||
Db      7 GGGGTGGTGGG 18

RESULT 2
AX023427/c
LOCUS      AX023427      18 bp      DNA      linear      PAT 15-SEP-2000
DEFINITION      Sequence 42 from Patent WO0014217.
ACCESSION      AX023427
VERSION      AX023427.1 GI:10183827
KEYWORDS      .
SOURCE      synthetic construct
ORGANISM      synthetic construct
      artificial sequences.
REFERENCE      1
AUTHORS      Lipford,G.B., Heeg,K. and Wagner,H.
TITLE      G-motif oligonucleotides and uses thereof
JOURNAL      Patent: WO 0014217-A 42 16-MAR-2000;
      LIPFORD GRAYSON B (DE); HEEG KLAUS (DE); WAGNER HERMANN (DE);
      CPG IMMUNOPHARMACEUTICALS GMBH (DE)
FEATURES
  source
    Location/Qualifiers
      1..18
      /organism="synthetic construct"
      /mol_type="genomic DNA"
      /db_xref="taxon:32630"
      /note="synthetic, no natural origin"
BASE COUNT      4 a      13 c      0 g      1 t
ORIGIN

Query Match      100.0%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 7e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGTGGTGGG 12
      |||||
Db      12 GGGGTGGTGGG 1

RESULT 3
A25058/c
LOCUS      A25058      17 bp      DNA      linear      PAT 01-MAR-1995
DEFINITION      Nucleoprotein N gene fragment.
ACCESSION      A25058
VERSION      A25058.1 GI:832954
KEYWORDS      .
SOURCE      Viral hemorrhagic septicemia virus
ORGANISM      Viral hemorrhagic septicemia virus
      Viruses; ssRNA negative-strand viruses; Mononegavirales;
      Rhabdoviridae; Novirhabdovirus.
REFERENCE      1 (bases 1 to 17)
AUTHORS      .
JOURNAL      Patent: FR 2659350-A 4 13-SEP-1991;
      Location/Qualifiers
FEATURES
  source
    Location/Qualifiers
      1..17
      /organism="Viral hemorrhagic septicemia virus"
      /mol_type="genomic DNA"
      /db_xref="taxon:11287"
BASE COUNT      4 a      10 c      2 g      1 t

CPG IMMUNOPHARMACEUTICALS GMBH (DE)
FEATURES
  source
    Location/Qualifiers
      1..18
      /organism="synthetic construct"
      /mol_type="genomic DNA"
      /db_xref="taxon:32630"
      /note="synthetic, no natural origin"
BASE COUNT      1 a      0 c      13 g      4 t
ORIGIN

Query Match      91.7%; Score 11; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GGGTGGTGGG 12
      |||||
Db      11 GGGTGGTGGG 1

RESULT 4
AR168836
LOCUS      AR168836      17 bp      DNA      linear      PAT 17-DEC-2001
DEFINITION      Sequence 62 from patent US 6288042.
ACCESSION      AR168836
VERSION      AR168836.1 GI:17904964
KEYWORDS      .
SOURCE      Unknown.
ORGANISM      Unknown.
      Unclassified.
REFERENCE      1 (bases 1 to 17)
AUTHORS      Rando,R.F., Ojwaug,J.O., Hogan,M.E., Wallace,T.L. and Cossum,P.A.
TITLE      Anti-viral guanosine-rich tetrad forming oligonucleotides
JOURNAL      Patent: US 6288042-A 62 11-SEP-2001;
      Location/Qualifiers
FEATURES
  source
    Location/Qualifiers
      1..17
      /organism="unknown"
      /mol_type="genomic DNA"
      /db_xref="taxon:32630"
      /note="synthetic, no natural origin"
BASE COUNT      0 a      0 c      12 g      5 t
ORIGIN

Query Match      91.7%; Score 11; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGTGGTGGG 11
      |||||
Db      6 GGGGTGGTGGG 16

RESULT 5
AR168838
LOCUS      AR168838      17 bp      DNA      linear      PAT 17-DEC-2001
DEFINITION      Sequence 64 from patent US 6288042.
ACCESSION      AR168838
VERSION      AR168838.1 GI:17904967
KEYWORDS      .
SOURCE      Unknown.
ORGANISM      Unknown.
      Unclassified.
REFERENCE      1 (bases 1 to 17)
AUTHORS      Rando,R.F., Ojwaug,J.O., Hogan,M.E., Wallace,T.L. and Cossum,P.A.
TITLE      Anti-viral guanosine-rich tetrad forming oligonucleotides
JOURNAL      Patent: US 6288042-A 64 11-SEP-2001;
      Location/Qualifiers
FEATURES
  source
    Location/Qualifiers
      1..17
      /organism="unknown"
      /mol_type="genomic DNA"
      /db_xref="taxon:32630"
      /note="synthetic, no natural origin"
BASE COUNT      0 a      0 c      12 g      5 t
ORIGIN

Query Match      91.7%; Score 11; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GGGTGGTGGG 12
      |||||
Db      3 GGGTGGTGGG 13

RESULT 6
AR168839
LOCUS      AR168839      17 bp      DNA      linear      PAT 17-DEC-2001
DEFINITION      Sequence 65 from patent US 6288042.
```



AR262438 LOCUS AR262438 17 bp DNA linear PAT 29-JAN-2003  
DEFINITION Sequence 64 from patent US 6323185.  
ACCESSION AR262438  
VERSION AR262438.1 GI:28073869  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Rando,R.F., Fennwald,S., Zendequi,J.G., Ojwang,J.O. and Hogan,M.E.  
TITLE Anti-viral guanosine-rich oligonucleotides and method of treating HIV  
JOURNAL Patent: US 6323185-A 64 27-NOV-2001;  
FEATURES Location/Qualifiers  
source 1..17  
BASE COUNT 0 a 0 c 12 g 5 t  
ORIGIN  
Query Match 91.7%; Score 11; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 GGGTGGTGGG 12  
Db 3 GGGTGGTGGG 13  
RESULT 12  
AR262439 LOCUS AR262439 17 bp DNA linear PAT 29-JAN-2003  
DEFINITION Sequence 65 from patent US 6323185.  
ACCESSION AR262439  
VERSION AR262439.1 GI:28073870  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Rando,R.F., Fennwald,S., Zendequi,J.G., Ojwang,J.O. and Hogan,M.E.  
TITLE Anti-viral guanosine-rich oligonucleotides and method of treating HIV  
JOURNAL Patent: US 6323185-A 65 27-NOV-2001;  
FEATURES Location/Qualifiers  
source 1..17  
BASE COUNT 0 a 0 c 12 g 4 t 1 others  
ORIGIN  
Query Match 91.7%; Score 11; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGTGGTGGG 11  
Db 6 GGGTGGTGGG 16  
RESULT 13  
AX284071 LOCUS AX284071 17 bp DNA linear PAT 20-NOV-2001  
DEFINITION Sequence 36 from Patent WO0179487.  
ACCESSION AX284071  
VERSION AX284071.1 GI:17044781  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE 1  
AUTHORS Degitz,K.K. and Besch,R.  
TITLE Polydesoxyribonucleotides for inhibiting the expression of the icam-1-gene

JOURNAL Patent: WO 0179487-A 36 25-OCT-2001;  
Degitz, Klaus Karl (DE) ; Besch, Robert (DE)  
FEATURES Location/Qualifiers  
source 1..17  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Beschreibung der kunstlichen Sequenz:Polydesoxyribonukleotid"  
BASE COUNT 0 a 0 c 12 g 5 t  
ORIGIN  
Query Match 91.7%; Score 11; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGTGGTGGG 11  
Db 6 GGGTGGTGGG 16  
RESULT 14  
AR078333 LOCUS AR078333 20 bp DNA linear PAT 31-AUG-2000  
DEFINITION Sequence 2 from patent US 5962426.  
ACCESSION AR078333  
VERSION AR078333.1 GI:10005079  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Glazer,P.M.  
TITLE Triple-helix forming oligonucleotides for targeted mutagenesis  
JOURNAL Patent: US 5962426-A 2 05-OCT-1999;  
FEATURES Location/Qualifiers  
source 1..20  
BASE COUNT 3 a 0 c 15 g 2 t  
ORIGIN  
Query Match 91.7%; Score 11; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.4e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGTGGTGGG 11  
Db 10 GGGTGGTGGG 20  
RESULT 15  
AR092032/c LOCUS AR092032 20 bp DNA linear PAT 08-SEP-2000  
DEFINITION Sequence 56 from patent US 5998141.  
ACCESSION AR092032  
VERSION AR092032.1 GI:10018786  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Acton,S.Laurene.  
TITLE Intronic and polymorphic SR-BI nucleic acids and uses therefor  
JOURNAL Patent: US 5998141-A 56 07-DEC-1999;  
FEATURES Location/Qualifiers  
source 1..20  
BASE COUNT 4 a 13 c 1 g 2 t  
ORIGIN  
Query Match 91.7%; Score 11; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.4e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTGGTGGG 11  
| | | | | | | | | |  
Db 13 GGGTGGTGGG 3

Search completed: October 27, 2003, 11:09:28  
Job time : 251.743 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:29 ; Search time 108 Seconds  
(without alignments)  
299.938 Million cell updates/sec

Title: US-09-331-204A-13  
Perfect score: 12  
Sequence: 1 ggggtggtg999 12

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 252756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 1643890

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq 19Jun03: \*  
1: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT: \*  
2: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT: \*  
3: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT: \*  
4: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT: \*  
5: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT: \*  
6: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT: \*  
7: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT: \*  
8: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT: \*  
9: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT: \*  
10: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT: \*  
11: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT: \*  
12: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT: \*  
13: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT: \*  
14: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT: \*  
15: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT: \*  
16: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT: \*  
17: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT: \*  
18: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT: \*  
19: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT: \*  
20: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT: \*  
21: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT: \*  
22: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT: \*  
23: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT: \*  
24: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT: \*  
25: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12	100.0	12	17	AAT36248
2	12	100.0	12	20	AAX90341
3	12	100.0	15	24	ABL39459
4	12	100.0	18	17	AAT36196
5	12	100.0	18	20	AAX90328
6	12	100.0	18	20	AAX90332
7	12	100.0	18	20	AAX90297
8	12	100.0	18	20	AAX90290
					CD28 expression in
					CD28 inhibiting ph
					Human ETPB allele-
					Triplex forming ol
					CD28 inhibiting ph
					CD28 inhibiting ph
					CD28 inhibiting ph
					Oligonucleotide RT
					CD28 inhibition ol

C	9	12	100.0	18	21	AAX99625	Nucleotide sequenc
	10	12	100.0	18	21	AAX99650	Nucleotide sequenc
	11	12	100.0	21	17	AAT36197	Triplex forming ol
	12	12	100.0	21	20	AAX90329	CD28 inhibiting ph
	13	12	100.0	21	20	AAX90291	CD28 inhibiting ol
C	14	11.6	96.7	15	24	ABL39458	Human ETPB allele-
C	15	11	91.7	12	23	ABH83464	Oligonucleotide pr
C	16	11	91.7	12	23	ABI20603	Oligonucleotide pr
C	17	11	91.7	13	23	ABC86820	Oligonucleotide SE
C	18	11	91.7	13	23	ABC86821	Oligonucleotide SE
C	19	11	91.7	13	23	ABF47470	Oligonucleotide SE
C	20	11	91.7	13	23	ABF47471	Oligonucleotide SE
C	21	11	91.7	13	23	ABH53376	Oligonucleotide SE
C	22	11	91.7	13	23	ABH53377	Oligonucleotide SE
C	23	11	91.7	16	18	AAT51684	Oligonucleotide SE
	24	11	91.7	17	18	AAT51680	Viral integrase in
	25	11	91.7	17	18	AAT51682	Viral integrase in
	26	11	91.7	17	19	AAX79259	Oligonucleotide #5
	27	11	91.7	17	19	AAX79263	Oligonucleotide #5
	28	11	91.7	17	19	AAX79264	Oligonucleotide #5
C	29	11	91.7	17	24	AAI68634	ICAM-1 triple heli
C	30	11	91.7	18	19	AAV02512	Transcriptional ac
C	31	11	91.7	19	22	AAD09693	Cryptosporidium pa
	32	11	91.7	20	15	AAQ55572	Sequence of B-133-
	33	11	91.7	20	16	AAQ81074	supF gene triplex
	34	11	91.7	20	18	AAT70012	Triplex-forming ol
	35	11	91.7	20	18	AAT47061	Oligonucleotide AG
C	36	11	91.7	20	20	AAX24525	Human SR-BI gene e
C	37	11	91.7	20	20	AAX24617	Human SR-BI gene e
C	38	11	91.7	20	24	AAS97785	Murine SAC1 gene-s
	39	11	91.7	21	15	AAQ79211	Guanosine rich oli
	40	11	91.7	21	18	AAT51529	Viral integrase in
	41	11	91.7	21	19	AAX79218	Oligonucleotide #1
	42	11	91.7	21	22	AAD09592	Cryptosporidium pa
C	43	11	91.7	22	24	AAL44899	Triplex forming ol
C	44	10.8	90.0	18	22	AAF89954	Probe for characte
C	45	10.4	86.7	12	23	ABI00175	Oligonucleotide pr

ALIGNMENTS

RESULT 1  
AAT36248  
ID AAT36248 standard; DNA; 12 BP.  
XX AAT36248;  
XX AAT36248;  
DT 25-MAR-2003 (updated)  
DT 16-APR-1997 (first entry)  
XX CD28 expression inhibiting oligonucleotide, RT18s.  
DE Reduction; T cell; CD28; gene expression; treatment; immune system;  
KW disorder; graft versus host disease; septic shock; viral disease;  
KW psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;  
KW multiple sclerosis; uveitis; rheumatoid arthritis; interleukin 2;  
KW systemic lupus erythematosus; inflammatory bowel disease;  
KW IL-2; production; antisense; inhibition; ss  
XX Synthetic.  
XX WO9624380-A1.  
PN 15-AUG-1996.  
PD 05-FEB-1996; 96WO-US01507.  
XX 09-FEB-1995; 95US-0387041.  
PR 18-SEP-1995; 95US-0529878.  
PR 09-FEB-1995; 95US-0387041.  
PR 18-SEP-1995; 95US-0529878.  
XX

PA (ICNC ) ICN PHARM INC.  
 XX Tam RC;  
 PI  
 XX WPI; 1996-384228/38.  
 DR  
 XX  
 PT Oligo:nucleotide which reduces CD28 gene expression in T cells -  
 PT for treating immune system diseases, e.g. graft vs. host disease,  
 PT septic shock, psoriasis, etc.  
 XX  
 XX Example 2; Page 45; 77pp; English.  
 PS  
 XX The present oligonucleotide reduces CD28 dependent interleukin-2  
 CC (IL-2) production and T cell CD28 gene expression, useful in the  
 CC treatment of CD28 mediated diseases, particularly immune system  
 CC disorders, e.g. graft versus host disease, septic shock, viral  
 CC disease, psoriasis, type I diabetes mellitus, thyroiditis,  
 CC sarcoïdes, multiple sclerosis, uveitis, rheumatoid arthritis,  
 CC systemic lupus erythematosus, inflammatory bowel disease, etc..  
 CC Reducing CD28 expression may reduce the effects of antigenic  
 CC stimulation of CD28 positive T cells, with a consequent reduction  
 CC in cytokine release.  
 CC (Updated on 25-MAR-2003 to correct PR field.)  
 XX  
 XX Sequence 12 BP; 0 A; 0 C; 10 G; 2 T; 0 other;  
 SQ  
 Query Match 100.0%; Score 12; DB 17; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1e+04;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGTGGTGGG 12  
 DB 1 GGGGTGGTGGG 12  
 RESULT 2  
 AAX90341  
 ID AAX90341 standard; DNA; 12 BP.  
 XX  
 AC AAX90341;  
 XX  
 DT 24-SEP-1999 (first entry)  
 XX  
 DE CD28 inhibiting phosphorothioate oligonucleotide RT18S.  
 XX  
 KW CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;  
 KW immune system mediated disease; gamma-interferon; IL-8;  
 KW phosphorothioate; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX US5932556-A.  
 PN  
 XX 03-AUG-1999.  
 PD  
 XX  
 PF 18-SEP-1995; 95US-0529878.  
 XX  
 PR 18-SEP-1995; 95US-0529878.  
 XX  
 PA (TAMR/) TAM R C.  
 XX  
 PI Tam RC;  
 XX  
 DR WPI; 1999-443609/37.  
 XX  
 PT Treatment of immune system-mediated diseases by inhibiting  
 PT expression of CD28, IL-2, gamma-interferon or IL-8  
 XX  
 PS Example; Column 24; 45pp; English.  
 XX  
 CC The present invention describes a method for inhibiting the expression  
 CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method  
 CC comprises subcutaneous administration of an oligonucleotide (OGN).

CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the  
 CC method. The OGNs are used for the treatment of immune system-mediated  
 CC diseases. The present sequence represents a CD28 inhibiting  
 CC phosphorothioate oligonucleotide used in the exemplification of the  
 CC present invention.  
 XX  
 SQ Sequence 12 BP; 0 A; 0 C; 10 G; 2 T; 0 other;  
 Query Match 100.0%; Score 12; DB 20; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1e+04;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGTGGTGGG 12  
 DB 1 GGGGTGGTGGG 12  
 RESULT 3  
 ABL39459  
 ID ABL39459 standard; DNA; 15 BP.  
 XX  
 AC ABL39459;  
 XX  
 DT 22-APR-2002 (first entry)  
 XX  
 DE Human ETVF allele-specific oligonucleotide primer 19.  
 XX  
 KW Human; electron-transfer flavoprotein beta polypeptide; ETVF;  
 KW electron acceptor; mitochondrial matrix; glutaric acidemia type II;  
 KW novel polymorphic site; novel polymorphism; ETVF genotype; ss; GAIL;  
 KW ETVF haplotype; transgenic animal; primer; probe; chromosome 19q13;  
 KW primer-extension oligonucleotide; single nucleotide polymorphism;  
 KW SNP.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WC200202580-A2.  
 XX  
 PD 10-JAN-2002.  
 XX  
 PF 05-JUL-2001; 2001WO-US21306.  
 XX  
 PR 05-JUL-2000; 2000US-215984P.  
 XX  
 PA (GENA-) GENAISSANCE PHARM INC.  
 XX  
 PI Bentivegna SC, Bieglecki KM, Kazemi A, Koshy B;  
 XX  
 DR WPI; 2002-154722/20.  
 XX  
 PT Novel isolated human electron-transfer-flavoprotein, beta  
 PT polynucleotide, useful for therapeutic purposes, for studying the  
 PT expression and function of the polynucleotide, and for expressing the  
 PT flavoprotein -  
 XX  
 PS Claim 17; Page 14; 143pp; English.  
 XX  
 CC The invention comprises DNA, cDNA and protein sequences of the human  
 CC electron-transfer flavoprotein, beta polypeptide (ETFB) gene (located on  
 CC chromosome 19q13.3-13.4). The invention specifically relates to the  
 CC identification of 27 novel polymorphic sites within the ETVF gene.  
 CC Electron-transfer flavoprotein (ETF) is an obligatory electron acceptor  
 CC for nine primary flavoprotein dehydrogenases and is located in the  
 CC mitochondrial matrix. ETF is composed of an alpha (ETFA) and a beta  
 CC (ETFB) subunit. Electrons accepted by ETF are transferred to the  
 CC mitochondrial respiratory chain by ETF dehydrogenases (ETPDHs).  
 CC Deficiency of ETF or ETVF leads to glutaric acidemia type II (GAIL).  
 CC Therefore ETVF is a pharmaceutically-important gene in the treatment of  
 CC GAIL. The novel ETVF polymorphisms identified in the invention are useful  
 CC for genotyping and haplotyping the ETVF gene of an individual. The ETVF  
 CC protein and nucleic acids of the invention are useful for studying the  
 CC expression and function of ETVF in vivo. The ETVF protein and nucleic  
 CC acids are also useful for testing the efficacy of therapeutic agents and



CC compounds for glutaric acidemia type II. The nucleic acids of the  
CC invention are useful in the production of a transgenic animal expressing  
CC the E7FB gene. Nucleic acids ABL39414-ABL39440 represent claimed E7FB  
CC allele-specific probes. Nucleic acids ABL39441-ABL39494 represent  
CC claimed E7FB allele-specific PCR primers. Nucleic acids ABL39495-ABL39548  
CC represent claimed E7FB primer-extension pligonucleotides.  
XX  
SQ Sequence 15 BP; 0 A; 0 C; 11 G; 3 T; 1 other;

Query Match 100.0%; Score 12; DB 24; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGTGGTGGGG 12  
Db 2 GGGGTGGTGGGG 13

RESULT 4  
AAT36196  
ID AAT36196 standard; DNA; 18 BP.  
XX  
AC AAT36196;  
XX  
DT 25-MAR-2003 (updated)  
DT 15-APR-1997 (first entry)  
XX

DE Triplex forming oligo targetting CD28 5'-UTR (nt 58-75).  
XX  
KW Reduction; T cell; CD28; gene expression; treatment; immune system;  
KW disorder; graft versus host disease; septic shock; viral disease;  
KW psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;  
KW multiple sclerosis; uveitis; rheumatoid arthritis; 5'-UTR;  
KW systemic lupus erythematosus; inflammatory bowel disease;  
KW triplex forming; oligonucleotide; 5'-untranslated region; ss  
XX  
OS Synthetic.

XX  
PN WO9624380-A1.  
XX  
PD 15-AUG-1996.  
XX  
PF 05-FEB-1996; 96WO-US01507.  
XX  
PR 09-FEB-1995; 95US-0387041.  
PR 18-SEP-1995; 95US-0529878.  
PR 09-FEB-1995; 95US-0387041.  
PR 18-SEP-1995; 95US-0529878.  
XX  
PA (ICNC ) ICN PHARM INC.  
XX  
PI Tam RC;  
XX  
DR WPI; 1996-384228/38.

XX  
PT Oligo:nucleotide which reduces CD28 gene expression in T cells -  
PT for treating immune system diseases, e.g. graft vs. host disease,  
PT septic shock, psoriasis, etc.  
XX  
PS Claim 9; Page 54; 77pp; English.

XX  
CC The present oligonucleotide reduces T cell CD28 gene expression,  
CC useful in the treatment of CD28 mediated diseases, particularly  
CC immune system disorders, e.g. graft versus host disease, septic  
CC shock, viral disease, psoriasis, type I diabetes mellitus,  
CC thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid  
CC arthritis, systemic lupus erythematosus, inflammatory bowel  
CC disease, etc.. Reducing CD28 expression may reduce the effects of  
CC antigenic stimulation of CD28 positive T cells, with a consequent  
CC reduction in cytokine release.  
CC (Updated on 25-MAR-2003 to correct PR field.)

XX  
SQ Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;

Query Match 100.0%; Score 12; DB 17; Length 18;  
Best Local Similarity 100.0%; Pred. No. 9.9e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGTGGTGGGG 12  
Db 7 GGGGTGGTGGGG 18

RESULT 5  
AAX90328  
ID AAX90328 standard; DNA; 18 BP.  
XX  
AC AAX90328;  
XX  
DT 24-SEP-1999 (first entry)  
XX

DE CD28 inhibiting phosphorothioate oligonucleotide RT03S.  
XX  
KW CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;  
KW immune system mediated disease; gamma-interferon; IL-8;  
KW phosphorothioate; ss.

XX  
OS Synthetic.  
XX  
PN US5932556-A.  
XX  
PD 03-AUG-1999.  
XX  
PF 18-SEP-1995; 95US-0529878.  
XX  
PR 18-SEP-1995; 95US-0529878.  
XX  
PA (TAMR/) TAM R C.  
XX  
PI Tam RC;  
XX  
DR WPI; 1999-443609/37.

XX  
PT Treatment of immune system-mediated diseases by inhibiting  
PT expression of CD28, IL-2, gamma-interferon or IL-8  
XX  
PS Example; Column 21; 45pp; English.

XX  
CC The present invention describes a method for inhibiting the expression  
CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method  
CC comprises subcutaneous administration of an oligonucleotide (OGN).  
CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the  
CC method. The OGNs are used for the treatment of immune system-mediated  
CC diseases. The present sequence represents a CD28 inhibiting  
CC phosphorothioate oligonucleotide used in the exemplification of the  
CC present invention.

XX  
SQ Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;  
Query Match 100.0%; Score 12; DB 20; Length 18;  
Best Local Similarity 100.0%; Pred. No. 9.9e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGGG 12  
Db 7 GGGGTGGTGGGG 18

RESULT 6  
AAX90332/c  
ID AAX90332 standard; DNA; 18 BP.  
XX  
AC AAX90332;  
XX  
DT 24-SEP-1999 (first entry)  
XX

DE CD28 inhibiting phosphorothioate oligonucleotide RTC06S.  
XX  
KW CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;  
KW immune system mediated disease; gamma-interferon; IL-8;  
KW phosphorothioate; ss.  
XX  
OS Synthetic.  
XX  
PN US5932556-A.  
XX  
PD 03-AUG-1999.  
XX  
PF 18-SEP-1995; 95US-0529878.  
XX  
PR 18-SEP-1995; 95US-0529878.  
XX  
PA (TAMR/) TAM R C.  
XX  
PI Tam RC;  
XX  
XX WPI; 1999-443609/37.  
DR Treatment of immune system-mediated diseases by inhibiting  
PT expression of CD28, IL-2, gamma-interferon or IL-8  
PT  
XX Example; Column 21; 45pp; English.  
PS  
XX The present invention describes a method for inhibiting the expression  
CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method  
CC comprises subcutaneous administration of an oligonucleotide (OGN).  
CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the  
CC method. The OGNs are used for the treatment of immune system-mediated  
CC diseases. The present sequence represents a CD28 inhibiting  
CC phosphorothioate oligonucleotide used in the exemplification of the  
CC present invention.  
XX  
XX Sequence 18 BP; 4 A; 13 C; 0 G; 1 T; 0 other;  
SQ  
Query Match 100.0%; Score 12; DB 20; Length 18;  
Best Local Similarity 100.0%; Pred. No. 9.9e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGTGGTGGG 12  
Db 18 GGGGTGGTGGG 7  
RESULT 7  
AAX90297/c  
ID AAX90297 standard; DNA; 18 BP.  
XX  
XX AAX90297;  
AC  
XX 24-SEP-1999 (first entry)  
DT  
XX Oligonucleotide RTC06 used in an Example from US5932556.  
DE  
XX CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;  
KW immune system mediated disease; gamma-interferon; IL-8; ss.  
XX  
XX Synthetic.  
OS  
XX US5932556-A.  
PN  
XX 03-AUG-1999.  
PD  
XX 18-SEP-1995; 95US-0529878.  
PF  
XX 18-SEP-1995; 95US-0529878.  
PR  
XX (TAMR/) TAM R C.  
PA  
XX Tam RC;  
PI

XX WPI; 1999-443609/37.  
DR Treatment of immune system-mediated diseases by inhibiting  
XX expression of CD28, IL-2, gamma-interferon or IL-8  
PT  
XX Example; Column 13; 45pp; English.  
PS  
XX The present invention describes a method for inhibiting the expression  
CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method  
CC comprises subcutaneous administration of an oligonucleotide (OGN).  
CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the  
CC method. The OGNs are used for the treatment of immune system-mediated  
CC diseases. AAX90292 to AAX90323 represent oligonucleotides used in the  
CC exemplification of the present invention.  
XX  
XX Sequence 18 BP; 4 A; 13 C; 0 G; 1 T; 0 other;  
SQ  
Query Match 100.0%; Score 12; DB 20; Length 18;  
Best Local Similarity 100.0%; Pred. No. 9.9e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGTGGTGGG 12  
Db 18 GGGGTGGTGGG 7  
RESULT 8  
AAX90290  
ID AAX90290 standard; DNA; 18 BP.  
XX  
XX AAX90290;  
AC  
XX 24-SEP-1999 (first entry)  
DT  
XX CD28 inhibition oligonucleotide RT03.  
DE  
XX CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;  
KW immune system mediated disease; gamma-interferon; IL-8; ss.  
XX  
XX Synthetic.  
OS  
XX US5932556-A.  
PN  
XX 03-AUG-1999.  
PD  
XX 18-SEP-1995; 95US-0529878.  
PF  
XX 18-SEP-1995; 95US-0529878.  
PR  
XX (TAMR/) TAM R C.  
PA  
XX Tam RC;  
PI  
XX WPI; 1999-443609/37.  
DR Treatment of immune system-mediated diseases by inhibiting  
XX expression of CD28, IL-2, gamma-interferon or IL-8  
PT  
XX Claim 5; Column 29; 45pp; English.  
PS  
XX The present invention describes a method for inhibiting the expression  
CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method  
CC comprises subcutaneous administration of an oligonucleotide (OGN).  
CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the  
CC method. The OGNs are used for the treatment of immune system-mediated  
CC diseases.  
XX  
XX Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;  
SQ  
Query Match 100.0%; Score 12; DB 20; Length 18;  
Best Local Similarity 100.0%; Pred. No. 9.9e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGTGGTGGG 12  
Db 18 GGGGTGGTGGG 7  
RESULT 8  
AAX90290  
ID AAX90290 standard; DNA; 18 BP.  
XX  
XX AAX90290;  
AC  
XX 24-SEP-1999 (first entry)  
DT  
XX CD28 inhibition oligonucleotide RT03.  
DE  
XX CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;  
KW immune system mediated disease; gamma-interferon; IL-8; ss.  
XX  
XX Synthetic.  
OS  
XX US5932556-A.  
PN  
XX 03-AUG-1999.  
PD  
XX 18-SEP-1995; 95US-0529878.  
PF  
XX 18-SEP-1995; 95US-0529878.  
PR  
XX (TAMR/) TAM R C.  
PA  
XX Tam RC;  
PI  
XX WPI; 1999-443609/37.  
DR Treatment of immune system-mediated diseases by inhibiting  
XX expression of CD28, IL-2, gamma-interferon or IL-8  
PT  
XX Claim 5; Column 29; 45pp; English.  
PS  
XX The present invention describes a method for inhibiting the expression  
CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method  
CC comprises subcutaneous administration of an oligonucleotide (OGN).  
CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the  
CC method. The OGNs are used for the treatment of immune system-mediated  
CC diseases.  
XX  
XX Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;  
SQ  
Query Match 100.0%; Score 12; DB 20; Length 18;  
Best Local Similarity 100.0%; Pred. No. 9.9e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGG 12  
| | | | | | | |  
Db 7 GGGGTGGTGGG 18

RESULT 9  
AAZ99625  
ID AAZ99625 standard; DNA; 18 BP.

XX  
AC AAZ99625;

XX  
DT 12-JUL-2000 (first entry)

XX  
DE Nucleotide sequence of G-motif oligonucleotide GR1.

XX  
KW G-motif oligonucleotide; vaccine; Toxoplasmosis; viral infection;  
KW antigen presenting cell activation; natural killer cell; septic shock;  
KW cytotoxic T-lymphocyte; inflammation; autoimmune disease;  
KW rheumatoid arthritis; Crohn's disease; sarcoidosis; multiple sclerosis;  
KW Kawasaki syndrome; graft-versus-host disease; transplant rejection;  
KW helper T cell response 1-mediated disease; Lyme arthritis;  
KW streptococcal induced arthritis; chronic inflammatory bowel disease;  
KW psoriasis vulgaris; experimental allergic encephalomyelitis;  
KW insulin-dependent diabetes mellitus; bacterial infection;  
KW parasitic infection; Leishmaniasis; spontaneous abortion; tumour; ss.

XX  
OS Synthetic.

XX  
PN WO200014217-A2.

XX  
PD 16-MAR-2000.

XX  
PF 03-SEP-1999; 99WO-EP06502.

XX  
PR 03-SEP-1998; 98EP-0116652.

XX  
PA (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.

XX  
PI Wagner H, Lipford GB, Heeg K;

XX  
DR WPI; 2000-256970/22.

XX  
PT Compositions comprising G-motif oligonucleotides useful for treating  
PT e.g. septic shock, rheumatoid arthritis, diabetes and human  
PT immunodeficiency virus infections -

XX  
PS Example 14; Page 32; 75pp; English.

XX  
CC The present sequence represents a G-motif oligonucleotide of the  
CC invention. The specification describes compositions comprising G-motif  
CC oligonucleotides. The G-motif oligonucleotides inhibit activation of  
CC antigen presenting cells by inhibiting the uptake of DNA by a cell, by  
CC stimulating natural killer cells, or by co-stimulating cytotoxic  
CC T-lymphocytes. The G-motif oligonucleotides may be used for the  
CC productions of vaccines for treating septic shock, inflammation,  
CC autoimmune diseases (e.g. rheumatoid arthritis, Crohn's disease,  
CC sarcoidosis, multiple sclerosis, Kawasaki syndrome, graft-versus-host  
CC disease and transplant rejection), helper T cell response 1-mediated  
CC diseases (e.g. Streptococcal induced arthritis, Lyme arthritis, chronic  
CC inflammatory bowel disease, psoriasis vulgaris, experimental allergic  
CC encephalomyelitis, and insulin-dependent diabetes mellitus), bacterial  
CC infections, parasitic infections (e.g. Leishmaniasis or Toxoplasmosis),  
CC viral infections (e.g. Cytomegalovirus and human immunodeficiency virus  
CC (HIV)-infections), spontaneous abortions and tumours. They may also be  
CC used to induce proliferation of bone marrow cells, especially macrophage  
CC precursor cells.

XX  
SQ Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;

Query Match 100.0%; Score 12; DB 21; Length 18;  
Best Local Similarity 100.0%; Pred. No. 9.9e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGG 12  
| | | | | | | |  
Db 7 GGGGTGGTGGG 18

RESULT 10  
AAZ99650/c  
ID AAZ99650 standard; DNA; 18 BP.

XX  
AC AAZ99650;

XX  
DT 12-JUL-2000 (first entry)

XX  
DE Nucleotide sequence of non-G-motif oligonucleotide GRF1comp.

XX  
KW G-motif oligonucleotide; vaccine; Toxoplasmosis; viral infection;  
KW antigen presenting cell activation; natural killer cell; septic shock;  
KW cytotoxic T-lymphocyte; inflammation; autoimmune disease;  
KW rheumatoid arthritis; Crohn's disease; sarcoidosis; multiple sclerosis;  
KW Kawasaki syndrome; graft-versus-host disease; transplant rejection;  
KW helper T cell response 1-mediated disease; Lyme arthritis;  
KW streptococcal induced arthritis; chronic inflammatory bowel disease;  
KW psoriasis vulgaris; experimental allergic encephalomyelitis;  
KW insulin-dependent diabetes mellitus; bacterial infection;  
KW parasitic infection; Leishmaniasis; spontaneous abortion; tumour; ss.

OS Synthetic.

XX  
PN WO200014217-A2.

XX  
PD 16-MAR-2000.

XX  
PF 03-SEP-1999; 99WO-EP06502.

XX  
PR 03-SEP-1998; 98EP-0116652.

XX  
PA (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.

XX  
PI Wagner H, Lipford GB, Heeg K;

XX  
DR WPI; 2000-256970/22.

XX  
PT Compositions comprising G-motif oligonucleotides useful for treating  
PT e.g. septic shock, rheumatoid arthritis, diabetes and human  
PT immunodeficiency virus infections -

XX  
PS Example 14; Page 32; 75pp; English.

XX  
CC The present sequence represents a non-G-motif oligonucleotide of the  
CC invention. The specification describes compositions comprising G-motif  
CC oligonucleotides. The G-motif oligonucleotides inhibit activation of  
CC antigen presenting cells by inhibiting the uptake of DNA by a cell, by  
CC stimulating natural killer cells, or by co-stimulating cytotoxic  
CC T-lymphocytes. The G-motif oligonucleotides may be used for the  
CC productions of vaccines for treating septic shock, inflammation,  
CC autoimmune diseases (e.g. rheumatoid arthritis, Crohn's disease,  
CC sarcoidosis, multiple sclerosis, Kawasaki syndrome, graft-versus-host  
CC disease and transplant rejection), helper T cell response 1-mediated  
CC diseases (e.g. Streptococcal induced arthritis, Lyme arthritis, chronic  
CC inflammatory bowel disease, psoriasis vulgaris, experimental allergic  
CC encephalomyelitis, and insulin-dependent diabetes mellitus), bacterial  
CC infections, parasitic infections (e.g. Leishmaniasis or Toxoplasmosis),  
CC viral infections (e.g. Cytomegalovirus and human immunodeficiency virus  
CC (HIV)-infections), spontaneous abortions and tumours. They may also be  
CC used to induce proliferation of bone marrow cells, especially macrophage  
CC precursor cells.

XX  
SQ Sequence 18 BP; 4 A; 13 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 12; DB 21; Length 18;  
Best Local Similarity 100.0%; Pred. No. 9.9e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGG 12  
Db 12 GGGGTGGTGGG 1

RESULT 11

AAT36197

ID AAT36197 standard; DNA; 21 BP.

XX

AC AAT36197;

XX 25-MAR-2003 (updated)

DT 15-APR-1997 (first entry)

XX

DE Triplex forming oligo targetting CD28 5'-UTR (nt 58-78).

XX

KW Reduction; T cell; CD28; gene expression; treatment; immune system;

KW disorder; graft versus host disease; septic shock; viral disease;

KW psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;

KW multiple sclerosis; uveitis; rheumatoid arthritis; 5'-UTR;

KW systemic lupus erythematosus; inflammatory bowel disease;

KW triplex forming; oligonucleotide; 5'-untranslated region; ss

XX

OS Synthetic.

XX

PN WO9624380-A1.

XX

PD 15-AUG-1996.

XX

PF 05-FEB-1996; 96WO-US01507.

XX

PR 09-FEB-1995; 95US-0387041.

PR 18-SEP-1995; 95US-0529878.

PR 09-FEB-1995; 95US-0387041.

PR 18-SEP-1995; 95US-0529878.

XX

PA (ICNC ) ICN PHARM INC.

XX

PI Tam RC;

XX

DR WPI; 1996-384228/38.

XX

PT Oligo:nucleotide which reduces CD28 gene expression in T cells -

PT for treating immune system diseases, e.g. graft vs. host disease,

PT septic shock, psoriasis, etc.

XX

PS Claim 10; Page 54; 77pp; English.

XX

CC The present oligonucleotide reduces T cell CD28 gene expression,

CC useful in the treatment of CD28 mediated diseases, particularly

CC immune system disorders, e.g. graft versus host disease, septic

CC shock, viral disease, psoriasis, type I diabetes mellitus,

CC thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid

CC arthritis, systemic lupus erythematosus, inflammatory bowel

CC disease, etc.. Reducing CD28 expression may reduce the effects of

CC antigenic stimulation of CD28 positive T cells, with a consequent

CC reduction in cytokine release.

CC (Updated on 25-MAR-2003 to correct PR field.)

XX

SQ Sequence 21 BP; 1 A; 0 C; 16 G; 4 T; 0 other;

Query Match 100.0%; Score 12; DB 17; Length 21;

Best Local Similarity 100.0%; Pred. No. 9.8e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGG 12

Db 10 GGGGTGGTGGG 21

RESULT 12

AAX90329

ID AAX90329 standard; DNA; 21 BP.

XX

AC AAX90329;

XX

DT 24-SEP-1999 (first entry)

XX

DE CD28 inhibiting phosphorothioate oligonucleotide RT04S.

XX

KW CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;

KW immune system mediated disease; gamma-interferon; IL-8;

KW phosphorothioate; ss.

XX

OS Synthetic.

XX

PN US5932556-A.

XX

PD 03-AUG-1999.

XX

PF 18-SEP-1995; 95US-0529878.

XX

PR 18-SEP-1995; 95US-0529878.

XX

PA (TAMR/) TAM R C.

XX

PI Tam RC;

XX

DR WPI; 1999-443609/37.

XX

PT Treatment of immune system-mediated diseases by inhibiting

PT expression of CD28, IL-2, gamma-interferon or IL-8

XX

PS Example; Column 21; 45pp; English.

XX

CC The present invention describes a method for inhibiting the expression

CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method

CC comprises subcutaneous administration of an oligonucleotide (OGN).

CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the

CC method. The OGNs are used for the treatment of immune system-mediated

CC diseases. The present sequence represents a CD28 inhibiting

CC phosphorothioate oligonucleotide used in the exemplification of the

CC present invention.

XX

SQ Sequence 21 BP; 1 A; 0 C; 16 G; 4 T; 0 other;

Query Match 100.0%; Score 12; DB 20; Length 21;

Best Local Similarity 100.0%; Pred. No. 9.8e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGG 12

Db 10 GGGGTGGTGGG 21

RESULT 13

AAX90291

ID AAX90291 standard; DNA; 21 BP.

XX

AC AAX90291;

XX

DT 24-SEP-1999 (first entry)

XX

DE CD28 inhibition oligonucleotide RT04.

XX

KW CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;

KW immune system mediated disease; gamma-interferon; IL-8; ss.

XX

OS Synthetic.

XX

PN US5932556-A.

XX

PD 03-AUG-1999.

XX

PF 18-SEP-1995; 95US-0529878.

XX 18-SEP-1995; 95US-0529878.  
PR (TAMR/) TAM R C.  
XX Tam RC;  
PI WPI; 1999-443609/37.  
XX Treatment of immune system-mediated diseases by inhibiting  
PT expression of CD28, IL-2, gamma-interferon or IL-8  
XX Claim 6; Column 29; 45pp; English.  
XX The present invention describes a method for inhibiting the expression  
CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method  
CC comprises subcutaneous administration of an oligonucleotide (OGN).  
CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the  
CC method. The OGNs are used for the treatment of immune system-mediated  
CC diseases.  
XX Sequence 21 BP; 1 A; 0 C; 16 G; 4 T; 0 other;  
SQ Query Match 100.0%; Score 12; DB 20; Length 21;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGTGGTGGGG 12  
Db 10 GGGGTGGTGGGG 21  
RESULT 14  
ABL39458/c  
ID ABL39458 standard; DNA; 15 BP.  
XX ABL39458;  
XX 22-APR-2002 (first entry)  
DT Human ETVB allele-specific oligonucleotide primer 18.  
XX Human; electron-transfer flavoprotein beta polypeptide; ETVB;  
KW electron acceptor; mitochondrial matrix; glutaric acidemia type II;  
KW novel polymorphic site; novel polymorphism; ETVB genotype; ss; GAIL;  
KW ETVB haplotype; transgenic animal; primer; probe; chromosome 19q13;  
KW primer-extension oligonucleotide; single nucleotide polymorphism;  
KW SNP.  
XX Homo sapiens.  
OS WO200202580-A2.  
XX 10-JAN-2002.  
PD 05-JUL-2001; 2001WO-US21306.  
XX 05-JUL-2000; 2000US-215984P.  
PR (GENA-) GENAISSANCE PHARM INC.  
XX Bentivegna SC, Bieglecki KM, Kazemi A, Koshy B;  
PI WPI; 2002-154722/20.  
XX Novel isolated human electron-transfer-flavoprotein, beta  
XX polynucleotide, useful for therapeutic purposes, for studying the  
PT expression and function of the polynucleotide, and for expressing the  
PT flavoprotein -  
XX Claim 17; Page 14; 143pp; English.  
PS The invention comprises DNA, cDNA and protein sequences of the human

CC electron-transfer flavoprotein, beta polypeptide (ETFB) gene (located on  
CC chromosome 19q13.3-13.4). The invention specifically relates to the  
CC identification of 27 novel polymorphic sites within the ETVB gene.  
CC Electron-transfer flavoprotein (ETFB) is an obligatory electron acceptor  
CC for nine primary flavoprotein dehydrogenases and is located in the  
CC mitochondrial matrix. ETF is composed of an alpha (ETFA) and a beta  
CC (ETFB) subunit. Electrons accepted by ETF are transferred to the  
CC mitochondrial respiratory chain by ETF dehydrogenases (ETFDHs).  
CC Deficiency of ETF or ETFDH leads to glutaric acidemia type II (GAIL).  
CC Therefore ETVB is a pharmaceutically-important gene in the treatment of  
CC GAIL. The novel ETVB polymorphisms identified in the invention are useful  
CC for genotyping and haplotyping the ETVB gene of an individual. The ETVB  
CC protein and nucleic acids of the invention are useful for studying the  
CC expression and function of ETVB in vivo. The ETVB protein and nucleic  
CC acids are also useful for testing the efficacy of therapeutic agents and  
CC compounds for glutaric acidemia type II. The nucleic acids of the  
CC invention are useful in the production of a transgenic animal expressing  
CC the ETVB gene. Nucleic acids ABL39414-ABL39440 represent claimed ETVB  
CC allele-specific probes. Nucleic acids ABL39441-ABL39494 represent  
CC claimed ETVB allele-specific PCR primers. Nucleic acids ABL39495-ABL39548  
CC represent claimed ETVB primer-extension oligonucleotides.  
XX Sequence 15 BP; 3 A; 10 C; 1 G; 0 U; 1 other;  
SQ Query Match 96.7%; Score 11.6; DB 24; Length 15;  
Best Local Similarity 91.7%; Pred. No. 1.5e+04;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGTGGTGGGG 12  
Db 14 RGGGTGGTGGGG 3  
RESULT 15  
ABH83464/c  
ID ABH83464 standard; DNA; 12 BP.  
XX ABH83464;  
AC ABH83464;  
XX 22-FEB-2002 (first entry)  
DT Oligonucleotide primer SEQ ID NO 283457 for detecting SNP TSC0011318.  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX Homo sapiens.  
OS WO200177384-A2.  
XX 18-OCT-2001.  
PD 06-APR-2001; 2001WO-IB00713.  
XX 07-APR-2000; 2000DE-1019173.  
PR (EPIG-) EPIGENOMICS AG.  
XX Olek A, Piepenbrock C, Berlin K;  
PI WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single nucleotide polymorphisms and cytosine  
PT methylation status -  
XX Claim 1; SEQ ID 283457; 29pp + Sequence Listing; German.  
PS This invention describes novel oligonucleotide primers or peptide nucleic  
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation.  
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and  
CC ABI00010-ABI82073 represent the oligomers described in the invention.  
CC NOTE: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

XX  
SQ Sequence 12 BP; 2 A; 10 C; 0 G; 0 U; 0 other;  
Query Match 91.7%; Score 11; DB 23; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.9e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGTGGTGGG 11  
| | | | | | | | | |  
Db 11 GCGGTGGTGGG 1

Search completed: October 27, 2003, 11:25:21  
Job time : 108 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:29 ; Search time 1054.51 Seconds  
(without alignments)  
276.576 Million cell updates/sec

Title: US-09-331-204A-13  
Perfect score: 12  
Sequence: 1 ggggtggtgggg 12

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 11152

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_estc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_est3:\*  
12: gb\_est4:\*  
13: gb\_est5:\*  
14: gb\_estfun:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	10.4	86.7	16	9 AI590540	AI590540 twllc02.x
C 2	10.4	86.7	19	9 AI807936	AI807936 wf52e09.x
C 3	10.4	86.7	19	28 AZ369361	AZ369361 lM0119123
C 4	10.4	86.7	19	28 AZ381798	AZ381798 lM0138G01

C 5	10.4	86.7	19	28	AZ447936	AI590540	16 bp	mrna	linear	EST 14-MAY-1999
C 6	10.4	86.7	19	28	AZ780591	twllc02.x1	NCI CGAP Brn52	Homo sapiens	cDNA clone	IMAGE:2259362 3'
C 7	10.4	86.7	19	28	AZ786308	similar to	TR:000599	O00599	CON1.	;', mRNA sequence.
C 8	10.4	86.7	20	28	AZ466238	AI590540	AI590540.1	GI:4599588		
C 9	10.4	86.7	21	28	AZ495585	EST.				
C 10	10.4	86.7	21	28	AZ774703	Homo sapiens (human)				
C 11	10.4	86.7	22	9	AI183338	Homo sapiens				
C 12	10.4	86.7	22	9	AI439277	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
C 13	10.4	86.7	22	28	AZ766712	1 (bases 1 to 16)				
C 14	10.4	86.7	22	28	AZ769521	NCI/NINDS-CGAP	http://www.ncbi.nlm.nih.gov/ncicgap.			
C 15	10	83.3	19	9	AA928040	National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BRGAP), Tumor Gene Index				
C 16	10	83.3	21	28	AZ758704	Unpublished				
C 17	10	83.3	22	9	AA923820	Contact: Robert Strausberg, Ph.D.				
C 18	10	83.3	22	9	AI354432	Email: cgapbs-r@mail.nih.gov				
C 19	9.4	78.3	16	9	AI569544	Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.				
C 20	9.4	78.3	16	9	AI684114	CDNA Library Preparation: Life Technologies, Inc.				
C 21	9.4	78.3	19	9	AA909236	CDNA Library Arrayed by: Greg Lennon, Ph.D.				
C 22	9.4	78.3	19	9	AI364573	DNA Sequencing by: Washington University Genome Sequencing Center				
C 23	9.4	78.3	21	28	AZ468862	Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:				
C 24	9.4	78.3	21	28	AZ512534					
C 25	9.4	78.3	21	28	AZ783943					
C 26	9.4	78.3	21	28	AZ788597					
C 27	9.4	78.3	21	28	AZ864022					
C 28	9.4	78.3	22	9	AI687266					
C 29	9.4	78.3	22	9	AI707945					
C 30	9.4	78.3	22	13	BQ585098					
C 31	9.4	78.3	22	28	AZ327083					
C 32	9.4	78.3	22	28	AZ454940					
C 33	9.4	78.3	22	28	AZ627938					
C 34	9.4	78.3	22	28	AZ953028					
C 35	9	75.0	20	14	D20001					
C 36	9	75.0	21	28	AZ399828					
C 37	8.8	73.3	12	13	BQ585390					
C 38	8.8	73.3	13	13	BQ595080					
C 39	8.8	73.3	14	13	BQ593114					
C 40	8.8	73.3	15	13	BQ590018					
C 41	8.8	73.3	16	9	AA937364					
C 42	8.8	73.3	16	9	AA968729					
C 43	8.8	73.3	16	9	AI209036					
C 44	8.8	73.3	16	9	AI446372					
C 45	8.8	73.3	16	9	AI648507					

ALIGNMENTS

RESULT 1  
AI590540/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AI590540  
twllc02.x1 NCI CGAP Brn52 Homo sapiens cDNA clone IMAGE:2259362 3', similar to TR:000599 O00599 CON1. ;', mRNA sequence.

AI590540  
AI590540.1 GI:4599588  
EST.

Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 16)  
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BRGAP), Tumor Gene Index

Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html  
Trace considered overall poor quality  
Insert Length: 353 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1  
POLYA=No.

FEATURES

source

Location/Qualifiers  
1. .16  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2259362"  
/tissue\_type="tumor, 5 pooled (see description)"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Brn52"  
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: SalI;  
Site 2: NotI; This library represents the normalized  
version of NCI CGAP Brn35. Cloned unidirectionally.  
Primer: Oligo dT. Average insert size 1.19 kb. Tumor  
types include: meningioma, oligodendroglioma, astrocytoma  
(grade II), medulloblastoma, astrocytoma (grade IV).  
Constructed by Life Technologies."

BASE COUNT  
ORIGIN

4 a 12 c 0 g 0 t  
Query Match 86.7%; Score 10.4; DB 9; Length 16;  
Best Local Similarity 91.7%; Pred. No. 6.9e+05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GGGGTGGTGGGG 12  
Db 14 GTGGTGGTGGGG 3

RESULT 2

AI807936/c

LOCUS AI807936 19 bp mRNA linear EST 19-DEC-1999  
DEFINITION W52e09.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone  
IMAGE:2359240 3' similar to TR:Q39600 Q39600 EXTENSIN. ; contains  
element MSr1 repetitive element ;, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 19)

NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: [cgaps@mail.nih.gov](mailto:cgaps@mail.nih.gov)

This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.

Trace considered overall poor quality

Insert Length: 724 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

FEATURES

source

Location/Qualifiers  
1. .19  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2359240"  
/lab\_host="DH10B"  
/clone\_lib="Soares\_NFL\_T\_GBC\_S1"  
/note="Organ: pooled; Vector: pR7T3D-Pac (Pharmacia) with  
a modified polylinker; Site 1: Not I; Site 2: Eco RI;  
Equal amounts of plasmid DNA from three normalized  
libraries (fetal lung NbHL19W, testis NHT, and B-cell

NCI CGAP GCBI1) were mixed, and ss circles were made in  
vitro. Following HAP purification, this DNA was used as  
tracer in a subtractive hybridization reaction. The driver  
was PCR-amplified cDNAs from pools of 5,000 clones made  
from the same 3 libraries. The pools consisted of  
I.M.A.G.E. clones 297480-302087, 682632-687239,  
726408-728711, and 729096-731399. Subtraction by Bento  
Soares and M. Fatima Bonaldo."

BASE COUNT  
ORIGIN

3 a 16 c 0 g 0 t  
Query Match 86.7%; Score 10.4; DB 9; Length 19;  
Best Local Similarity 91.7%; Pred. No. 6.9e+05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY

1 GGGGTGGTGGGG 12

Db

17 GGGGTGGGGGGG 6

RESULT 3

AZ369361

LOCUS

DEFINITION

AZ369361 19 bp DNA linear GSS 02-OCT-2000  
1M0119I23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0119I23 R, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 19)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

Unpublished

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)

Insert Length: 10000 Std Error: 0.00

Plate: 0119 row: I column: 23

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1. .19

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0119I23"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, P-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to



10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 0 c 18 g 1 t  
ORIGIN

Query Match 86.7%; Score 10.4; DB 28; Length 19;  
Best Local Similarity 91.7%; Pred. No. 6.9e+05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGTGGTGGGG 12  
|||||  
Db 2 GGGTGGGGGG 13

RESULT 4  
AZ381798  
LOCUS  
DEFINITION  
1M0138G01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0138G01 R, genomic survey sequence.  
AZ381798  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)

REFERENCE  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D.,Weiss,R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0138 row: G column: 01  
Seq primer: CACACAGGAACACGTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers  
1..19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0138G01"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The

FEATURES  
source

adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 0 c 15 g 4 t  
ORIGIN

Query Match 86.7%; Score 10.4; DB 28; Length 19;  
Best Local Similarity 91.7%; Pred. No. 6.9e+05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGTGGTGGGG 12  
|||||  
Db 7 GTGGTGGTGGGG 18

RESULT 5  
AZ447936/c  
LOCUS  
DEFINITION  
1M0245018F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0245018 F, genomic survey sequence.  
AZ447936  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)

REFERENCE  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D.,Weiss,R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0245 row: O column: 18  
Seq primer: CGTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers  
1..19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0245018"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were

FEATURES  
source

ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 1 a 18 c 0 g 0 t  
ORIGIN  
Query Match 86.7%; Score 10.4; DB 28; Length 19;  
Best Local Similarity 91.7%; Pred. No. 6.9e+05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GGGGTGGTGGGG 12  
|||||  
Db 18 GGGGTGGGGGG 7

RESULT 6  
AZ780591  
LOCUS 2M0018B09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC2M0018B09 F, genomic survey sequence.

ACCESSION AZ780591  
VERSION AZ780591.1 GI:12912422  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 19)  
REFERENCE  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.  
and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0018 row: B column: 09  
Seq primer: CGTTGTAACGACGGCCACT  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers  
1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0018B09"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4

FEATURES  
source  
1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0018B09"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 0 c 18 g 1 t  
ORIGIN  
Query Match 86.7%; Score 10.4; DB 28; Length 19;  
Best Local Similarity 91.7%; Pred. No. 6.9e+05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GGGGTGGTGGGG 12  
|||||  
Db 3 GGGGTGGGGGG 14

RESULT 7  
AZ786308  
LOCUS 2M0031B17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC2M0031B17 R, genomic survey sequence.

ACCESSION AZ786308  
VERSION AZ786308.1 GI:12923936  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 19)  
REFERENCE  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.  
and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0031 row: B column: 17  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers  
1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0031B17"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA

FEATURES  
source  
1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0031B17"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 2 a 1 c 15 g 1 t  
ORIGIN  
Query Match 86.7%; Score 10.4; DB 28; Length 19;  
Best Local Similarity 91.7%; Pred. No. 6.9e+05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GGGGTGGTGGGG 12  
||| |||||  
Db 5 GGGGAGGTGGGG 16

RESULT 8  
AZ466238  
LOCUS  
DEFINITION  
1M0276J16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0276J16 R, genomic survey sequence.

ACCESSION  
AZ466238  
VERSION  
AZ466238.1 GI:10624363  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)

ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS  
1 (bases 1 to 20)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0276 row: J column: 16  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.

Location/Qualifiers  
1. .20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0276J16"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a

FEATURES  
source

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 4 a 0 c 12 g 4 t  
ORIGIN  
Query Match 86.7%; Score 10.4; DB 28; Length 20;  
Best Local Similarity 91.7%; Pred. No. 6.9e+05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GGGGTGGTGGGG 12  
||| |||||  
Db 5 GGAGTGGTGGGG 16

RESULT 9  
AZ495585/c  
LOCUS  
DEFINITION  
1M0331H02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0331H02 R, genomic survey sequence.

ACCESSION  
AZ495585  
VERSION  
AZ495585.1 GI:10671122  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)

ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS  
1 (bases 1 to 21)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0331 row: H column: 02  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 21.

Location/Qualifiers  
1. .21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0331H02"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 2 a 16 c 1 g 2 t  
ORIGIN

Query Match 86.7%; Score 10.4; DB 28; Length 21;  
Best Local Similarity 91.7%; Pred. No. 6.9e+05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGGG 12  
|||||  
Db 21 GGGGTGGGGGG 10

RESULT 10  
AZ774703/c  
LOCUS  
DEFINITION  
2M0004G14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
Clone UUGC2M0004G14 F, genomic survey sequence.

ACCESSION  
AZ774703  
VERSION  
AZ774703.1 GI:12900261

KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
1 (bases 1 to 21)

AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.  
and Wright,D., Weiss,R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## JOURNAL

## COMMENT

Unpublished  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0004 row: G column: 14

Seq primer: CGTTGTAACGACGGCCAGT

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

## FEATURES

## source

1..21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0004G14"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 2 a 19 c 0 g 0 t  
ORIGIN

Query Match 86.7%; Score 10.4; DB 28; Length 21;  
Best Local Similarity 91.7%; Pred. No. 6.9e+05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGGG 12  
|||||  
Db 17 GGGGGGTGGGG 6

RESULT 11  
AII83338/c

## LOCUS

## DEFINITION

AII83338 22 bp mRNA linear EST 28-OCT-1998  
Qd41a12.x1 Soares\_fetal\_heart NBHH19W Homo sapiens cDNA clone  
IMAGE:1732030 3' similar to TR:Q18444 Q18444 COSMID C34D4. ; mRNA  
sequence.

## ACCESSION

AII83338

## VERSION

AII83338.1 GI:3733976

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 22)

## AUTHORS

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

## TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

## JOURNAL

## COMMENT

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.

Trace considered overall poor quality

Insert Length: 698 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

## FEATURES

## source

1..22

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:1732030"

/sex="unknown"

/dev\_stage="19 weeks"

/lab\_host="DH10B (ampicillin resistant)"

/clone\_lib="Soares\_fetal\_heart NBHH19W"

/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a

modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer [5'

TGTTACCAATCTGAGTGGGAGCGCGCATCTTTTTTTTTTTT 3'],

double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of a modified pT7T3 vector

(Pharmacia). Library went through one round of

normalization to a Cot = 5. Library constructed by

M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbHL19W."

BASE COUNT 4 a 16 c 0 g 2 t

Query Match 86.7%; Score 10.4; DB 9; Length 22;  
Best Local Similarity 91.7%; Pred. No. 7e+05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGG 12  
| | | | | | | | | |  
Db 12 GGGGTGGTGGG 1

RESULT 12  
AI439277/c  
LOCUS AI439277 22 bp mRNA linear EST 09-MAR-1999  
DEFINITION ti54a02.x1 NCI CGAP Lym12 Homo sapiens cDNA clone IMAGE:2134250 3' similar to TR:Q17089 Q17089 COLLAGEN ;contains element MER22 repetitive element ;, mRNA sequence.

ACCESSION AI439277 GI:4303196  
VERSION AI439277.1  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Life Technologies catalog #: 11547-015  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.

FEATURES source  
1..22  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2134250"  
/tissue\_type="lymphoma, follicular mixed small and large cell"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Lym12"  
/note="Organ: lymph node; Vector: pCMV-SPORT6; Site\_1: SalI; Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.25 kb. Life Technologies catalog #: 11547-015"

BASE COUNT 1 a 17 c 1 g 3 t

QY 1 GGGGTGGTGGG 12  
| | | | | | | | | |  
Db 17 GGGGGGTGGGG 6

RESULT 13  
AZ766712/c  
LOCUS AZ766712 22 bp DNA linear GSS 16-FEB-2001

DEFINITION IM0564A03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0564A03 R, genomic survey sequence.

ACCESSION AZ766712  
VERSION AZ766712.1 GI:12884063  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)  
Insert Length: 10000 Std Error: 0.00  
Plate: 0564 row: A column: 03  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 22.

FEATURES source  
1..22  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0564A03"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 1 a 21 c 0 g 0 t

ORIGIN  
Query Match 86.7%; Score 10.4; DB 28; Length 22;  
Best Local Similarity 91.7%; Pred. No. 7e+05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGG 12  
| | | | | | | | | |  
Db 21 GGGGTGGGGGG 10

RESULT 14  
AZ769521/c

LOCUS AZ769521 22 bp DNA linear GSS 16-FEB-2001  
DEFINITION IM0570018F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0570018 F, genomic survey sequence.  
ACCESSION AZ769521  
VERSION AZ769521.1 GI:12889741  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0570 row: 0 column: 18  
Seq primer: CGTTGTAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 22.

FEATURES source  
1..22  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0570018"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 1 a 21 c 0 g 0 t  
ORIGIN  
Query Match 86.7%; Score 10.4; DB 28; Length 22;  
Best Local Similarity 91.7%; Pred. No. 7e+05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GGGGTGGTGGG 12  
|||||  
Db 20 GGGGGGTGGG 9

RESULT 15

AA928040 19 bp mRNA linear EST 22-APR-1998  
LOCUS O158G09.s1 NCI CGAP HN4 Homo sapiens cDNA clone IMAGE:1486912 3', similar to TR:O04216 O04216 EXTENSIN ; contains element MSRI  
DEFINITION repetitive element ;, mRNA sequence.  
ACCESSION AA928040  
VERSION AA928040.1 GI:3077196  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 19)  
AUTHORS NCI/NIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute / National Institute of Dental Research, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaps-r@mail.nih.gov  
Tissue Procurement: John Ensley, M.D.  
cDNA Library Preparation: Stratagene, Inc.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 1.  
FEATURES source  
Location/Qualifiers  
1..19  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1486912"  
/tissue\_type="squamous cell carcinoma"  
/lab\_host="SOLR (kanamycin resistant)"  
/clone\_lib="NCI CGAP HN4"  
/note="Organ: pharynx; Vector: Bluescript SK-; Site\_1: EcoRI; Site\_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5 kb. 5' adaptor sequence: 5' GAATTCGGCAG 3' 3' adaptor sequence: 5' (GA )10ACTAGTCTCGAGTTTITTTTTTTT 3'"

BASE COUNT 2 a 1 c 11 g 5 t  
ORIGIN  
Query Match 83.3%; Score 10; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 GGTGGTGGG 12  
|||||  
Db 3 GGTGGTGGG 12

Search completed: October 27, 2003, 13:59:29  
Job time : 1055.51 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:34 ; Search time 27.5429 Seconds  
(without alignments)  
192.304 Million cell updates/sec

Title: US-09-331-204A-13  
Perfect score: 12  
Sequence: 1 ggggtgtgtggg 12

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 376294

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA: \*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq: \*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq: \*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq: \*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq: \*  
5: /cgn2\_6/ptodata/1/ina/PTUS\_COMB.seq: \*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12	100.0	18	2	US-08-529-878B-3
2	12	100.0	18	2	US-08-529-878B-10
3	12	100.0	18	2	US-08-529-878B-44
4	12	100.0	18	2	US-08-529-878B-48
5	12	100.0	21	2	US-08-529-878B-4
6	12	100.0	21	2	US-08-529-878B-45
7	11	91.7	17	3	US-09-017-974-62
8	11	91.7	17	3	US-09-017-974-64
9	11	91.7	17	3	US-09-017-974-65
10	11	91.7	17	4	US-08-682-255A-62
11	11	91.7	17	4	US-08-682-255A-64
12	11	91.7	17	4	US-08-682-255A-65
13	11	91.7	17	4	US-09-429-130-62
14	11	91.7	17	4	US-09-429-130-64
15	11	91.7	17	4	US-09-429-130-65
16	11	91.7	20	2	US-08-476-712-2
17	11	91.7	20	2	US-08-890-980-56
18	11	91.7	20	3	US-08-890-979-56
19	11	91.7	20	3	US-09-032-894-56
20	11	91.7	20	3	US-09-031-626-56
21	11	91.7	20	4	US-09-411-291-2
22	11	91.7	20	5	PCT-US93-07743-14
23	11	91.7	21	1	US-08-145-704-11
24	11	91.7	21	3	US-08-987-574-11
25	11	91.7	21	3	US-08-535-168-11
26	11	91.7	21	3	US-09-017-974-11
27	11	91.7	21	4	US-08-682-255A-11

28	11	91.7	21	4	US-09-429-130-11	Sequence 11, Appl
29	11	91.7	21	5	PCT-US96-11786-11	Sequence 11, Appl
30	10.4	86.7	15	1	US-08-580-242-2	Sequence 2, Appl
31	10.4	86.7	15	5	PCT-US94-06331A-22	Sequence 22, Appl
32	10.4	86.7	18	1	US-08-469-802B-13	Sequence 13, Appl
33	10.4	86.7	18	2	US-08-267-803B-31	Sequence 31, Appl
34	10.4	86.7	20	3	US-09-513-729B-63	Sequence 63, Appl
35	10.4	86.7	20	3	US-09-487-368A-174	Sequence 174, Appl
36	10.4	86.7	20	3	US-09-662-249A-20	Sequence 20, Appl
37	10.4	86.7	20	3	US-09-662-249A-21	Sequence 21, Appl
38	10.4	86.7	20	3	US-09-662-249A-22	Sequence 22, Appl
39	10.4	86.7	20	4	US-09-629-644A-174	Sequence 174, Appl
40	10.4	86.7	20	4	US-09-198-452A-3980	Sequence 3980, Ap
41	10.4	86.7	21	1	US-08-145-704-10	Sequence 10, Appl
42	10.4	86.7	21	3	US-08-987-574-10	Sequence 10, Appl
43	10.4	86.7	21	3	US-08-535-168-10	Sequence 10, Appl
44	10.4	86.7	21	3	US-09-017-974-10	Sequence 10, Appl
45	10.4	86.7	21	4	US-08-682-255A-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1  
US-08-529-878B-3  
; Sequence 3, Application US/08529878B  
; Patent No. 5932556  
; GENERAL INFORMATION:  
; APPLICANT: Tam, Robert C.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
; TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Crockett & Fish  
; STREET: 3000 S. Augusta Court  
; CITY: La Habra  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 90631  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Wordperfect 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/529,878B  
; FILING DATE: 13-SEP-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fish, Robert D.  
; REGISTRATION NUMBER: 33,880  
; REFERENCE/DOCKET NUMBER: 213/003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 714-525-3433  
; TELEFAX: 714-525-3303  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
; US-08-529-878B-3

Query Match 100.0%; Score 12; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGTGTGGG 12

Db 7 GGGGTGTGTGGG 18

```

RESULT 3
US-08-529-878B-44
; Sequence 44, Application US/08529878B
; Patent No. 5932556
; GENERAL INFORMATION:
; APPLICANT: Tam, Robert C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESS: Crockett & Fish
; STREET: 3000 S. Augusta Court
; CITY: La Habra
; STATE: California
; COUNTRY: United States of America
; ZIP: 90631
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1

```

Query Match 100.0%; Score 12; DB 2; Length 18;



Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGG 12  
| | | | | | | | | |  
Db 18 GGGGTGGTGGG 7

## RESULT 5

US-08-529-878B-4  
; Sequence 4, Application US/08529878B  
; Patent No. 5932556  
; GENERAL INFORMATION:  
; APPLICANT: Tam, Robert C.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
; REGULATION OF CD28 EXPRESSION  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Crockett & Fish  
; STREET: 3000 S. Augusta Court  
; CITY: La Habra  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 90631  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Wordperfect 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/529,878B  
; FILING DATE: 13-SEP-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fish, Robert D.  
; REGISTRATION NUMBER: 33,880  
; REFERENCE/DOCKET NUMBER: 213/003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 714-525-3433  
; TELEFAX: 714-525-3303  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 21 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
US-08-529-878B-4

Query Match 100.0%; Score 12; DB 2; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGG 12  
| | | | | | | | | |  
Db 10 GGGGTGGTGGG 21

## RESULT 6

US-08-529-878B-45  
; Sequence 45, Application US/08529878B  
; Patent No. 5932556  
; GENERAL INFORMATION:  
; APPLICANT: Tam, Robert C.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
; REGULATION OF CD28 EXPRESSION  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Crockett & Fish  
; STREET: 3000 S. Augusta Court  
; CITY: La Habra  
; STATE: California

COUNTRY: United States of America  
ZIP: 90631  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Wordperfect 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/529,878B  
; FILING DATE: 13-SEP-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fish, Robert D.  
; REGISTRATION NUMBER: 33,880  
; REFERENCE/DOCKET NUMBER: 213/003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 714-525-3433  
; TELEFAX: 714-525-3303  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 45:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 21 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
US-08-529-878B-45

Query Match 100.0%; Score 12; DB 2; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGG 12  
| | | | | | | | | |  
Db 10 GGGGTGGTGGG 21

## RESULT 7

US-09-017-974-62  
; Sequence 62, Application US/09017974  
; Patent No. 628042  
; GENERAL INFORMATION:  
; APPLICANT: Rando, Robert F.  
; APPLICANT: Ojwang, Joshua O.  
; APPLICANT: Hogan, Michael E.  
; APPLICANT: Wallace, Thomas L.  
; APPLICANT: Cossam, Paul A.  
; TITLE OF INVENTION: Anti-Viral Guanosine-Rich  
; Tetrads Forming Oligonucleotides  
; NUMBER OF SEQUENCES: 88  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Conley, Rose & Tayon, P.C.  
; STREET: 600 Travis, Suite 1800  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: U.S.A.  
; ZIP: 77002-2912  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: MS Word 97 (saved as .txt file)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/017,974  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/037,374  
; FILING DATE: 04-FEB-97  
; APPLICATION NUMBER:  
; FILING DATE: 09-DEC-97  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McDaniel, C. Steven

REGISTRATION NUMBER: 33,962  
REFERENCE/DOCKET NUMBER: 1472-06223  
TELEPHONE: 713/238-8010  
TELEFAX: 713/238-8008  
INFORMATION FOR SEQ ID NO: 62:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-017-974-62

Query Match 91.7%; Score 11; DB 3; Length 17;  
Best Local Similarity 100.0%; Pred.No. 3.3e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGG 11  
| | | | | | | | | |  
Db 6 GGGGTGGTGGG 16

RESULT 8  
US-09-017-974-64  
; Sequence 64, Application US/09017974  
; Patent No. 6288042  
; GENERAL INFORMATION:  
; APPLICANT: Rando, Robert F.  
; APPLICANT: Ojwang, Joshua O.  
; APPLICANT: Hogan, Michael E.  
; APPLICANT: Wallace, Thomas L.  
; APPLICANT: Cossum, Paul A.  
; TITLE OF INVENTION: Anti-Viral Guanosine-Rich  
; TITLE OF INVENTION: Tetrad Forming Oligonucleotides  
; NUMBER OF SEQUENCES: 88  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Conley, Rose & Tayon, P.C.  
; STREET: 600 Travis, Suite 1800  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: U.S.A.  
; ZIP: 77002-2912  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: MS Word 97 (saved as .txt file)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/017,974  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/037,374  
; FILING DATE: 04-FEB-97  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McDaniel, C. Steven  
; REGISTRATION NUMBER: 33,962  
; REFERENCE/DOCKET NUMBER: 1472-06223  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 713/238-8010  
; TELEFAX: 713/238-8008  
; INFORMATION FOR SEQ ID NO: 64:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-09-017-974-64

Query Match 91.7%; Score 11; DB 3; Length 17;  
Best Local Similarity 100.0%; Pred.No. 3.3e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 GGGTGGTGGG 12  
| | | | | | | | | |  
Db 3 GGGTGGTGGG 13

RESULT 9  
US-09-017-974-65  
; Sequence 65, Application US/09017974  
; Patent No. 6288042  
; GENERAL INFORMATION:  
; APPLICANT: Rando, Robert F.  
; APPLICANT: Ojwang, Joshua O.  
; APPLICANT: Hogan, Michael E.  
; APPLICANT: Wallace, Thomas L.  
; APPLICANT: Cossum, Paul A.  
; TITLE OF INVENTION: Anti-Viral Guanosine-Rich  
; TITLE OF INVENTION: Tetrad Forming Oligonucleotides  
; NUMBER OF SEQUENCES: 88  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Conley, Rose & Tayon, P.C.  
; STREET: 600 Travis, Suite 1800  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: U.S.A.  
; ZIP: 77002-2912  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: MS Word 97 (saved as .txt file)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/017,974  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/037,374  
; FILING DATE: 04-FEB-97  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McDaniel, C. Steven  
; REGISTRATION NUMBER: 33,962  
; REFERENCE/DOCKET NUMBER: 1472-06223  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 713/238-8010  
; TELEFAX: 713/238-8008  
; INFORMATION FOR SEQ ID NO: 65:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 5  
; OTHER INFORMATION: /note= "C-5 propynl dU"  
US-09-017-974-65

Query Match 91.7%; Score 11; DB 3; Length 17;  
Best Local Similarity 100.0%; Pred.No. 3.3e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGTGGTGGG 11  
| | | | | | | | | |  
Db 6 GGGGTGGTGGG 16

RESULT 10

```
; APPLICANT: Rando, Robert F.
; APPLICANT: Fennewald, Susan
; APPLICANT: Zendegeui, Joseph G.
; APPLICANT: Oiwang, Joshua O.
; APPLICANT: Hogan, Michael E.
; APPLICANT: Pommier, Eyves
; APPLICANT: Mazumder, Abhijit
; TITLE OF INVENTION: Anti-Viral Guanosine-Rich
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Conley, Rose & Tayon, P.C.
; STREET: 600 Travis, Suite 1850
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77002-2912
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS Windows 95
; SOFTWARE: MS Word 97 (saved as .txt file)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/682,255A
; FILING DATE: 17-JULY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/535,168
; FILING DATE: 23-OCT-95
; APPLICATION NUMBER: 60/001,505
; FILING DATE: 19-JULY-95
; APPLICATION NUMBER: 60/014,007
; FILING DATE: 25-MARCH-96
; APPLICATION NUMBER: 60/013,688
; FILING DATE: 19-MARCH-96
; APPLICATION NUMBER: 60/015,714
; FILING DATE: 17-APRIL-96
; APPLICATION NUMBER: 60/016,271
; FILING DATE: 23-APRIL-96
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniel, C. Steven
; REGISTRATION NUMBER: 33,962
; REFERENCE/DOCKET NUMBER: 1472-06214
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/238-8010
; TELEFAX: 713/238-8008
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-682-255A-64

Query Match          91.7%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches      11; Conservative    0; Mismatches    0; Indels

QY      2   GGGTGGTGGG 12
        |||         |||
DB      3   GGGTGGTGGG 13

RESULT 12
US-08-682-255A-65
; Sequence 65, Application US/08682255A
; Patent No. 6323185
; GENERAL INFORMATION:
; APPLICANT: Rando, Robert F.
; APPLICANT: Fennewald, Susan
; APPLICANT: Zendegeui, Joseph G.
; APPLICANT: Oiwang, Joshua O.
```

APPLICANT: Hogan, Michael E.  
APPLICANT: Pommier, Yves  
APPLICANT: Mazumder, Abhijit  
TITLE OF INVENTION: Anti-Viral Guanosine-Rich  
TITLE OF INVENTION: Oligonucleotides  
NUMBER OF SEQUENCES: 87  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Conley, Rose & Tayon, P.C.  
STREET: 600 Travis, Suite 1850  
CITY: Houston  
STATE: Texas  
COUNTRY: U.S.A.  
ZIP: 77002-2912  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: MS Windows 95  
SOFTWARE: MS Word 97 (saved as .txt file)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/682,255A  
FILING DATE: 17-JULY-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/535,168  
FILING DATE: 23-OCT-95  
APPLICATION NUMBER: 60/001,505  
FILING DATE: 19-JULY-95  
APPLICATION NUMBER: 60/014,007  
FILING DATE: 25-MARCH-96  
APPLICATION NUMBER: 60/013,688  
FILING DATE: 19-MARCH-96  
APPLICATION NUMBER: 60/015,714  
FILING DATE: 17-APRIL-96  
APPLICATION NUMBER: 60/016,271  
FILING DATE: 23-APRIL-96  
ATTORNEY/AGENT INFORMATION:  
NAME: McDaniel, C. Steven  
REGISTRATION NUMBER: 33,962  
REFERENCE/DOCKET NUMBER: 1472-06214  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713/238-8010  
TELEFAX: 713/238-8008  
INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 5  
OTHER INFORMATION: /note= "C-5 propynl du"  
US-08-682-255A-65

Query Match 91.7%; Score 11; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGG 11  
|||||  
Db 6 GGGGTGGTGGG 16

RESULT 13  
US-09-429-130-62  
; Sequence 62, Application US/09429130  
; Patent No. 6355785  
; GENERAL INFORMATION:  
; APPLICANT: Rando, Robert F.  
; Fennwald, Susan  
; Zendequi, Joseph G.  
; Ojwang, Joshua O.

Hogan, Michael E.  
Pommier, Yves  
Mazumder, Abhijit  
60/015,714  
TITLE OF INVENTION: Anti-Viral Guanosine-Rich  
TITLE OF INVENTION: Oligonucleotides  
NUMBER OF SEQUENCES: 87  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Conley, Rose & Tayon, P.C.  
STREET: 600 Travis, Suite 1850  
CITY: Houston  
STATE: Texas  
COUNTRY: U.S.A.  
ZIP: 77002-2912  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: MS Windows 95  
SOFTWARE: MS Word 97 (saved as .txt file)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/429,130  
FILING DATE: 28-Oct-1999  
CLASSIFICATION: <Unknown>  
19-JULY-95  
25-MARCH-96  
19-MARCH-96  
17-APRIL-96  
23-APRIL-96  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/682,255  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 60/001,505  
FILING DATE: 19-JULY-95  
APPLICATION NUMBER: 60/014,007  
FILING DATE: 25-MARCH-96  
APPLICATION NUMBER: 60/013,688  
FILING DATE: 19-MARCH-96  
APPLICATION NUMBER: 60/016,271  
FILING DATE: 17-APRIL-96  
ATTORNEY/AGENT INFORMATION:  
NAME: McDaniel, C. Steven  
REGISTRATION NUMBER: 33,962  
REFERENCE/DOCKET NUMBER: 1472-06214  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713/238-8010  
TELEFAX: 713/238-8008  
INFORMATION FOR SEQ ID NO: 62:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 62:  
US-09-429-130-62

Query Match 91.7%; Score 11; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGG 11  
|||||  
Db 6 GGGGTGGTGGG 16

RESULT 14  
US-09-429-130-64  
; Sequence 64, Application US/09429130  
; Patent No. 6355785  
; GENERAL INFORMATION:  
; APPLICANT: Rando, Robert F.  
; Fennwald, Susan  
; Zendequi, Joseph G.

Ojwang, Joshua O.  
Hogan, Michael E.  
Pommier, Yves  
Mazumder, Abhijit  
60/015,714  
TITLE OF INVENTION: Anti-Viral Guanosine-Rich  
Oligonucleotides  
NUMBER OF SEQUENCES: 87  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Conley, Rose & Tayon, P.C.  
STREET: 600 Travis, Suite 1850  
CITY: Houston  
STATE: Texas  
COUNTRY: U.S.A.  
ZIP: 77002-2912  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: MS Windows 95  
SOFTWARE: MS Word 97 (saved as .txt file)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/429,130  
FILING DATE: 28-Oct-1999  
CLASSIFICATION: <Unknown>  
19-JULY-95  
25-MARCH-96  
19-MARCH-96  
17-APRIL-96  
23-APRIL-96  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/682,255  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 60/001,505  
FILING DATE: 19-JULY-95  
APPLICATION NUMBER: 60/014,007  
FILING DATE: 25-MARCH-96  
APPLICATION NUMBER: 60/013,688  
FILING DATE: 19-MARCH-96  
APPLICATION NUMBER: 60/016,271  
FILING DATE: 17-APRIL-96  
ATTORNEY/AGENT INFORMATION:  
NAME: McDaniel, C. Steven  
REGISTRATION NUMBER: 33,962  
REFERENCE/DOCKET NUMBER: 1472-06214  
TELEPHONE: 713/238-8010  
TELEFAX: 713/238-8008  
INFORMATION FOR SEQ ID NO: 64:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 64:  
US-09-429-130-64

Query Match 91.7%; Score 11; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred.No. 3.3e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGTGGTGGG 12  
Db 3 GGGTGGTGGG 13

RESULT 15  
US-09-429-130-65  
Sequence 65, Application US/09429130  
Patent No. 6355785  
GENERAL INFORMATION:  
APPLICANT: Rando, Robert F.  
Fennewald, Susan

Zendegui, Joseph G.  
Ojwang, Joshua O.  
Hogan, Michael E.  
Pommier, Yves  
Mazumder, Abhijit  
60/015,714  
TITLE OF INVENTION: Anti-Viral Guanosine-Rich  
Oligonucleotides  
NUMBER OF SEQUENCES: 87  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Conley, Rose & Tayon, P.C.  
STREET: 600 Travis, Suite 1850  
CITY: Houston  
STATE: Texas  
COUNTRY: U.S.A.  
ZIP: 77002-2912  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: MS Windows 95  
SOFTWARE: MS Word 97 (saved as .txt file)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/429,130  
FILING DATE: 28-Oct-1999  
CLASSIFICATION: <Unknown>  
19-JULY-95  
25-MARCH-96  
19-MARCH-96  
17-APRIL-96  
23-APRIL-96  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/682,255  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 60/001,505  
FILING DATE: 19-JULY-95  
APPLICATION NUMBER: 60/014,007  
FILING DATE: 25-MARCH-96  
APPLICATION NUMBER: 60/013,688  
FILING DATE: 19-MARCH-96  
APPLICATION NUMBER: 60/016,271  
FILING DATE: 17-APRIL-96  
ATTORNEY/AGENT INFORMATION:  
NAME: McDaniel, C. Steven  
REGISTRATION NUMBER: 33,962  
REFERENCE/DOCKET NUMBER: 1472-06214  
TELEPHONE: 713/238-8010  
TELEFAX: 713/238-8008  
INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 5  
OTHER INFORMATION: /note= "C-5 propynl du"  
SEQUENCE DESCRIPTION: SEQ ID NO: 65:  
US-09-429-130-65

Query Match 91.7%; Score 11; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred.No. 3.3e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTGGTGGG 11  
Db 6 GGGTGGTGGG 16

Search completed: October 27, 2003, 14:03:36  
Job time : 28.5429 secs

---

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 11:25:34 ; Search time 258.629 Seconds  
(without alignments)  
124.432 Million cell updates/sec

Title: US-09-331-204A-13  
Perfect score: 12  
Sequence: 1 ggggtggtgggg 12

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1792395 seqs, 1340900451 residues

Total number of hits satisfying chosen parameters: 408622

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA:\*

1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*

2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*

3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*

4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*

5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*

6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*

7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*

8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*

9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*

10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*

11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*

12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*

13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*

14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*

15: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*

16: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*

17: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
C 1	12	100.0	17	11	US-09-740-332-2132 Sequence 2132, Ap
C 2	12	100.0	17	11	US-09-740-332-2133 Sequence 2133, Ap
C 3	12	100.0	17	11	US-09-740-332-2422 Sequence 2422, Ap
C 4	12	100.0	17	11	US-09-740-332-2423 Sequence 2423, Ap
C 5	12	100.0	17	12	US-09-817-879-2132 Sequence 2132, Ap
C 6	12	100.0	17	12	US-09-817-879-2133 Sequence 2133, Ap
C 7	12	100.0	17	12	US-09-817-879-2422 Sequence 2422, Ap
C 8	12	100.0	17	12	US-09-817-879-2423 Sequence 2423, Ap
C 9	11	91.7	19	12	US-10-148-687-39 Sequence 39, Appl
C 10	11	91.7	20	11	US-09-779-152-56 Sequence 56, Appl
C 11	11	91.7	20	14	US-10-023-610-56 Sequence 56, Appl
C 12	11	91.7	21	12	US-10-184-085A-365 Sequence 365, App
C 13	11	91.7	21	12	US-10-184-085A-366 Sequence 366, App
C 14	11	91.7	21	12	US-10-184-085A-367 Sequence 367, App
C 15	11	91.7	21	12	US-10-184-085A-368 Sequence 368, App
C 16	11	91.7	21	12	US-10-184-085A-370 Sequence 370, App

C 17	11	91.7	21	12	US-10-184-085A-371 Sequence 371, App
C 18	11	91.7	21	12	US-10-184-085A-373 Sequence 373, App
C 19	11	91.7	21	12	US-10-184-085A-374 Sequence 374, App
C 20	11	91.7	21	12	US-10-184-085A-375 Sequence 375, App
C 21	11	91.7	21	12	US-10-184-085A-376 Sequence 376, App
C 22	11	91.7	21	12	US-10-184-085A-405 Sequence 405, App
C 23	11	91.7	21	12	US-10-184-085A-408 Sequence 408, App
C 24	11	91.7	21	12	US-10-184-085A-506 Sequence 506, App
C 25	11	91.7	21	12	US-10-148-687-38 Sequence 38, Appl
C 26	10.4	86.7	17	11	US-09-780-533A-49 Sequence 49, Appl
C 27	10.4	86.7	17	11	US-09-780-533A-932 Sequence 932, App
C 28	10.4	86.7	17	11	US-09-780-533A-933 Sequence 933, App
C 29	10.4	86.7	17	11	US-09-780-533A-934 Sequence 934, App
C 30	10.4	86.7	17	11	US-09-780-533A-935 Sequence 935, App
C 31	10.4	86.7	17	11	US-09-848-754A-2390 Sequence 2390, Ap
C 32	10.4	86.7	17	11	US-09-848-754A-2869 Sequence 2869, Ap
C 33	10.4	86.7	17	11	US-09-848-754A-3378 Sequence 3378, Ap
C 34	10.4	86.7	17	11	US-09-848-754A-3379 Sequence 3379, Ap
C 35	10.4	86.7	17	12	US-10-238-700-446 Sequence 446, App
C 36	10.4	86.7	17	12	US-10-238-700-447 Sequence 447, App
C 37	10.4	86.7	19	12	US-10-251-117-671 Sequence 671, App
C 38	10.4	86.7	19	12	US-10-251-117-978 Sequence 978, App
C 39	10.4	86.7	20	9	US-09-854-883-174 Sequence 174, App
C 40	10.4	86.7	20	11	US-09-904-968A-105 Sequence 105, App
C 41	10.4	86.7	20	12	US-10-083-246A-118 Sequence 118, App
C 42	10.4	86.7	22	12	US-10-214-417A-32 Sequence 32, Appl
C 43	10.4	86.7	22	12	US-10-214-417A-35 Sequence 35, Appl
C 44	10	83.3	16	14	US-10-206-839-38 Sequence 38, Appl
C 45	10	83.3	19	12	US-10-240-046A-62 Sequence 62, Appl

ALIGNMENTS

RESULT 1

US-09-740-332-2132/c

; Sequence 2132, Application US/09740332

; Publication No. US20030125270A1

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals Inc.

; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat

; TITLE OF INVENTION: Hepatitis C Virus Infection

; FILE REFERENCE: RPI 400/003

; CURRENT APPLICATION NUMBER: US/09/740,332

; CURRENT FILING DATE: 2001-03-26

; NUMBER OF SEQ ID NOS: 9704

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 2132

; LENGTH: 17

; TYPE: RNA

; ORGANISM: artificial sequence

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION:

; OTHER INFORMATION: oligonucleotide substrate

US-09-740-332-2132

Query Match 100.0%; Score 12; DB 11; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGG 12

Db 16 GGGGTGGTGGG 5

RESULT 2

US-09-740-332-2133/c

; Sequence 2133, Application US/09740332

; Publication No. US20030125270A1

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals Inc.

; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat

```
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2133
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-2133
```

```
Query Match          100.0%; Score 12; DB 11; Length 17;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GGGGTGGTGGGG 12
        |||||
Db      13 GGGGTGGTGGGG 2
```

## RESULT 3

```
US-09-740-332-2422
; Sequence 2422, Application US/09740332
; Publication No. US20030125270A1
```

## GENERAL INFORMATION:

```
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2422
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-2422
```

```
Query Match          100.0%; Score 12; DB 11; Length 17;
Best Local Similarity 83.3%; Pred. No. 9e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GGGGTGGTGGGG 12
        |||||
Db      6 GGGGUGGUGGGG 17
```

## RESULT 4

```
US-09-740-332-2423
; Sequence 2423, Application US/09740332
; Publication No. US20030125270A1
```

## GENERAL INFORMATION:

```
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2423
; LENGTH: 17
; TYPE: RNA
```

```
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-2423
```

```
Query Match          100.0%; Score 12; DB 11; Length 17;
Best Local Similarity 83.3%; Pred. No. 9e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GGGGTGGTGGGG 12
        |||||
Db      3 GGGGUGGUGGGG 14
```

## RESULT 5

```
US-09-817-879-2132/c
; Sequence 2132, Application US/09817879
; Publication No. US20030171311A1
```

## GENERAL INFORMATION:

```
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MBHB00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2132
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-2132
```

```
Query Match          100.0%; Score 12; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GGGGTGGTGGGG 12
        |||||
Db      16 GGGGTGGTGGGG 5
```

## RESULT 6

```
US-09-817-879-2133/c
; Sequence 2133, Application US/09817879
; Publication No. US20030171311A1
```

## GENERAL INFORMATION:

```
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MBHB00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2133
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-2133
```

```
Query Match          100.0%; Score 12; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 9e+03;
```



```
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGTGGTGGG 12
Db 13 GGGGTGGTGGG 2

RESULT 7
US-09-817-879-2422
; Sequence 2422, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: MH800-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2422
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-2422
Query Match 100.0%; Score 12; DB 12; Length 17;
Best Local Similarity 83.3%; Pred. No. 9e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGG 12
Db 6 GGGGUGGUGGG 17

RESULT 8
US-09-817-879-2423
; Sequence 2423, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: MH800-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2423
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-2423
Query Match 100.0%; Score 12; DB 12; Length 17;
Best Local Similarity 83.3%; Pred. No. 9e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGG 12
Db 3 GGGGUGGUGGG 14

RESULT 9
US-10-148-687-39/c
; Sequence 56, Application US/10023610
; Publication No. US20030023059A1
; GENERAL INFORMATION:
; APPLICANT: WINTER, Gerhard
; APPLICANT: SLADE, Martin Basil
; APPLICANT: WILLIAMS, Keith Leslie
; APPLICANT: GOOLEY, Andrew Arthur
; APPLICANT: Macquarie Research Ltd
; TITLE OF INVENTION: Cryptosporidium sporozoite antigens
; FILE REFERENCE: 047763-5019-US
; CURRENT APPLICATION NUMBER: US/10/148,687
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: PCT/AU00/01492
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: AU PQ4400
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primers
US-10-148-687-39
Query Match 91.7%; Score 11; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGGTGGTGGG 12
Db 17 GGGGTGGTGGG 7

RESULT 10
US-09-779-152-56/c
; Sequence 56, Application US/09779152
; Publication No. US20030044782A1
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Ordovas, Jose M.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS AND
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS
; FILE REFERENCE: MNI-172CP2
; CURRENT APPLICATION NUMBER: US/09/779,152
; CURRENT FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 08/890,979
; PRIOR FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-779-152-56
Query Match 91.7%; Score 11; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGG 11
Db 13 GGGGTGGTGGG 3

RESULT 11
US-10-023-610-56/c
; Sequence 56, Application US/10023610
; Publication No. US20030023059A1
; GENERAL INFORMATION:
```

; APPLICANT: Acton, Susan L.  
; TITLE OF INVENTION: SR-BI NUCLEIC ACIDS AND USES THEREFOR  
; FILE REFERENCE: MIA-005.03  
; CURRENT APPLICATION NUMBER: US/10/023,610  
; CURRENT FILING DATE: 2001-12-17  
; EARLIER APPLICATION NUMBER: 09/686,106  
; EARLIER FILING DATE: 2000-10-10  
; EARLIER APPLICATION NUMBER: 09/032,894  
; EARLIER FILING DATE: 1998-02-27  
; EARLIER APPLICATION NUMBER: 08/890,980  
; EARLIER FILING DATE: 1997-07-10  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 56  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Human  
US-10-023-610-56

Query Match 91.7%; Score 11; DB 14; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.5e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGGTGGG 11  
|||||  
Db 13 GGGGTGGTGGG 3

RESULT 12  
US-10-184-085A-365/c  
; Sequence 365, Application US/10184085A  
; Publication No. US20030152950A1  
; GENERAL INFORMATION:  
; APPLICANT: Garner, Harold R.  
; APPLICANT: Minna, John D.  
; APPLICANT: Luebke, Kevin, J.  
; APPLICANT: Balog, Robert P.  
; TITLE OF INVENTION: Identification of Chemically Modified Polymers  
; FILE REFERENCE: 119929-1035  
; CURRENT APPLICATION NUMBER: US/10/184, 085A  
; CURRENT FILING DATE: 2002-10-01  
; PRIOR APPLICATION NUMBER: US 60/301,370  
; PRIOR FILING DATE: 2001-06-27  
; NUMBER OF SEQ ID NOS: 1291  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 365  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-184-085A-365

Query Match 91.7%; Score 11; DB 12; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2.5e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGGTGGTGGG 12  
|||||  
Db 21 GGGGTGGTGGG 11

RESULT 13  
US-10-184-085A-366/c  
; Sequence 366, Application US/10184085A  
; Publication No. US20030152950A1  
; GENERAL INFORMATION:  
; APPLICANT: Garner, Harold R.  
; APPLICANT: Minna, John D.  
; APPLICANT: Luebke, Kevin, J.  
; APPLICANT: Balog, Robert P.  
; TITLE OF INVENTION: Identification of Chemically Modified Polymers  
; FILE REFERENCE: 119929-1035  
; CURRENT APPLICATION NUMBER: US/10/184, 085A  
; CURRENT FILING DATE: 2002-10-01

; PRIOR APPLICATION NUMBER: US 60/301,370  
; PRIOR FILING DATE: 2001-06-27  
; NUMBER OF SEQ ID NOS: 1291  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 366  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-184-085A-366

Query Match 91.7%; Score 11; DB 12; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2.5e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGGTGGG 11  
|||||  
Db 21 GGGGTGGTGGG 11

RESULT 14  
US-10-184-085A-367/c  
; Sequence 367, Application US/10184085A  
; Publication No. US20030152950A1  
; GENERAL INFORMATION:  
; APPLICANT: Garner, Harold R.  
; APPLICANT: Minna, John D.  
; APPLICANT: Luebke, Kevin, J.  
; APPLICANT: Balog, Robert P.  
; TITLE OF INVENTION: Identification of Chemically Modified Polymers  
; FILE REFERENCE: 119929-1035  
; CURRENT APPLICATION NUMBER: US/10/184, 085A  
; CURRENT FILING DATE: 2002-10-01  
; PRIOR APPLICATION NUMBER: US 60/301,370  
; PRIOR FILING DATE: 2001-06-27  
; NUMBER OF SEQ ID NOS: 1291  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 367  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-184-085A-367

Query Match 91.7%; Score 11; DB 12; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2.5e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGGTGGG 11  
|||||  
Db 20 GGGGTGGTGGG 10

RESULT 15  
US-10-184-085A-368/c  
; Sequence 368, Application US/10184085A  
; Publication No. US20030152950A1  
; GENERAL INFORMATION:  
; APPLICANT: Garner, Harold R.  
; APPLICANT: Minna, John D.  
; APPLICANT: Luebke, Kevin, J.  
; APPLICANT: Balog, Robert P.  
; TITLE OF INVENTION: Identification of Chemically Modified Polymers  
; FILE REFERENCE: 119929-1035  
; CURRENT APPLICATION NUMBER: US/10/184, 085A  
; CURRENT FILING DATE: 2002-10-01  
; PRIOR APPLICATION NUMBER: US 60/301,370  
; PRIOR FILING DATE: 2001-06-27  
; NUMBER OF SEQ ID NOS: 1291  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 368  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-184-085A-368

Query Match 91.7%; Score 11; DB 12; Length 21;  
Best Local Similarity 100.0%; Pred. NO. 2.5e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGTGGTGGG 11  
Db 19 GGGGTGGTGGG 9

Search completed: October 27, 2003, 19:00:53  
Job time : 258.629 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:35 ; Search time 1570.86 Seconds  
(without alignments)  
253.343 Million cell updates/sec

Title: US-09-331-204A-13  
Perfect score: 12  
Sequence: 1 999gtggtg999 12  
Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 33363688 seqs, 16581889874 residues  
Total number of hits satisfying chosen parameters: 2938060

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents\_NA.Main:\*  
1: /cgn2\_6/ptodata/1/pna/PCTUS\_COMB.seq.\*  
2: /cgn2\_6/ptodata/1/pna/PCTUS\_COMB.seq.old:\*  
3: /cgn2\_6/ptodata/1/pna/US06\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/pna/US07\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/pna/US080\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/pna/US081\_COMB.seq.\*  
7: /cgn2\_6/ptodata/1/pna/US082\_COMB.seq.\*  
8: /cgn2\_6/ptodata/1/pna/US083\_COMB.seq.\*  
9: /cgn2\_6/ptodata/1/pna/US084\_COMB.seq.\*  
10: /cgn2\_6/ptodata/1/pna/US085\_COMB.seq.\*  
11: /cgn2\_6/ptodata/1/pna/US086\_COMB.seq.\*  
12: /cgn2\_6/ptodata/1/pna/US087\_COMB.seq.\*  
13: /cgn2\_6/ptodata/1/pna/US088\_COMB.seq.\*  
14: /cgn2\_6/ptodata/1/pna/US089\_COMB.seq.\*  
15: /cgn2\_6/ptodata/1/pna/US090\_COMB.seq.\*  
16: /cgn2\_6/ptodata/1/pna/US091\_COMB.seq.\*  
17: /cgn2\_6/ptodata/1/pna/US092A\_COMB.seq.\*  
18: /cgn2\_6/ptodata/1/pna/US092B\_COMB.seq.\*  
19: /cgn2\_6/ptodata/1/pna/US093A\_COMB.seq.\*  
20: /cgn2\_6/ptodata/1/pna/US093B\_COMB.seq.\*  
21: /cgn2\_6/ptodata/1/pna/US094\_COMB.seq.\*  
22: /cgn2\_6/ptodata/1/pna/US095A\_COMB.seq.\*  
23: /cgn2\_6/ptodata/1/pna/US095B\_COMB.seq.\*  
24: /cgn2\_6/ptodata/1/pna/US095C\_COMB.seq.\*  
25: /cgn2\_6/ptodata/1/pna/US095D\_COMB.seq.\*  
26: /cgn2\_6/ptodata/1/pna/US096A\_COMB.seq.\*  
27: /cgn2\_6/ptodata/1/pna/US096B\_COMB.seq.\*  
28: /cgn2\_6/ptodata/1/pna/US096C\_COMB.seq.\*  
29: /cgn2\_6/ptodata/1/pna/US096D\_COMB.seq.\*  
30: /cgn2\_6/ptodata/1/pna/US096E\_COMB.seq.\*  
31: /cgn2\_6/ptodata/1/pna/US097A\_COMB.seq.\*  
32: /cgn2\_6/ptodata/1/pna/US097B\_COMB.seq.\*  
33: /cgn2\_6/ptodata/1/pna/US097C\_COMB.seq.\*  
34: /cgn2\_6/ptodata/1/pna/US098A\_COMB.seq.\*  
35: /cgn2\_6/ptodata/1/pna/US098B\_COMB.seq.\*  
36: /cgn2\_6/ptodata/1/pna/US098C\_COMB.seq.\*  
37: /cgn2\_6/ptodata/1/pna/US098D\_COMB.seq.\*  
38: /cgn2\_6/ptodata/1/pna/US099A\_COMB.seq.\*  
39: /cgn2\_6/ptodata/1/pna/US099B\_COMB.seq.\*  
40: /cgn2\_6/ptodata/1/pna/US099C\_COMB.seq.\*  
41: /cgn2\_6/ptodata/1/pna/US099D\_COMB.seq.\*  
42: /cgn2\_6/ptodata/1/pna/US099E\_COMB.seq.\*  
43: /cgn2\_6/ptodata/1/pna/US099F\_COMB.seq.\*

44: /cgn2\_6/ptodata/1/pna/US100A\_COMB.seq.\*  
45: /cgn2\_6/ptodata/1/pna/US100B\_COMB.seq.\*  
46: /cgn2\_6/ptodata/1/pna/US101A\_COMB.seq.\*  
47: /cgn2\_6/ptodata/1/pna/US101B\_COMB.seq.\*  
48: /cgn2\_6/ptodata/1/pna/US102A\_COMB.seq.\*  
49: /cgn2\_6/ptodata/1/pna/US102B\_COMB.seq.\*  
50: /cgn2\_6/ptodata/1/pna/US103A\_COMB.seq.\*  
51: /cgn2\_6/ptodata/1/pna/US103B\_COMB.seq.\*  
52: /cgn2\_6/ptodata/1/pna/US104A\_COMB.seq.\*  
53: /cgn2\_6/ptodata/1/pna/US104B\_COMB.seq.\*  
54: /cgn2\_6/ptodata/1/pna/US6000\_COMB.seq.\*  
55: /cgn2\_6/ptodata/1/pna/US6001\_COMB.seq.\*  
56: /cgn2\_6/ptodata/1/pna/US6002\_COMB.seq.\*  
57: /cgn2\_6/ptodata/1/pna/US6003\_COMB.seq.\*  
58: /cgn2\_6/ptodata/1/pna/US6004\_COMB.seq.\*  
59: /cgn2\_6/ptodata/1/pna/US6005\_COMB.seq.\*  
60: /cgn2\_6/ptodata/1/pna/US6006\_COMB.seq.\*  
61: /cgn2\_6/ptodata/1/pna/US6007\_COMB.seq.\*  
62: /cgn2\_6/ptodata/1/pna/US6008\_COMB.seq.\*  
63: /cgn2\_6/ptodata/1/pna/US6009\_COMB.seq.\*  
64: /cgn2\_6/ptodata/1/pna/US6010\_COMB.seq.\*  
65: /cgn2\_6/ptodata/1/pna/US6011\_COMB.seq.\*  
66: /cgn2\_6/ptodata/1/pna/US6012\_COMB.seq.\*  
67: /cgn2\_6/ptodata/1/pna/US6013\_COMB.seq.\*  
68: /cgn2\_6/ptodata/1/pna/US6014\_COMB.seq.\*  
69: /cgn2\_6/ptodata/1/pna/US6015\_COMB.seq.\*  
70: /cgn2\_6/ptodata/1/pna/US6016\_COMB.seq.\*  
71: /cgn2\_6/ptodata/1/pna/US6017\_COMB.seq.\*  
72: /cgn2\_6/ptodata/1/pna/US6018\_COMB.seq.\*  
73: /cgn2\_6/ptodata/1/pna/US6019\_COMB.seq.\*  
74: /cgn2\_6/ptodata/1/pna/US6020\_COMB.seq.\*  
75: /cgn2\_6/ptodata/1/pna/US6021\_COMB.seq.\*  
76: /cgn2\_6/ptodata/1/pna/US6022\_COMB.seq.\*  
77: /cgn2\_6/ptodata/1/pna/US6023A\_COMB.seq.\*  
78: /cgn2\_6/ptodata/1/pna/US6023B\_COMB.seq.\*  
79: /cgn2\_6/ptodata/1/pna/US6024\_COMB.seq.\*  
80: /cgn2\_6/ptodata/1/pna/US6025\_COMB.seq.\*  
81: /cgn2\_6/ptodata/1/pna/US6026\_COMB.seq.\*  
82: /cgn2\_6/ptodata/1/pna/US6027\_COMB.seq.\*  
83: /cgn2\_6/ptodata/1/pna/US6028\_COMB.seq.\*  
84: /cgn2\_6/ptodata/1/pna/US6029\_COMB.seq.\*  
85: /cgn2\_6/ptodata/1/pna/US6030\_COMB.seq.\*  
86: /cgn2\_6/ptodata/1/pna/US6031\_COMB.seq.\*  
87: /cgn2\_6/ptodata/1/pna/US6032\_COMB.seq.\*  
88: /cgn2\_6/ptodata/1/pna/US6033\_COMB.seq.\*  
89: /cgn2\_6/ptodata/1/pna/US6034\_COMB.seq.\*  
90: /cgn2\_6/ptodata/1/pna/US6035\_COMB.seq.\*  
91: /cgn2\_6/ptodata/1/pna/US6036\_COMB.seq.\*  
92: /cgn2\_6/ptodata/1/pna/US6037\_COMB.seq.\*  
93: /cgn2\_6/ptodata/1/pna/US6038\_COMB.seq.\*  
94: /cgn2\_6/ptodata/1/pna/US6039\_COMB.seq.\*  
95: /cgn2\_6/ptodata/1/pna/US6040\_COMB.seq.\*  
96: /cgn2\_6/ptodata/1/pna/US6041\_COMB.seq.\*  
97: /cgn2\_6/ptodata/1/pna/US6042\_COMB.seq.\*  
98: /cgn2\_6/ptodata/1/pna/US6043\_COMB.seq.\*  
99: /cgn2\_6/ptodata/1/pna/US6044\_COMB.seq.\*  
100: /cgn2\_6/ptodata/1/pna/US6045\_COMB.seq.\*  
101: /cgn2\_6/ptodata/1/pna/US6046\_COMB.seq.\*  
102: /cgn2\_6/ptodata/1/pna/US6047\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Score	Match	Length	DB	ID	Description
	No.						
1	12	100.0	12	19	US-09-331-204-3		Sequence 3, Appl
2	12	100.0	12	19	US-09-331-204A-13		Sequence 13, Appl
3	12	100.0	15	1	PCT-US01-21306-49		Sequence 49, Appl
4	12	100.0	15	2	PCT-US01-21306-49		Sequence 49, Appl

C 5 12 100.0 17 32 US-09-740-332-2132 Sequence 2132, Ap  
C 6 12 100.0 17 32 US-09-740-332-2133 Sequence 2133, Ap  
C 7 12 100.0 17 32 US-09-740-332-2422 Sequence 2422, Ap  
C 8 12 100.0 17 32 US-09-740-332-2423 Sequence 2423, Ap  
C 9 12 100.0 17 34 US-09-817-879-2132 Sequence 2132, Ap  
C 10 12 100.0 17 34 US-09-817-879-2133 Sequence 2133, Ap  
C 11 12 100.0 17 34 US-09-817-879-2422 Sequence 2422, Ap  
C 12 12 100.0 17 34 US-09-817-879-2423 Sequence 2423, Ap  
C 13 12 100.0 17 34 US-10-303-778-2132 Sequence 13820, A  
C 14 12 100.0 17 50 US-08-387-041A-3 Sequence 3, Appli  
C 15 12 100.0 18 8 US-08-387-041A-10 Sequence 10, Appli  
C 16 12 100.0 18 8 US-09-331-204-1 Sequence 1, Appli  
C 17 12 100.0 18 19 US-09-331-204A-4 Sequence 4, Appli  
C 18 12 100.0 18 19 US-09-331-204A-21 Sequence 21, Appli  
C 19 12 100.0 18 33 US-09-786-436-17 Sequence 17, Appli  
C 20 12 100.0 18 33 US-09-786-436-42 Sequence 42, Appli  
C 21 12 100.0 18 33 US-09-786-436-42 Sequence 9770, Ap  
C 22 12 100.0 18 50 US-10-310-188-9770 Sequence 72857, A  
C 23 12 100.0 19 49 US-10-293-338-6664 Sequence 6664, Ap  
C 24 12 100.0 19 50 US-10-310-188-46976 Sequence 46976, A  
C 25 12 100.0 19 50 US-10-310-188-64788 Sequence 64788, A  
C 26 12 100.0 20 50 US-10-303-778-16068 Sequence 16068, A  
C 27 12 100.0 20 50 US-10-310-188-31313 Sequence 31313, A  
C 28 12 100.0 20 50 US-10-310-188-78501 Sequence 78501, A  
C 29 12 100.0 21 8 US-08-387-041A-4 Sequence 4, Appli  
C 30 12 100.0 21 19 US-09-331-204-6 Sequence 6, Appli  
C 31 12 100.0 21 19 US-09-331-204A-6 Sequence 6, Appli  
C 32 12 100.0 21 49 US-10-293-338-2091 Sequence 2091, Ap  
C 33 12 100.0 21 50 US-10-310-188-31329 Sequence 31329, A  
C 34 12 100.0 21 50 US-10-310-188-72837 Sequence 72837, A  
C 35 12 100.0 21 50 US-10-310-188-78761 Sequence 78761, A  
C 36 12 100.0 22 50 US-10-310-188-42141 Sequence 42141, A  
C 37 11.6 96.7 15 1 PCT-US01-21306-48 Sequence 48, Appli  
C 38 11.6 96.7 15 2 PCT-US01-21306-48 Sequence 48, Appli  
C 39 11 91.7 17 1 PCT-US96-11786B-62 Sequence 62, Appli  
C 40 11 91.7 17 1 PCT-US96-11786B-64 Sequence 64, Appli  
C 41 11 91.7 17 1 PCT-US96-11786B-65 Sequence 65, Appli  
C 42 11 91.7 17 1 PCT-US98-01974-62 Sequence 62, Appli  
C 43 11 91.7 17 1 PCT-US98-01974-64 Sequence 64, Appli  
C 44 11 91.7 17 1 PCT-US98-01974-65 Sequence 65, Appli  
C 45 11 91.7 17 2 PCT-US96-11786B-62 Sequence 62, Appli

ALIGNMENTS

RESULT 1  
US-09-331-204-3  
; Sequence 3, Application US/09331204  
; GENERAL INFORMATION:  
; APPLICANT: Tam, Robert  
; TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN  
; TITLE OF INVENTION: IMMUNE RESPONSE  
; FILE REFERENCE: ICNSequence  
; CURRENT APPLICATION NUMBER: US/09/331,204  
; CURRENT FILING DATE: 1999-08-20  
; PRIOR APPLICATION NUMBER: PCT/US97/23927  
; PRIOR FILING DATE: 1997-12-19  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: An oligomer  
; OTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic  
; OTHER INFORMATION: acid. This term includes oligomers consisting of  
; OTHER INFORMATION: naturally occurring bases, sugars and intersugar (

Query Match 100.0%; Score 12; DB 19; Length 12;  
Best Local Similarity 100.0%; Pred. No. 8.7e+04;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGTGGTGGG 12  
Db 1 GGGGTGGTGGG 12  
RESULT 2  
US-09-331-204A-13  
; Sequence 13, Application US/09331204A  
; GENERAL INFORMATION:  
; APPLICANT: ICN Pharmaceuticals, Inc.  
; APPLICANT: Tam, Robert  
; TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Resi  
; FILE REFERENCE: 216/013-US1  
; CURRENT APPLICATION NUMBER: US/09/331,204A  
; CURRENT FILING DATE: 1999-08-20  
; PRIOR APPLICATION NUMBER: PCT/US97/23927  
; PRIOR FILING DATE: 1997-12-19  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 13  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: synthetic construct  
US-09-331-204A-13  
Query Match 100.0%; Score 12; DB 19; Length 12;  
Best Local Similarity 100.0%; Pred. No. 8.7e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGG 12  
Db 1 GGGGTGGTGGG 12

RESULT 3  
PCT-US01-21306-49  
; Sequence 49, Application PC/TUS0121306  
; GENERAL INFORMATION:  
; APPLICANT: Genaissance Pharmaceuticals, Inc.  
; APPLICANT: Bentivegna, Steven C  
; APPLICANT: Bieglecki, Karyn M.  
; APPLICANT: Kazemi, Amir  
; APPLICANT: Koshy, Beena  
; TITLE OF INVENTION: Haplotypes of the ETVB Gene  
; FILE REFERENCE: MWH-0902PCT ETVB  
; CURRENT APPLICATION NUMBER: PCT/US01/21306  
; CURRENT FILING DATE: 2001-07-06  
; PRIOR APPLICATION NUMBER: 60/215,984  
; PRIOR FILING DATE: 2000-07-05  
; NUMBER OF SEQ ID NOS: 141  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 49  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US01-21306-49  
Query Match 100.0%; Score 12; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.7e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGG 12  
Db 2 GGGGTGGTGGG 13

RESULT 4  
PCT-US01-21306-49  
; Sequence 49, Application PC/TUS0121306  
; GENERAL INFORMATION:  
; APPLICANT: Genaissance Pharmaceuticals, Inc.

APPLICANT: Bentivegna, Steven C  
APPLICANT: Bieglecki, Karyn M.  
APPLICANT: Kazemi, Amir  
APPLICANT: Koshy, Beena  
TITLE OF INVENTION: Haplotypes of the E7FB Gene  
FILE REFERENCE: MWH-0902PCT E7FB  
CURRENT APPLICATION NUMBER: PCT/US01/21306  
CURRENT FILING DATE: 2001-07-06  
PRIOR APPLICATION NUMBER: 60/215,984  
PRIOR FILING DATE: 2000-07-05  
NUMBER OF SEQ ID NOS: 141  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 49  
LENGTH: 15  
TYPE: DNA  
ORGANISM: Homo sapiens  
PCT-US01-21306-49

Query Match 100.0%; Score 12; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.7e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGGTGGGG 12  
Db 2 GGGGTGGTGGGG 13

RESULT 5

US-09-740-332-2132/c  
Sequence 2132, Application US/09740332  
GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals Inc.  
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection  
FILE REFERENCE: RPI 400/003  
CURRENT APPLICATION NUMBER: US/09/740,332  
CURRENT FILING DATE: 2001-03-26  
NUMBER OF SEQ ID NOS: 9704  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 2132  
LENGTH: 17  
TYPE: RNA

ORGANISM: artificial sequence  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION:  
OTHER INFORMATION: oligonucleotide substrate

US-09-740-332-2132

Query Match 100.0%; Score 12; DB 32; Length 17;  
Best Local Similarity 100.0%; Pred. No. 8.7e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGGTGGGG 12  
Db 16 GGGGTGGTGGGG 5

RESULT 6

US-09-740-332-2133/c  
Sequence 2133, Application US/09740332  
GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals Inc.  
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection  
FILE REFERENCE: RPI 400/003  
CURRENT APPLICATION NUMBER: US/09/740,332  
CURRENT FILING DATE: 2001-03-26  
NUMBER OF SEQ ID NOS: 9704  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 2133  
LENGTH: 17  
TYPE: RNA

ORGANISM: artificial sequence  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION:  
OTHER INFORMATION: oligonucleotide substrate  
US-09-740-332-2133

Query Match 100.0%; Score 12; DB 32; Length 17;  
Best Local Similarity 100.0%; Pred. No. 8.7e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGGTGGGG 12  
Db 13 GGGGTGGTGGGG 2

RESULT 7

US-09-740-332-2422  
Sequence 2422, Application US/09740332  
GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals Inc.  
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection  
FILE REFERENCE: RPI 400/003  
CURRENT APPLICATION NUMBER: US/09/740,332  
CURRENT FILING DATE: 2001-03-26  
NUMBER OF SEQ ID NOS: 9704  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 2422  
LENGTH: 17  
TYPE: RNA

ORGANISM: artificial sequence  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION:  
OTHER INFORMATION: oligonucleotide substrate  
US-09-740-332-2422

Query Match 100.0%; Score 12; DB 32; Length 17;  
Best Local Similarity 83.3%; Pred. No. 8.7e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGGTGGGG 12  
Db 6 GGGGUGGUGGGG 17

RESULT 8

US-09-740-332-2423  
Sequence 2423, Application US/09740332  
GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals Inc.  
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection  
FILE REFERENCE: RPI 400/003  
CURRENT APPLICATION NUMBER: US/09/740,332  
CURRENT FILING DATE: 2001-03-26  
NUMBER OF SEQ ID NOS: 9704  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 2423  
LENGTH: 17  
TYPE: RNA

ORGANISM: artificial sequence  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION:  
OTHER INFORMATION: oligonucleotide substrate  
US-09-740-332-2423

Query Match 100.0%; Score 12; DB 32; Length 17;  
Best Local Similarity 83.3%; Pred. No. 8.7e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGG 12  
||||:||||  
Db 3 GGGUGGUGGG 14

RESULT 9

US-09-817-879-2132/c  
; Sequence 2132, Application US/09817879  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate  
; FILE REFERENCE: MBH00-801-F  
; CURRENT APPLICATION NUMBER: US/09/817,879  
; CURRENT FILING DATE: 2001-03-26  
; NUMBER OF SEQ ID NOS: 9703  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2132  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION:  
; OTHER INFORMATION: oligonucleotide substrate  
US-09-817-879-2132

Query Match 100.0%; Score 12; DB 34; Length 17;  
Best Local Similarity 100.0%; Pred. No. 8.7e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGG 12  
||||:||||  
Db 16 GGGGTGGTGGG 5

RESULT 10

US-09-817-879-2133/c  
; Sequence 2133, Application US/09817879  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate  
; FILE REFERENCE: MBH00-801-F  
; CURRENT APPLICATION NUMBER: US/09/817,879  
; CURRENT FILING DATE: 2001-03-26  
; NUMBER OF SEQ ID NOS: 9703  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2133  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION:  
; OTHER INFORMATION: oligonucleotide substrate  
US-09-817-879-2133

Query Match 100.0%; Score 12; DB 34; Length 17;  
Best Local Similarity 100.0%; Pred. No. 8.7e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGG 12  
||||:||||  
Db 13 GGGGTGGTGGG 2

RESULT 11

US-09-817-879-2422  
; Sequence 2422, Application US/09817879  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate

; TITLE OF INVENTION: Hepatitis C Virus Infection  
; FILE REFERENCE: MBH00-801-F  
; CURRENT APPLICATION NUMBER: US/09/817,879  
; CURRENT FILING DATE: 2001-03-26  
; NUMBER OF SEQ ID NOS: 9703  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2422  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION:  
; OTHER INFORMATION: oligonucleotide substrate  
US-09-817-879-2422

Query Match 100.0%; Score 12; DB 34; Length 17;  
Best Local Similarity 83.3%; Pred. No. 8.7e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGG 12  
||||:||||  
Db 6 GGGUGGUGGG 17

RESULT 12

US-09-817-879-2423  
; Sequence 2423, Application US/09817879  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate  
; FILE REFERENCE: MBH00-801-F  
; CURRENT APPLICATION NUMBER: US/09/817,879  
; CURRENT FILING DATE: 2001-03-26  
; NUMBER OF SEQ ID NOS: 9703  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2423  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION:  
; OTHER INFORMATION: oligonucleotide substrate  
US-09-817-879-2423

Query Match 100.0%; Score 12; DB 34; Length 17;  
Best Local Similarity 83.3%; Pred. No. 8.7e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGG 12  
||||:||||  
Db 3 GGGUGGUGGG 14

RESULT 13

US-10-303-778-13820  
; Sequence 13820, Application US/10303778  
; GENERAL INFORMATION:  
; APPLICANT: RosettaGenomics  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL  
; FILE REFERENCE: 47416  
; CURRENT APPLICATION NUMBER: US/10/303,778  
; CURRENT FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 17608  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 13820  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-303-778-13820

Query Match 100.0%; Score 12; DB 50; Length 17;  
Best Local Similarity 100.0%; Pred. No. 8.7e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGG 12  
| | | | | | | | | |  
Db 6 GGGGTGGTGGG 17

RESULT 14

US-08-387-041A-3  
; Sequence 3, Application US/08387041A  
; GENERAL INFORMATION:  
; APPLICANT: Tam, Robert C.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATION  
; TITLE OF INVENTION: OF CD28 EXPRESSION  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/387,041A  
; FILING DATE: 02-FEB-1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Halluin, Albert P.  
; REGISTRATION NUMBER: 25,227  
; REFERENCE/DOCKET NUMBER: 8250-011  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-854-3660  
; TELEFAX: 415-854-3694  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
; US-08-387-041A-3

Query Match 100.0%; Score 12; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 8.8e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGG 12  
| | | | | | | | | |  
Db 7 GGGGTGGTGGG 18

RESULT 15

US-08-387-041A-10/C  
; Sequence 10, Application US/08387041A  
; GENERAL INFORMATION:  
; APPLICANT: Tam, Robert C.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATION  
; TITLE OF INVENTION: OF CD28 EXPRESSION  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York

; COUNTRY: United States of America  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/387,041A  
; FILING DATE: 02-FEB-1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Halluin, Albert P.  
; REGISTRATION NUMBER: 25,227  
; REFERENCE/DOCKET NUMBER: 8250-011  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-854-3660  
; TELEFAX: 415-854-3694  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
; US-08-387-041A-10

Query Match 100.0%; Score 12; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 8.8e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGG 12  
| | | | | | | | | |  
Db 18 GGGGTGGTGGG 7

Search completed: October 27, 2003, 17:52:54  
Job time : 1570.86 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 11:09:34 ; Search time 204.686 Seconds  
(without alignments)  
97.777 Million cell updates/sec

Title: US-09-331-204A-13

Perfect score: 12

Sequence: 1 ggggtgtgggg 12

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2231628 seqs, 833900706 residues

Total number of hits satisfying chosen parameters: 264402

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_NA\_New:\*  
1: /cgn2\_6/ptodata/1/pna/PCT\_NEW\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq:\*  
7: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
C 1	12	100.0	17	6	US-10-669-841-4725
C 2	12	100.0	17	6	US-10-669-841-4726
3	12	100.0	17	6	US-10-669-841-5015
4	12	100.0	17	6	US-10-669-841-5016
5	12	100.0	18	1	PCT-US02-38216-9770
6	12	100.0	18	1	PCT-US02-38216-72857
7	12	100.0	19	1	PCT-US02-38216-46976
C 8	12	100.0	19	1	PCT-US02-38216-64788
9	12	100.0	20	1	PCT-US02-38216-31313
10	12	100.0	20	1	PCT-US02-38216-78501
11	12	100.0	21	1	PCT-US02-38216-31329
12	12	100.0	21	1	PCT-US02-38216-72837
13	12	100.0	21	1	PCT-US02-38216-78761
14	12	100.0	22	1	PCT-US02-38216-42141
15	11	91.7	17	1	PCT-US02-38216-39287
16	11	91.7	18	1	PCT-US02-38216-10573
17	11	91.7	18	1	PCT-US02-38216-31330
18	11	91.7	18	1	PCT-US02-38216-56500
C 19	11	91.7	18	5	US-09-943-944E-22
20	11	91.7	19	1	PCT-US02-38216-78687
21	11	91.7	20	1	PCT-US02-38216-10564
22	11	91.7	20	1	PCT-US02-38216-41184
23	11	91.7	20	1	PCT-US02-38216-63924
24	11	91.7	20	1	PCT-US02-38216-64021
25	11	91.7	20	1	PCT-US02-38216-64022
26	11	91.7	20	5	US-09-978-333B-2

27	11	91.7	20	5	US-09-978-333C-2	Sequence 2, Appli
28	11	91.7	22	1	PCT-US02-38216-39252	Sequence 39252, A
29	11	91.7	22	1	PCT-US02-38216-63970	Sequence 63970, A
30	11	91.7	22	1	PCT-US02-38216-83087	Sequence 83087, A
31	10.4	86.7	15	1	PCT-US02-38216-34808	Sequence 34808, A
32	10.4	86.7	15	1	PCT-US02-38216-72787	Sequence 72787, A
33	10.4	86.7	15	1	PCT-US02-38216-84942	Sequence 84942, A
34	10.4	86.7	15	1	PCT-US02-38216-84968	Sequence 84968, A
35	10.4	86.7	16	1	PCT-US02-38216-9718	Sequence 9718, Ap
36	10.4	86.7	16	1	PCT-US02-38216-31332	Sequence 31332, A
37	10.4	86.7	16	1	PCT-US02-38216-51833	Sequence 51833, A
38	10.4	86.7	16	1	PCT-US02-38216-60635	Sequence 60635, A
39	10.4	86.7	16	1	PCT-US02-38216-61028	Sequence 61028, A
40	10.4	86.7	16	1	PCT-US02-38216-64024	Sequence 64024, A
41	10.4	86.7	16	1	PCT-US02-38216-72823	Sequence 72823, A
C 42	10.4	86.7	16	1	PCT-US02-38216-73073	Sequence 73073, A
43	10.4	86.7	16	1	PCT-US02-38216-75530	Sequence 75530, A
44	10.4	86.7	17	1	PCT-US02-38216-9811	Sequence 9811, Ap
C 45	10.4	86.7	17	1	PCT-US02-38216-26671	Sequence 26671, A

ALIGNMENTS

RESULT 1  
US-10-669-841-4725/c  
; Sequence 4725, Application US/10669841  
; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics, Inc.  
; APPLICANT: Lawrence, Blatt  
; APPLICANT: Dennis, Macejak  
; APPLICANT: James, McSwiggan  
; APPLICANT: David, Morrissey  
; APPLICANT: Pamela, Pavco  
; APPLICANT: Patrice, Lee  
; APPLICANT: Kenneth, Draper  
; APPLICANT: Elisabeth, Roberts  
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEI  
; TITLE OF INVENTION: VIRUS REPLICATION  
; FILE REFERENCE: 400/042US (MBHB02-249-E)  
; CURRENT APPLICATION NUMBER: US/10/669,841  
; CURRENT FILING DATE: 2003-09-23  
; PRIOR APPLICATION NUMBER: PCT/US02/09187  
; PRIOR FILING DATE: 2002-03-26  
; PRIOR APPLICATION NUMBER: US 60/296,876  
; PRIOR FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 60/335,059  
; PRIOR FILING DATE: 2001-10-24  
; PRIOR APPLICATION NUMBER: US 60/337,055  
; PRIOR FILING DATE: 2001-12-05  
; PRIOR APPLICATION NUMBER: US 60/358,580  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: US 60/363,124  
; PRIOR FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: US 09/817,879  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: US 09/740,332  
; PRIOR FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: US 09/611,931  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: US 09/504,321  
; PRIOR FILING DATE: 2000-02-15  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 16207  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4725  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid  
; FEATURE:  
; NAME/KEY: misc\_feature

LOCATION:  
OTHER INFORMATION: oligonucleotide substrate  
US-10-669-841-4725

Query Match 100.0%; Score 12; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGGTGGG 12  
| | | | | | | | | |  
Db 16 GGGGTGGTGGG 5

RESULT 2

US-10-669-841-4726/c  
Sequence 4726, Application US/10669841  
GENERAL INFORMATION:  
APPLICANT: Sirna Therapeutics, Inc.  
APPLICANT: Lawrence, Blatt  
APPLICANT: Dennis, Macejak  
APPLICANT: James, McSwiggen  
APPLICANT: David, Morrissey  
APPLICANT: Pamela, Pavco  
APPLICANT: Patrice, Lee  
APPLICANT: Kenneth, Draper  
APPLICANT: Elisabeth, Roberts  
TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPA  
TITLE OF INVENTION: VIRUS REPLICATION  
FILE REFERENCE: 400/042US (MEHB02-249-E)  
CURRENT APPLICATION NUMBER: US/10/669,841  
CURRENT FILING DATE: 2003-09-23  
PRIOR APPLICATION NUMBER: PCT/US02/09187  
PRIOR FILING DATE: 2002-03-26  
PRIOR APPLICATION NUMBER: US 60/296,876  
PRIOR FILING DATE: 2001-06-08  
PRIOR APPLICATION NUMBER: US 60/335,059  
PRIOR FILING DATE: 2001-10-24  
PRIOR APPLICATION NUMBER: US 60/337,055  
PRIOR FILING DATE: 2001-12-05  
PRIOR APPLICATION NUMBER: US 60/358,580  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: US 60/363,124  
PRIOR FILING DATE: 2002-03-11  
PRIOR APPLICATION NUMBER: US 09/817,879  
PRIOR FILING DATE: 2001-03-26  
PRIOR APPLICATION NUMBER: US 09/740,332  
PRIOR FILING DATE: 2000-12-18  
PRIOR APPLICATION NUMBER: US 09/611,931  
PRIOR FILING DATE: 2000-07-07  
PRIOR APPLICATION NUMBER: US 09/504,321  
PRIOR FILING DATE: 2000-02-15  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 16207  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 4726  
LENGTH: 17  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid  
NAME/KEY: misc\_feature  
LOCATION:  
OTHER INFORMATION: oligonucleotide substrate  
US-10-669-841-4726

Query Match 100.0%; Score 12; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGGTGGG 12  
| | | | | | | | | |  
Db 13 GGGGTGGTGGG 2

RESULT 3

US-10-669-841-5015  
Sequence 5015, Application US/10669841  
GENERAL INFORMATION:  
APPLICANT: Sirna Therapeutics, Inc.  
APPLICANT: Lawrence, Blatt  
APPLICANT: Dennis, Macejak  
APPLICANT: James, McSwiggen  
APPLICANT: David, Morrissey  
APPLICANT: Pamela, Pavco  
APPLICANT: Patrice, Lee  
APPLICANT: Kenneth, Draper  
APPLICANT: Elisabeth, Roberts  
TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HE  
TITLE OF INVENTION: VIRUS REPLICATION  
FILE REFERENCE: 400/042US (MEHB02-249-E)  
CURRENT APPLICATION NUMBER: US/10/669,841  
CURRENT FILING DATE: 2003-09-23  
PRIOR APPLICATION NUMBER: PCT/US02/09187  
PRIOR FILING DATE: 2002-03-26  
PRIOR APPLICATION NUMBER: US 60/296,876  
PRIOR FILING DATE: 2001-06-08  
PRIOR APPLICATION NUMBER: US 60/335,059  
PRIOR FILING DATE: 2001-10-24  
PRIOR APPLICATION NUMBER: US 60/337,055  
PRIOR FILING DATE: 2001-12-05  
PRIOR APPLICATION NUMBER: US 60/358,580  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: US 60/363,124  
PRIOR FILING DATE: 2002-03-11  
PRIOR APPLICATION NUMBER: US 09/817,879  
PRIOR FILING DATE: 2001-03-26  
PRIOR APPLICATION NUMBER: US 09/740,332  
PRIOR FILING DATE: 2000-12-18  
PRIOR APPLICATION NUMBER: US 09/611,931  
PRIOR FILING DATE: 2000-07-07  
PRIOR APPLICATION NUMBER: US 09/504,321  
PRIOR FILING DATE: 2000-02-15  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 16207  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 5015  
LENGTH: 17  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid  
NAME/KEY: misc\_feature  
LOCATION:  
OTHER INFORMATION: oligonucleotide substrate  
US-10-669-841-5015

Query Match 100.0%; Score 12; DB 6; Length 17;  
Best Local Similarity 83.3%; Pred. No. 1.4e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGGTGGG 12  
| | | | | | | | | |  
Db 6 GGGGTGGTGGG 17

RESULT 4

US-10-669-841-5016  
Sequence 5016, Application US/10669841  
GENERAL INFORMATION:  
APPLICANT: Sirna Therapeutics, Inc.  
APPLICANT: Lawrence, Blatt  
APPLICANT: Dennis, Macejak  
APPLICANT: James, McSwiggen  
APPLICANT: David, Morrissey

APPLICANT: Pamela, Pavco  
APPLICANT: Patrice, Lee  
APPLICANT: Kenneth, Draper  
APPLICANT: Elisabeth, Roberts  
TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPA  
FILE REFERENCE: 400/042US (MBHB02-249-E)  
CURRENT APPLICATION NUMBER: US/10/669,841  
CURRENT FILING DATE: 2003-09-23  
PRIOR APPLICATION NUMBER: PCT/US02/09187  
PRIOR FILING DATE: 2002-03-26  
PRIOR APPLICATION NUMBER: US 60/296,876  
PRIOR FILING DATE: 2001-06-08  
PRIOR APPLICATION NUMBER: US 60/335,059  
PRIOR FILING DATE: 2001-10-24  
PRIOR APPLICATION NUMBER: US 60/337,055  
PRIOR FILING DATE: 2001-12-05  
PRIOR APPLICATION NUMBER: US 60/358,580  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: US 60/363,124  
PRIOR FILING DATE: 2002-03-11  
PRIOR APPLICATION NUMBER: US 09/817,879  
PRIOR FILING DATE: 2001-03-26  
PRIOR APPLICATION NUMBER: US 09/740,332  
PRIOR FILING DATE: 2000-12-18  
PRIOR APPLICATION NUMBER: US 09/611,931  
PRIOR FILING DATE: 2000-07-07  
PRIOR APPLICATION NUMBER: US 09/504,321  
PRIOR FILING DATE: 2000-02-15  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 16207  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 5016  
LENGTH: 17  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION:  
OTHER INFORMATION: oligonucleotide substrate  
US-10-669-841-5016

Query Match 100.0%; Score 12; DB 6; Length 17;  
Best Local Similarity 83.3%; Pred. No. 1.4e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTGGTGGGG 12  
Db 3 GGGGUGGUGGGG 14

RESULT 5  
PCT-US02-38216-9770  
Sequence 9770, Application PC/TUS0238216  
GENERAL INFORMATION:  
APPLICANT: Rosetta Genomics LTD  
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
TITLE OF INVENTION: GENES AND USES THEREOF  
FILE REFERENCE: 55002  
CURRENT APPLICATION NUMBER: PCT/US02/38216  
CURRENT FILING DATE: 2002-11-12  
NUMBER OF SEQ ID NOS: 86841  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 9770  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Homo sapiens  
PCT-US02-38216-9770

Query Match 100.0%; Score 12; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.4e+04;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGTGGTGGGG 12  
Db 2 GGGTGGTGGGG 13  
RESULT 6  
PCT-US02-38216-72857  
Sequence 72857, Application PC/TUS0238216  
GENERAL INFORMATION:  
APPLICANT: Rosetta Genomics LTD  
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
TITLE OF INVENTION: GENES AND USES THEREOF  
FILE REFERENCE: 55002  
CURRENT APPLICATION NUMBER: PCT/US02/38216  
CURRENT FILING DATE: 2002-11-12  
NUMBER OF SEQ ID NOS: 86841  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 72857  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Homo sapiens  
PCT-US02-38216-72857

Query Match 100.0%; Score 12; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.4e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTGGTGGGG 12  
Db 1 GGGTGGTGGGG 12

RESULT 7  
PCT-US02-38216-46976  
Sequence 46976, Application PC/TUS0238216  
GENERAL INFORMATION:  
APPLICANT: Rosetta Genomics LTD  
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
TITLE OF INVENTION: GENES AND USES THEREOF  
FILE REFERENCE: 55002  
CURRENT APPLICATION NUMBER: PCT/US02/38216  
CURRENT FILING DATE: 2002-11-12  
NUMBER OF SEQ ID NOS: 86841  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 46976  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Homo sapiens  
PCT-US02-38216-46976

Query Match 100.0%; Score 12; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.4e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTGGTGGGG 12  
Db 8 GGGTGGTGGGG 19

RESULT 8  
PCT-US02-38216-64788/c  
Sequence 64788, Application PC/TUS0238216  
GENERAL INFORMATION:  
APPLICANT: Rosetta Genomics LTD  
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
TITLE OF INVENTION: GENES AND USES THEREOF  
FILE REFERENCE: 55002  
CURRENT APPLICATION NUMBER: PCT/US02/38216  
CURRENT FILING DATE: 2002-11-12  
NUMBER OF SEQ ID NOS: 86841  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 64788

```

; SEQ ID NO 64788
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-64788

Query Match      100.0%; Score 12; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGTGGTGGGG 12
Db      14 GGGGTGGTGGGG 3

RESULT 9
PCT-US02-38216-31313
; Sequence 31313, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31313
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-31313

Query Match      100.0%; Score 12; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGTGGTGGGG 12
Db      1 GGGGTGGTGGGG 12

RESULT 10
PCT-US02-38216-78501
; Sequence 78501, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 78501
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-78501

Query Match      100.0%; Score 12; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGTGGTGGGG 12
Db      6 GGGGTGGTGGGG 17

RESULT 11
PCT-US02-38216-31329
; Sequence 31329, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31329
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-31329

Query Match      100.0%; Score 12; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGTGGTGGGG 12
Db      1 GGGGTGGTGGGG 12

RESULT 12
PCT-US02-38216-72837
; Sequence 72837, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 72837
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-72837

Query Match      100.0%; Score 12; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGTGGTGGGG 12
Db      1 GGGGTGGTGGGG 12

RESULT 13
PCT-US02-38216-78761
; Sequence 78761, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 78761
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-78761

Query Match      100.0%; Score 12; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGTGGTGGGG 12
Db      1 GGGGTGGTGGGG 12
```

```

; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31329
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-31329

Query Match      100.0%; Score 12; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGTGGTGGGG 12
Db      1 GGGGTGGTGGGG 12

RESULT 12
PCT-US02-38216-72837
; Sequence 72837, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 72837
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-72837

Query Match      100.0%; Score 12; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGTGGTGGGG 12
Db      8 GGGGTGGTGGGG 19

RESULT 13
PCT-US02-38216-78761
; Sequence 78761, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 78761
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-78761

Query Match      100.0%; Score 12; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGTGGTGGGG 12
```

Db 9 GGGTGGTGGG 20  
|||||

RESULT 14  
PCT-US02-38216-42141  
; Sequence 42141, Application PC/TUS0238216  
; GENERAL INFORMATION:  
; APPLICANT: Rosetta Genomics LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
; TITLE OF INVENTION: GENES AND USES THEREOF  
; FILE REFERENCE: 55002  
; CURRENT APPLICATION NUMBER: PCT/US02/38216  
; CURRENT FILING DATE: 2002-11-12  
; NUMBER OF SEQ ID NOS: 86841  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 42141  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US02-38216-42141

Query Match 100.0%; Score 12; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTGGTGGG 12  
|||||  
Db 6 GGGTGGTGGG 17

RESULT 15  
PCT-US02-38216-39287  
; Sequence 39287, Application PC/TUS0238216  
; GENERAL INFORMATION:  
; APPLICANT: Rosetta Genomics LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
; TITLE OF INVENTION: GENES AND USES THEREOF  
; FILE REFERENCE: 55002  
; CURRENT APPLICATION NUMBER: PCT/US02/38216  
; CURRENT FILING DATE: 2002-11-12  
; NUMBER OF SEQ ID NOS: 86841  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 39287  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US02-38216-39287

Query Match 91.7%; Score 11; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.7e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGTGGTGGG 12  
|||||  
Db 7 GGTGGTGGG 17

Search completed: October 27, 2003, 18:22:56  
Job time : 205.686 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:29 ; Search time 162 Seconds  
(without alignments)  
299.938 Million cell updates/sec

Title: US-09-331-204A-8  
Perfect score: 18  
Sequence: 1 ttggagggggaggtggg 18

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues  
Total number of hits satisfying chosen parameters: 1643890

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_19Jun03:\*  
1: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.\*  
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.\*  
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.\*  
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.\*  
5: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.\*  
6: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.\*  
7: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.\*  
8: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.\*  
9: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.\*  
10: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.\*  
11: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.\*  
12: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.\*  
13: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.\*  
14: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.\*  
15: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.\*  
16: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.\*  
17: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.\*  
18: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.\*  
19: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.\*  
20: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.\*  
21: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.\*  
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.\*  
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.\*  
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.\*  
25: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	17 AAT36243	CD28 expression in
2	18	100.0	18	20 AAX90336	CD28 inhibiting ph
3	16.4	91.1	18	17 AAT36242	CD28 expression in
4	16.4	91.1	18	17 AAT36196	Triplex forming ol
5	16.4	91.1	18	20 AAX90328	CD28 inhibiting ph
6	16.4	91.1	18	20 AAX90335	CD28 inhibiting ph
7	16.4	91.1	18	20 AAX90290	CD28 inhibition ol
8	16.4	91.1	18	21 AAZ99625	Nucleotide sequenc

C	9	16.4	91.1	18	21	AAZ99650	Nucleotide sequenc
	10	16.4	91.1	21	17	AAT36197	Triplex forming ol
	11	16.4	91.1	21	20	AAX90329	CD28 inhibiting ph
	12	16.4	91.1	21	20	AAX90291	CD28 inhibition ol
	13	14.8	82.2	22	22	AAF16593	Gastric acid produ
C	14	14.4	80.0	17	21	AAF01954	Hammerhead ribozym
	15	13.8	76.7	20	22	AAD12117	Rat PTP1B antisens
	16	13.8	76.7	20	24	ABK85192	Rat PTP1B antisens
	17	13.8	76.7	20	24	ABK37361	Rat PTP1B mRNA lev
	18	13.8	76.7	21	11	AAQ06932	MMY24 nucleotide c
	19	13.8	76.7	21	18	AAQ98040	Human or simian im
C	20	13.4	74.4	17	24	ABV91221	Human POSHL1 scann
C	21	13.4	74.4	17	24	ABV91222	Human POSHL1 scann
C	22	13.4	74.4	17	24	ABV91223	Human POSHL1 scann
	23	13.4	74.4	19	17	AAV56945	HIV-1 proviral DNA
	24	13.4	74.4	19	24	AAD41090	Primer ON-DHFR-F1
	25	13.4	74.4	19	24	ABT03925	Human pol kappa 76
C	26	13.4	74.4	20	21	AAZ75053	Human biallelic ma
	27	13.2	73.3	18	17	AAT36244	CD28 expression in
	28	13.2	73.3	18	20	AAX90337	CD28 inhibiting ph
C	29	13.2	73.3	21	24	ABK99294	Hepatitis C virus
	30	13	72.2	20	24	ABT08387	Human CC3 promoter
C	31	12.8	71.1	17	20	AAX14740	Triple helix formi
	32	12.8	71.1	17	20	AAV55680	Human tissue kalli
C	33	12.8	71.1	17	21	AAF05272	Hammerhead ribozym
C	34	12.8	71.1	17	23	ABK00045	Human NOGO Hammerh
C	35	12.8	71.1	17	23	ABK00894	Human NOGO Inozyme
	36	12.8	71.1	17	24	AAL43484	Human tissue kalli
	37	12.8	71.1	18	18	AAT95456	Primer for breast
	38	12.8	71.1	18	22	AAH49336	C. glutamicum ATCC
C	39	12.8	71.1	20	21	AAZ37997	Human GLC1A gene e
	40	12.8	71.1	20	22	AAD12118	Rat PTP1B antisens
	41	12.8	71.1	20	24	ABK85193	Rat PTP1B antisens
	42	12.8	71.1	20	24	ABK37362	Rat PTP1B mRNA lev
	43	12.8	71.1	21	18	AAV06186	Primer used when o
	44	12.8	71.1	21	21	AAA47231	Primer 1 for human
C	45	12.8	71.1	22	24	AAD45780	Human promoter -14

ALIGNMENTS

RESULT 1

AAT36243

ID AAT36243 standard; DNA; 18 BP.

XX AAT36243;

XX 25-MAR-2003 (updated)

DT 16-APR-1997 (first entry)

XX CD28 expression inhibiting oligonucleotide, RT09s.

DE Reduction; T cell; CD28; gene expression; treatment; immune system;  
XX disorder; graft versus host disease; septic shock; viral disease;  
KW psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;  
KW multiple sclerosis; uveitis; rheumatoid arthritis; interleukin 2;  
KW systemic lupus erythematosus; inflammatory bowel disease;  
KW IL-2; production; antisense; inhibition; ss

XX Synthetic.

XX WO9624380-A1.

PN 15-AUG-1996.

XX 05-FEB-1996; 96WO-US01507.

XX 09-FEB-1995; 95US-0387041.

XX 18-SEP-1995; 95US-0529878.

XX 09-FEB-1995; 95US-0387041.

XX 18-SEP-1995; 95US-0529878.

PA (ICNC ) ICN PHARM INC.  
XX Tam RC;  
XX WPI; 1996-384228/38.  
XX Oligo:nucleotide which reduces CD28 gene expression in T cells -  
PT for treating immune system diseases, e.g. graft vs. host disease,  
PT septic shock, psoriasis, etc.  
XX Example 2; Page 45; 77pp; English.  
XX The present oligonucleotide reduces CD28 dependent interleukin-2  
CC (IL-2) production and T cell CD28 gene expression, useful in the  
CC treatment of CD28 mediated diseases, particularly immune system  
CC disorders, e.g. graft versus host disease, septic shock, viral  
CC disease, psoriasis, type I diabetes mellitus, thyroiditis,  
CC sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis,  
CC systemic lupus erythematosus, inflammatory bowel disease, etc..  
CC Reducing CD28 expression may reduce the effects of antigenic  
CC stimulation of CD28 positive T cells, with a consequent reduction  
CC in cytokine release.  
CC (Updated on 25-MAR-2003 to correct PR field.)  
XX Sequence 18 BP; 2 A; 0 C; 13 G; 3 T; 0 other;  
SQ

Query Match 100.0%; Score 18; DB 17; Length 18;  
Best Local Similarity 100.0%; Pred. NO. 3.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGAGGTGGG 18  
Db 1 TTGGAGGGGGAGGTGGG 18

RESULT 2  
AAX90336  
ID AAX90336 standard; DNA; 18 BP.  
XX  
AC AAX90336;  
XX  
DT 24-SEP-1999 (first entry)  
XX  
DE CD28 inhibiting phosphorothioate oligonucleotide RT09S.  
XX  
XX CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;  
KW immune system mediated disease; gamma-interferon; IL-8;  
KW phosphorothioate; ss.  
XX  
OS Synthetic.  
XX  
PN US932556-A.  
XX  
PD 03-AUG-1999.  
XX  
PF 18-SEP-1995; 95US-0529878.  
XX  
PR 18-SEP-1995; 95US-0529878.  
XX  
PA (TAMR/) TAM R C.  
XX  
XX Tam RC;  
PI  
XX WPI; 1999-443609/37.  
XX  
XX Treatment of immune system-mediated diseases by inhibiting  
PT expression of CD28, IL-2, gamma-interferon or IL-8  
XX  
XX Example; Column 24; 45pp; English.  
XX  
XX The present invention describes a method for inhibiting the expression  
CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method  
CC comprises subcutaneous administration of an oligonucleotide (OGN).

CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the  
CC method. The OGNs are used for the treatment of immune system-mediated  
CC diseases. The present sequence represents a CD28 inhibiting  
CC phosphorothioate oligonucleotide used in the exemplification of the  
CC present invention.  
XX  
SQ Sequence 18 BP; 2 A; 0 C; 13 G; 3 T; 0 other;  
Query Match 100.0%; Score 18; DB 20; Length 18;  
Best Local Similarity 100.0%; Pred. NO. 3.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGAGGTGGG 18  
Db 1 TTGGAGGGGGAGGTGGG 18

RESULT 3  
AAT36242  
ID AAT36242 standard; DNA; 18 BP.  
XX  
AC AAT36242;  
XX  
DT 25-MAR-2003 (updated)  
DT 16-APR-1997 (first entry)  
XX  
DE CD28 expression inhibiting oligonucleotide, RT05S.  
XX  
XX Reduction; T cell; CD28; gene expression; treatment; immune system;  
KW disorder; graft versus host disease; septic shock; viral disease;  
KW psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;  
KW multiple sclerosis; uveitis; rheumatoid arthritis; interleukin 2;  
KW systemic lupus erythematosus; inflammatory bowel disease;  
KW IL-2; production; antisense; inhibition; ss  
XX  
OS Synthetic.  
XX  
PN WO9624380-A1.  
XX  
PD 15-AUG-1996.  
XX  
PF 05-FEB-1996; 96WO-US01507.  
XX  
PR 09-FEB-1995; 95US-0387041.  
PR 18-SEP-1995; 95US-0529878.  
PR 09-FEB-1995; 95US-0387041.  
PR 18-SEP-1995; 95US-0529878.  
XX  
PA (ICNC ) ICN PHARM INC.  
XX  
XX Tam RC;  
PI  
XX WPI; 1996-384228/38.  
XX  
XX Oligo:nucleotide which reduces CD28 gene expression in T cells -  
PT for treating immune system diseases, e.g. graft vs. host disease,  
PT septic shock, psoriasis, etc.  
XX  
XX Example 2; Page 45; 77pp; English.  
XX  
XX The present oligonucleotide reduces CD28 dependent interleukin-2  
CC (IL-2) production and T cell CD28 gene expression, useful in the  
CC treatment of CD28 mediated diseases, particularly immune system  
CC disorders, e.g. graft versus host disease, septic shock, viral  
CC disease, psoriasis, type I diabetes mellitus, thyroiditis,  
CC sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis,  
CC systemic lupus erythematosus, inflammatory bowel disease, etc..  
CC Reducing CD28 expression may reduce the effects of antigenic  
CC stimulation of CD28 positive T cells, with a consequent reduction  
CC in cytokine release.  
CC (Updated on 25-MAR-2003 to correct PR field.)  
XX  
XX Sequence 18 BP; 3 A; 0 C; 13 G; 2 T; 0 other;  
SQ

Query Match 91.1%; Score 16.4; DB 17; Length 18;  
Best Local Similarity 94.4%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGAGGTGGGG 18  
Db 1 TTGGAGGGGGAGGTGGGG 18

RESULT 4

AAT36196

ID AAT36196 standard; DNA; 18 BP.

XX

AC AAT36196;

XX 25-MAR-2003 (updated)

DT 15-APR-1997 (first entry)

XX

DE Triplex forming oligo targetting CD28 5'-UTR (nt 58-75).

XX

KW Reduction; T cell; CD28; gene expression; treatment; immune system;

KW disorder; graft versus host disease; septic shock; viral disease;

KW psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;

KW multiple sclerosis; uveitis; rheumatoid arthritis; 5'-UTR;

KW systemic lupus erythematosus; inflammatory bowel disease;

KW triplex forming; oligonucleotide; 5'-untranslated region; ss

XX

OS Synthetic.

XX

PN WO9624380-A1.

XX

PD 15-AUG-1996.

XX

PF 05-FEB-1996; 96WO-US01507.

XX

PR 09-FEB-1995; 95US-0387041.

PR 18-SEP-1995; 95US-0529878.

PR 09-FEB-1995; 95US-0387041.

PR 18-SEP-1995; 95US-0529878.

XX (ICNC ) ICN PHARM INC.

PA

XX

PI Tam RC;

XX

DR WPI; 1996-384228/38.

XX Oligo:nucleotide which reduces CD28 gene expression in T cells -

PT for treating immune system diseases, e.g. graft vs. host disease,

PT septic shock, psoriasis, etc.

XX

PS Claim 9; Page 54; 77pp; English.

XX

CC The present oligonucleotide reduces T cell CD28 gene expression,

CC useful in the treatment of CD28 mediated diseases, particularly

CC immune system disorders, e.g. graft versus host disease, septic

CC shock, viral disease, psoriasis; type I diabetes mellitus,

CC thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid

CC arthritis, systemic lupus erythematosus, inflammatory bowel

CC disease, etc.. Reducing CD28 expression may reduce the effects of

CC antigenic stimulation of CD28 positive T cells, with a consequent

CC reduction in cytokine release.

CC (Updated on 25-MAR-2003 to correct PR field.)

XX

SQ Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;

Query Match

Best Local Similarity 91.1%; Score 16.4; DB 17; Length 18;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGAGGTGGGG 18  
Db 1 TTGGAGGGGGAGGTGGGG 18



```
PN US5932556-A.
XX
PD 03-AUG-1999.
XX
PF 18-SEP-1995; 95US-0529878.
XX
PR 18-SEP-1995; 95US-0529878.
XX
PA (TAMR/) TAM R C.
XX
PI Tam RC;
XX
DR WPI; 1999-443609/37.
XX
PT Treatment of immune system-mediated diseases by inhibiting
PT expression of CD28, IL-2, gamma-interferon or IL-8
XX
PS Example; Column 24; 45pp; English.
XX
CC The present invention describes a method for inhibiting the expression
CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method
CC comprises subcutaneous administration of an oligonucleotide (OGN).
CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the
CC method. The OGNs are used for the treatment of immune system-mediated
CC diseases. The present sequence represents a CD28 inhibiting
CC phosphorothioate oligonucleotide used in the exemplification of the
CC present invention.
XX
SQ Sequence 18 BP; 3 A; 0 C; 13 G; 2 T; 0 other;
Query Match 91.1%; Score 16.4; DB 20; Length 18;
Best Local Similarity 94.4%; Pred. NO. 1.4e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TTGGAGGGGGAGGTGGG 18
Db 1 TTGGAGGGGGAGGTGGG 18
RESULT 7
AAX90290
ID AAX90290 standard; DNA; 18 BP.
XX
AC AAX90290;
XX
DT 24-SEP-1999 (first entry)
XX
DE CD28 inhibition oligonucleotide RT03.
XX
KW CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
KW immune system mediated disease; gamma-interferon; IL-8; ss.
XX
OS Synthetic.
XX
PN US5932556-A.
XX
PD 03-AUG-1999.
XX
PF 18-SEP-1995; 95US-0529878.
XX
PR 18-SEP-1995; 95US-0529878.
XX
PA (TAMR/) TAM R C.
XX
PI Tam RC;
XX
DR WPI; 1999-443609/37.
XX
PT Treatment of immune system-mediated diseases by inhibiting
PT expression of CD28, IL-2, gamma-interferon or IL-8
XX
PS Claim 5; Column 29; 45pp; English.
XX
CC The present invention describes a method for inhibiting the expression
CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method
CC comprises subcutaneous administration of an oligonucleotide (OGN).
CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the
CC method. The OGNs are used for the treatment of immune system-mediated
CC diseases. The present sequence represents a CD28 inhibiting
CC phosphorothioate oligonucleotide used in the exemplification of the
CC present invention.
XX
SQ Sequence 18 BP; 3 A; 0 C; 13 G; 2 T; 0 other;
Query Match 91.1%; Score 16.4; DB 20; Length 18;
Best Local Similarity 94.4%; Pred. NO. 1.4e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TTGGAGGGGGAGGTGGG 18
Db 1 TTGGAGGGGGAGGTGGG 18
RESULT 8
AAX99625
ID AAX99625 standard; DNA; 18 BP.
XX
AC AAX99625;
XX
DT 12-JUL-2000 (first entry)
XX
DE Nucleotide sequence of G-motif oligonucleotide GR1.
XX
KW G-motif oligonucleotide; vaccine; Toxoplasmosis; viral infection;
KW antigen presenting cell activation; natural killer cell; septic shock;
KW cytotoxic T-lymphocyte; inflammation; autoimmune disease;
KW rheumatoid arthritis; Crohn's disease; sarcoidosis; multiple sclerosis;
KW Kawasaki syndrome; graft-versus-host disease; transplant rejection;
KW helper T cell response 1-mediated disease; Lyme arthritis;
KW Streptococcal induced arthritis; chronic inflammatory bowel disease;
KW psoriasis vulgaris; experimental allergic encephalomyelitis;
KW insulin-dependent diabetes mellitus; bacterial infection;
KW parasitic infection; Leishmaniasis; spontaneous abortion; tumour; ss.
XX
OS Synthetic.
XX
PN WO200014217-A2.
XX
PD 16-MAR-2000.
XX
PF 03-SEP-1999; 99WO-EP06502.
XX
PR 03-SEP-1998; 98EP-0116652.
XX
PA (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.
XX
PI Wagner H, Lipford GB, Heeg K;
XX
DR WPI; 2000-256970/22.
XX
PT Compositions comprising G-motif oligonucleotides useful for treating
PT e.g. septic shock, rheumatoid arthritis, diabetes and human
PT immunodeficiency virus infections -
XX
PS Example 14; Page 32; 75pp; English.
XX
CC The present sequence represents a G-motif oligonucleotide of the
CC invention. The specification describes compositions comprising G-motif
CC oligonucleotides. The G-motif oligonucleotides inhibit activation of
CC antigen presenting cells by inhibiting the uptake of DNA by a cell, by
CC stimulating natural killer cells, or by co-stimulating cytotoxic
CC T-lymphocytes. The G-motif oligonucleotides may be used for the
CC productions of vaccines for treating septic shock, inflammation,
CC autoimmune diseases (e.g. rheumatoid arthritis, Crohn's disease,
CC sarcoidosis, multiple sclerosis, Kawasaki syndrome, graft-versus-host
CC disease and transplant rejection), helper T cell response 1-mediated
CC diseases (e.g. Streptococcal induced arthritis, Lyme arthritis, chronic
CC inflammatory bowel disease, psoriasis vulgaris, experimental allergic
```

CC encephalomyelitis, and insulin-dependent diabetes mellitus), bacterial  
CC infections, parasitic infections (e.g. Leishmaniasis or Toxoplasmosis),  
CC viral infections (e.g. Cytomegalovirus and human immunodeficiency virus  
CC (HIV)-infections), spontaneous abortions and tumours. They may also be  
CC used to induce proliferation of bone marrow cells, especially macrophage  
CC precursor cells.  
XX  
SQ Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;

Query Match 91.1%; Score 16.4; DB 21; Length 18;  
Best Local Similarity 94.4%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTGAGGGGGAGGTGGGG 18  
|||  
Db 1 TTGAGGGGGTGGTGGGG 18

RESULT 9  
AAZ99650/c  
ID AAZ99650 standard; DNA; 18 BP.

XX  
AC AAZ99650;

XX  
DT 12-JUL-2000 (first entry)

XX  
DE Nucleotide sequence of non-G-motif oligonucleotide GRP1comp.

XX G-motif oligonucleotide; vaccine; Toxoplasmosis; viral infection;  
KW antigen presenting cell activation; natural killer cell; septic shock;  
KW cytotoxic T-lymphocyte; inflammation; autoimmune disease;  
KW rheumatoid arthritis; Crohn's disease; sarcoidosis; multiple sclerosis;  
KW Kawasaki syndrome; graft-versus-host disease; transplant rejection;  
KW helper T cell response 1-mediated disease; Lyme arthritis;  
KW Streptococcal induced arthritis; chronic inflammatory bowel disease;  
KW psoriasis vulgaris; experimental allergic encephalomyelitis;  
KW insulin-dependent diabetes mellitus; bacterial infection;  
KW parasitic infection; leishmaniasis; spontaneous abortion; tumour; ss.

XX  
OS Synthetic.

XX  
PN WO200014217-A2.

XX  
PD 16-MAR-2000.

XX  
PF 03-SEP-1999; 99WO-EP06502.

XX  
PR 03-SEP-1998; 98EP-0116652.

XX  
PA (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.

XX  
PI Wagner H, Lipford GB, Heeg K;

XX  
DR WPI; 2000-256970/22.

XX  
PT Compositions comprising G-motif oligonucleotides useful for treating  
PT e.g. septic shock, rheumatoid arthritis, diabetes and human  
PT immunodeficiency virus infections -

XX  
PS Example 14; Page 32; 75pp; English.

XX  
CC The present sequence represents a non-G-motif oligonucleotide of the  
CC invention. The specification describes compositions comprising G-motif  
CC oligonucleotides. The G-motif oligonucleotides inhibit activation of  
CC antigen presenting cells by inhibiting the uptake of DNA by a cell, by  
CC stimulating natural killer cells, or by co-stimulating cytotoxic  
CC T-lymphocytes. The G-motif oligonucleotides may be used for the  
CC productions of vaccines for treating septic shock, inflammation,  
CC autoimmune diseases (e.g. rheumatoid arthritis, Crohn's disease,  
CC sarcoidosis, multiple sclerosis, Kawasaki syndrome, graft-versus-host  
CC disease and transplant rejection), helper T cell response 1-mediated  
CC diseases (e.g. Streptococcal induced arthritis, Lyme arthritis, chronic  
CC inflammatory bowel disease, psoriasis vulgaris, experimental allergic

CC encephalomyelitis, and insulin-dependent diabetes mellitus), bacterial  
CC infections, parasitic infections (e.g. Leishmaniasis or Toxoplasmosis),  
CC viral infections (e.g. Cytomegalovirus and human immunodeficiency virus  
CC (HIV)-infections), spontaneous abortions and tumours. They may also be  
CC used to induce proliferation of bone marrow cells, especially macrophage  
CC precursor cells.  
XX  
SQ Sequence 18 BP; 4 A; 13 C; 0 G; 1 T; 0 other;

Query Match 91.1%; Score 16.4; DB 21; Length 18;  
Best Local Similarity 94.4%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTGAGGGGGAGGTGGGG 18  
|||  
Db 18 TTGAGGGGGTGGTGGGG 1

RESULT 10  
AAT36197  
ID AAT36197 standard; DNA; 21 BP.

XX  
AC AAT36197;

XX  
DT 25-MAR-2003 (updated)

DT 15-APR-1997 (first entry)

XX  
DE Triplex forming oligo targetting CD28 5'-UTR (nt 58-78).

XX Reduction; T cell; CD28; gene expression; treatment; immune system;  
KW disorder; graft versus host disease; septic shock; viral disease;  
KW psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;  
KW multiple sclerosis; uveitis; rheumatoid arthritis; 5'-UTR;  
KW systemic lupus erythematosus; inflammatory bowel disease;  
KW triplex forming; oligonucleotide; 5'-untranslated region; ss

XX  
OS Synthetic.

XX  
PN WO9624380-A1.

XX  
PD 15-AUG-1996.

XX  
PF 05-FEB-1996; 96WO-US01507.

XX  
PR 09-FEB-1995; 95US-0387041.

XX  
PR 18-SEP-1995; 95US-0529878.

XX  
PR 09-FEB-1995; 95US-0387041.

XX  
PR 18-SEP-1995; 95US-0529878.

XX  
PA (ICNC ) ICN PHARM INC.

XX  
PI Tam RC;

XX  
DR WPI; 1996-384228/38.

XX  
PS Claim 10; Page 54; 77pp; English.

XX  
CC The present oligonucleotide reduces T cell CD28 gene expression,  
CC useful in the treatment of CD28 mediated diseases, particularly  
CC immune system disorders, e.g. graft versus host disease, septic  
CC shock, viral disease, psoriasis, type I diabetes mellitus,  
CC thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid  
CC arthritis, systemic lupus erythematosus, inflammatory bowel  
CC disease, etc.. Reducing CD28 expression may reduce the effects of  
CC antigenic stimulation of CD28 positive T cells, with a consequent  
CC reduction in cytokine release.  
CC (Updated on 25-MAR-2003 to correct PR field.)

XX  
SQ Sequence 21 BP; 1 A; 0 C; 16 G; 4 T; 0 other;

Query Match 91.1%; Score 16.4; DB 17; Length 21;  
Best Local Similarity 94.4%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTGGAGGGGGAGGTGGG 18  
|||||  
Db 4 TTGGAGGGGGTGGTGGG 21

## RESULT 11

AAX90329  
ID AAX90329 standard; DNA; 21 BP.

XX AC AAX90329;

DT 24-SEP-1999 (first entry)

XX CD28 inhibiting phosphorothioate oligonucleotide RT04S.

KW CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;  
KW immune system mediated disease; gamma-interferon; IL-8;  
XX phosphorothioate; ss.

OS Synthetic.

XX US5932556-A.

PD 03-AUG-1999.

XX 18-SEP-1995; 95US-0529878.

PR 18-SEP-1995; 95US-0529878.

XX (TAMR/) TAM R C.

PI Tam RC;

XX WPI; 1999-443609/37.

XX Treatment of immune system-mediated diseases by inhibiting  
PT expression of CD28, IL-2, gamma-interferon or IL-8

PS Example; Column 21; 45pp; English.

XX The present invention describes a method for inhibiting the expression  
CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method  
CC comprises subcutaneous administration of an oligonucleotide (OGN).  
CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the  
CC method. The OGNs are used for the treatment of immune system-mediated  
CC diseases. The present sequence represents a CD28 inhibiting  
CC phosphorothioate oligonucleotide used in the exemplification of the  
CC present invention.

SQ Sequence 21 BP; 1 A; 0 C; 16 G; 4 T; 0 other;

Query Match 91.1%; Score 16.4; DB 20; Length 21;  
Best Local Similarity 94.4%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTGGAGGGGGAGGTGGG 18  
|||||  
Db 4 TTGGAGGGGGTGGTGGG 21

## RESULT 12

AAX90291

ID AAX90291 standard; DNA; 21 BP.

XX AC AAX90291;

DT 24-SEP-1999 (first entry)

XX

DE CD28 inhibition oligonucleotide RT04.  
XX CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;  
KW immune system mediated disease; gamma-interferon; IL-8; ss.  
XX Synthetic.  
OS US5932556-A.  
XX 03-AUG-1999.  
PD 18-SEP-1995; 95US-0529878.  
XX 18-SEP-1995; 95US-0529878.  
XX (TAMR/) TAM R C.  
XX Tam RC;  
XX WPI; 1999-443609/37.  
DR Treatment of immune system-mediated diseases by inhibiting  
XX expression of CD28, IL-2, gamma-interferon or IL-8  
PT Claim 6; Column 29; 45pp; English.  
XX The present invention describes a method for inhibiting the expression  
CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method  
CC comprises subcutaneous administration of an oligonucleotide (OGN).  
CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the  
CC method. The OGNs are used for the treatment of immune system-mediated  
CC diseases.

XX Sequence 21 BP; 1 A; 0 C; 16 G; 4 T; 0 other;

Query Match 91.1%; Score 16.4; DB 20; Length 21;  
Best Local Similarity 94.4%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTGGAGGGGGAGGTGGG 18  
|||||  
Db 4 TTGGAGGGGGTGGTGGG 21

## RESULT 13

AAF16593

ID AAF16593 standard; DNA; 22 BP.

XX AC AAF16593;

DT 13-MAR-2001 (first entry)

XX Gastric acid production inhibiting oligonucleotide SEQ ID NO: 79.

KW Gastric acid disturbance; gastric reflux; gastritis; dyspepsia;  
KW stomach ulcer; duodenal ulcer; Helicobacter pylori; antisense;  
XX DNA-RNA hybrid; ss.

OS Synthetic.

XX WO200071164-A1.

PD 30-NOV-2000.

XX 24-MAY-2000; 2000WO-AU00498.

PR 24-MAY-1999; 99AU-0000510.

XX (TACH/) TACHAS G.

PI Tachas G;

XX WPI; 2001-025093/03.

XX Treating gastric acid disturbance by administering an oligonucleotide  
PT which modulates the activity of a polypeptide involved in gastric acid  
PT production or secretion -  
XX  
XX Example 3; Page 145; 164pp; English.  
XX  
CC The present invention provides oligonucleotides, and methods for their  
CC use, which are useful in modulating the action of proteins involved in  
CC gastric acid production. The target protein is preferably the histamine  
CC H2 receptor or one of the proteins which form part of the gastric proton  
CC pump. The sequences and methods of the invention are useful in the  
CC treatment of gastric reflux, gastritis, dyspepsia, stomach ulcers,  
CC duodenal ulcers and other gastric acid disturbances, most of which are  
CC caused by Helicobacter pylori.  
XX  
SQ Sequence 22 BP; 0 A; 0 C; 16 G; 3 T; 3 other;  
  
Query Match 82.2%; Score 14.8; DB 22; Length 22;  
Best Local Similarity 81.2%; Pred. NO. 5.8e+03;  
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 TGGAGGGGGAGGTGGG 17  
|||:|||||:|||||  
Db 2 TGGMGGGGGGMGGKGG 17  
  
RESULT 14  
AAF01954/c  
ID AAF01954 standard; DNA; 17 BP.  
XX  
AC AAF01954;  
XX  
DT 16-FEB-2001 (first entry)  
XX  
DE Hammerhead ribozyme substrate #249.  
XX  
KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;  
KW interferon alpha; ss.  
XX  
OS Homo sapiens.  
XX  
XX WO200061729-A2.  
PN  
XX 19-OCT-2000.  
PD  
XX 11-APR-2000; 2000WO-US09721.  
PF  
XX 12-APR-1999; 99US-0129390.  
PR  
XX (RIBO-) RIBOZYME PHARM INC.  
PA  
XX Blatt L, Zwick M, Pavco P, McSwiggen J;  
PI  
XX WPI; 2000-647423/62.  
DR  
XX  
XX Enzymatic and antisense nucleic acid inhibition of repressor genes,  
PT useful for producing e.g. granulocyte colony stimulating factor  
PT protein, interferon alpha and erythropoietin -  
XX  
XX Claim 37; Page 61; 164pp; English.  
PS  
XX The present invention relates to enzymatic and antisense nucleic acid  
CC molecules that act as inhibitors of the expression of repressor genes  
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA  
CC transcription factor gene, IRF-2 and/or the CAAT Displacement  
CC Protein (CDP). Inhibition of the repressors removes prevents  
CC inhibition (and consequently increases expression of) genes involved in  
CC the production of erythropoietin, granulocyte colony stimulating factor  
CC protein and interferon alpha.  
XX  
SQ Sequence 17 BP; 2 A; 12 C; 0 G; 3 T; 0 other;

Query Match 80.0%; Score 14.4; DB 21; Length 17;  
Best Local Similarity 93.8%; Pred. NO. 8.4e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 3 GGAGGGGAGGTGGG 18  
|||||:|||||  
Db 16 GGAGGGGTAGTGGG 1  
  
RESULT 15  
AAD12117  
ID AAD12117 standard; DNA; 20 BP.  
XX  
AC AAD12117;  
XX  
DT 25-SEP-2001 (first entry)  
XX  
DE Rat PTP1B antisense oligonucleotide (ISIS# 113721).  
XX  
KW Rat; PTP1B; protein phosphatase 1B inhibitor; antisense; gene therapy;  
KW infection; inflammation; tumour; prophylaxis; phosphorothioate; ss.  
XX  
OS Rattus norvegicus.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..20  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "Phosphorothioate backbone"  
FT modified\_base 1..5  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "Methoxyethyl residues"  
FT modified\_base 16..20  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "Methoxyethyl residues"  
FT modified\_base 4..5  
FT /\*tag= d  
FT /mod\_base= m5c  
FT modified\_base 19  
FT /\*tag= e  
FT /mod\_base= m5c  
XX  
PN US6261840-B1.  
XX  
XX 17-JUL-2001.  
PD  
XX 18-JAN-2000; 2000US-0487368.  
PF  
XX 18-JAN-2000; 2000US-0487368.  
PR  
XX (ISIS-) ISIS PHARM INC.  
PA  
XX Cowser LM, Wyatt J;  
PI  
XX WPI; 2001-432181/46.  
DR  
XX  
PT New antisense compounds capable of modulating expression of human  
PT protein phosphatase 1B, useful for diagnosis, prophylaxis and treatment  
PT of diseases associated with expression of protein phosphatase -  
XX  
PS Example 17; Column 51-52; 71pp; English.  
XX  
CC The invention is directed to antisense compounds, particularly  
CC oligonucleotides which are targeted to a DNA encoding protein  
CC phosphatase 1B (PTP1B) to modulate its expression. The antisense  
CC compounds are useful for diagnosis, prophylaxis and treatment of  
CC diseases associated with the expression of PTP1B, to prevent or  
CC delay infection, inflammation and tumour formation and as a  
CC research reagent. The PTP1B DNA is useful in gene therapy.  
CC  
CC The present sequence is an antisense oligonucleotide with a

CC phosphorothioate backbone. This oligo is targetted to rat  
CC PTP1B to inhibit its expression.

XX  
SQ Sequence 20 BP; 2 A; 3 C; 13 G; 2 T; 0 other;

Query Match 76.7%; Score 13.8; DB 22; Length 20;  
Best Local Similarity 88.2%; Pred. No. 1.4e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGGAGGGGGAGGTGGGG 18  
||| ||||| |||||  
Db 1 TGGCCGGGGAGGTGGGG 17

Search completed: October 27, 2003, 11:25:21  
Job time : 163 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 11:09:34 ; Search time 307.029 Seconds  
(without alignments)  
97.777 Million cell updates/sec

Title: US-09-331-204A-7  
Perfect score: 18  
Sequence: 1 ttggagggaggaggagg 18

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2231628 seqs, 833900706 residues

Total number of hits satisfying chosen parameters: 264402

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents NA New:\*

- 1: /cgn2\_6/ptodata/1/pna/PCT\_NEW\_COMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq:\*
- 3: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq:\*
- 4: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq:\*
- 6: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	17	94.4	19	1	PCT-US02-38216-47426 Sequence 47426, A
2	15	83.3	18	1	PCT-US02-38216-6227 Sequence 6227, Ap
3	14.8	82.2	22	1	PCT-US02-38216-18159 Sequence 18159, A
4	14.4	80.0	16	1	PCT-US02-38216-39032 Sequence 39032, A
5	14.4	80.0	17	1	PCT-US02-38216-38911 Sequence 38911, A
6	14.4	80.0	18	1	PCT-US02-38216-6229 Sequence 6229, Ap
7	14.4	80.0	18	1	PCT-US02-38216-39031 Sequence 39031, A
8	14.4	80.0	18	1	PCT-US02-38216-41647 Sequence 41647, A
9	14.4	80.0	19	1	PCT-US02-38216-38912 Sequence 38912, A
10	14.4	80.0	21	1	PCT-US03-11936A-126 Sequence 126, App
11	14	77.8	17	1	PCT-US02-38216-6220 Sequence 6220, Ap
12	14	77.8	17	1	PCT-US02-38216-38954 Sequence 38954, A
13	14	77.8	19	1	PCT-US02-38216-26652 Sequence 26652, A
14	13.8	76.7	17	1	PCT-US02-38216-18314 Sequence 18314, A
15	13.8	76.7	18	1	PCT-US02-38216-14763 Sequence 14763, A
16	13.8	76.7	19	1	PCT-US02-38216-18278 Sequence 18278, A
17	13.8	76.7	22	1	PCT-US02-38216-58271 Sequence 58271, A
18	13.4	74.4	16	1	PCT-US02-38216-39060 Sequence 39060, A
19	13.4	74.4	16	1	PCT-US02-38216-60967 Sequence 60967, A
20	13.4	74.4	16	1	PCT-US02-38216-61070 Sequence 61070, A
21	13.4	74.4	17	1	PCT-US02-38216-5920 Sequence 5920, Ap
22	13.4	74.4	17	1	PCT-US02-38216-18231 Sequence 18231, A
23	13.4	74.4	17	1	PCT-US02-38216-38987 Sequence 38987, A
24	13.4	74.4	17	1	PCT-US02-38216-48877 Sequence 48877, A
25	13.4	74.4	17	1	PCT-US02-38216-58278 Sequence 58278, A
26	13.4	74.4	17	1	PCT-US02-38216-58297 Sequence 58297, A

27	13.4	74.4	17	1	PCT-US02-38216-60884 Sequence 60884, A
28	13.4	74.4	18	1	PCT-US02-38216-18290 Sequence 18290, A
c 29	13.4	74.4	18	1	PCT-US02-38216-25803 Sequence 25803, A
30	13.4	74.4	18	1	PCT-US02-38216-38927 Sequence 38927, A
31	13.4	74.4	18	1	PCT-US02-38216-39001 Sequence 39001, A
32	13.4	74.4	18	1	PCT-US02-38216-39023 Sequence 39023, A
33	13.4	74.4	18	1	PCT-US02-38216-41601 Sequence 41601, A
c 34	13.4	74.4	19	1	PCT-US02-38216-6296 Sequence 6296, Ap
c 35	13.4	74.4	19	1	PCT-US02-38216-26644 Sequence 26644, A
36	13.4	74.4	19	1	PCT-US02-38216-38922 Sequence 38922, A
37	13.4	74.4	19	1	PCT-US02-38216-60003 Sequence 60003, A
38	13.4	74.4	20	1	PCT-US02-38216-39088 Sequence 39088, A
39	13.4	74.4	20	1	PCT-US02-38216-52911 Sequence 52911, A
40	13.4	74.4	21	1	PCT-US02-38216-38986 Sequence 38986, A
41	13.4	74.4	22	1	PCT-US02-38216-27400 Sequence 27400, A
42	13.2	73.3	18	1	PCT-US02-38216-18060 Sequence 18060, A
43	13.2	73.3	20	1	PCT-US02-38216-992 Sequence 992, App
c 44	13.2	73.3	22	1	PCT-US02-38216-26562 Sequence 26562, A
45	13	72.2	15	1	PCT-US02-38216-61080 Sequence 61080, A

ALIGNMENTS

RESULT 1  
PCT-US02-38216-47426  
; Sequence 47426, Application PC/TUS0238216  
; GENERAL INFORMATION:  
; APPLICANT: Rosetta Genomics LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
; TITLE OF INVENTION: GENES AND USES THEREOF  
; FILE REFERENCE: 55002  
; CURRENT APPLICATION NUMBER: PCT/US02/38216  
; CURRENT FILING DATE: 2002-11-12  
; NUMBER OF SEQ ID NOS: 86841  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 47426  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US02-38216-47426

Query Match 94.4%; Score 17; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGAGGGGAGGAGGGG 18  
| | | | | | | | | | | | | | | | | |  
Db 3 TGGAGGGGAGGAGGGG 19

RESULT 2  
PCT-US02-38216-6227/c  
; Sequence 6227, Application PC/TUS0238216  
; GENERAL INFORMATION:  
; APPLICANT: Rosetta Genomics LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
; TITLE OF INVENTION: GENES AND USES THEREOF  
; FILE REFERENCE: 55002  
; CURRENT APPLICATION NUMBER: PCT/US02/38216  
; CURRENT FILING DATE: 2002-11-12  
; NUMBER OF SEQ ID NOS: 86841  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 6227  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US02-38216-6227

Query Match 83.3%; Score 15; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 9.1e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



; TITLE OF INVENTION: GENES AND USES THEREOF  
; FILE REFERENCE: 55002  
; CURRENT APPLICATION NUMBER: PCT/US02/38216  
; CURRENT FILING DATE: 2002-11-12  
; NUMBER OF SEQ ID NOS: 86841  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 41647  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US02-38216-41647

Query Match 80.0%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 1.5e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGGGGAGGAGGGG 18  
|||||  
Db 1 GGAGGGGTGGAGGGG 16

RESULT 9  
PCT-US02-38216-38912  
; Sequence 38912, Application PC/TUS0238216  
; GENERAL INFORMATION:

; APPLICANT: Rosetta Genomics LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
; TITLE OF INVENTION: GENES AND USES THEREOF

; FILE REFERENCE: 55002  
; CURRENT APPLICATION NUMBER: PCT/US02/38216  
; CURRENT FILING DATE: 2002-11-12  
; NUMBER OF SEQ ID NOS: 86841

; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 38912  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US02-38216-38912

Query Match 80.0%; Score 14.4; DB 1; Length 19;  
Best Local Similarity 93.8%; Pred. No. 1.5e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGGGGAGGAGGGG 18  
|||||  
Db 3 GGAGGAGGAGGAGGGG 18

RESULT 10  
PCT-US03-11936A-126/c  
; Sequence 126, Application PC/TUS0311936A  
; GENERAL INFORMATION:

; APPLICANT: Crea, Roberto  
; TITLE OF INVENTION: UNIVERSAL LIBRARIES FOR IMMUNOGLOBULINS  
; FILE REFERENCE: 1551.2001003

; CURRENT APPLICATION NUMBER: PCT/US03/11936A  
; CURRENT FILING DATE: 2003-04-16  
; PRIOR APPLICATION NUMBER: 60/373,558  
; PRIOR FILING DATE: 2002-04-17

; NUMBER OF SEQ ID NOS: 423  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 126  
; LENGTH: 21  
; TYPE: DNA

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: oligonucleotide  
PCT-US03-11936A-126

Query Match 80.0%; Score 14.4; DB 1; Length 21;  
Best Local Similarity 93.8%; Pred. No. 1.5e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGGGGAGGAGGGG 18  
|||||  
Db 17 GGAGGGGGAGGAGGAG 2

RESULT 11  
PCT-US02-38216-6220/c  
; Sequence 6220, Application PC/TUS0238216  
; GENERAL INFORMATION:  
; APPLICANT: Rosetta Genomics LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
; TITLE OF INVENTION: GENES AND USES THEREOF  
; FILE REFERENCE: 55002  
; CURRENT APPLICATION NUMBER: PCT/US02/38216  
; CURRENT FILING DATE: 2002-11-12  
; NUMBER OF SEQ ID NOS: 86841

; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 6220  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US02-38216-6220

Query Match 77.8%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.1e+04;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGAGGGGGAGGAGG 16  
|||||  
Db 14 GGAGGGGGAGGAGG 1

RESULT 12  
PCT-US02-38216-38954  
; Sequence 38954, Application PC/TUS0238216  
; GENERAL INFORMATION:

; APPLICANT: Rosetta Genomics LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
; TITLE OF INVENTION: GENES AND USES THEREOF

; FILE REFERENCE: 55002  
; CURRENT APPLICATION NUMBER: PCT/US02/38216  
; CURRENT FILING DATE: 2002-11-12  
; NUMBER OF SEQ ID NOS: 86841

; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 38954  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US02-38216-38954

Query Match 77.8%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.1e+04;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGGGGGAGGAGGG 17  
|||||  
Db 2 GAGGGGGAGGAGGG 15

RESULT 13  
PCT-US02-38216-26652/c  
; Sequence 26652, Application PC/TUS0238216  
; GENERAL INFORMATION:

; APPLICANT: Rosetta Genomics LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
; TITLE OF INVENTION: GENES AND USES THEREOF

; FILE REFERENCE: 55002  
; CURRENT APPLICATION NUMBER: PCT/US02/38216  
; CURRENT FILING DATE: 2002-11-12  
; NUMBER OF SEQ ID NOS: 86841

; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 26652  
; LENGTH: 19



```
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-26652

Query Match      77.8%; Score 14; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 AGGGGAGGAGGGG 18
      |||||
Db      14 AGGGGAGGAGGGG 1

RESULT 14
PCT-US02-38216-18314
; Sequence 18314, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18314
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-18314

Query Match      76.7%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 TGGAGGGGAGGAGGGG 18
      |||||
Db      1 TGGAGAGGGAAGAGGGG 17

RESULT 15
PCT-US02-38216-14763
; Sequence 14763, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14763
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-14763

Query Match      76.7%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2.4e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TTGGAGGGGAGGAGGG 17
      |||||
Db      1 TGGGAGGGAGGAGGG 17

Search completed: October 27, 2003, 18:22:55
Job time : 307.029 secs
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: October 27, 2003, 10:32:29 ; Search time 1581.77 Seconds  
(without alignments)  
276.576 Million cell updates/sec

Title: US-09-331-204A-7  
Perfect score: 18  
Sequence: 1 ttggagggggaggagggg 18  
Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 22781392 seqs, 12152238056 residues  
Total number of hits satisfying chosen parameters: 11152  
Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :				EST:*	
1:	em_estba:*			1:	em_estba:*
2:	em_esthum:*			2:	em_esthum:*
3:	em_estin:*			3:	em_estin:*
4:	em_estmu:*			4:	em_estmu:*
5:	em_estov:*			5:	em_estov:*
6:	em_estpl:*			6:	em_estpl:*
7:	em_estro:*			7:	em_estro:*
8:	em_htc:*			8:	em_htc:*
9:	gb_est1:*			9:	gb_est1:*
10:	gb_est2:*			10:	gb_est2:*
11:	gb_htc:*			11:	gb_htc:*
12:	gb_est3:*			12:	gb_est3:*
13:	gb_est4:*			13:	gb_est4:*
14:	gb_est5:*			14:	gb_est5:*
15:	em_estfun:*			15:	em_estfun:*
16:	em_estom:*			16:	em_estom:*
17:	em_gss_hum:*			17:	em_gss_hum:*
18:	em_gss_inv:*			18:	em_gss_inv:*
19:	em_gss_pln:*			19:	em_gss_pln:*
20:	em_gss_vrt:*			20:	em_gss_vrt:*
21:	em_gss_fun:*			21:	em_gss_fun:*
22:	em_gss_mam:*			22:	em_gss_mam:*
23:	em_gss_mus:*			23:	em_gss_mus:*
24:	em_gss_pro:*			24:	em_gss_pro:*
25:	em_gss_rod:*			25:	em_gss_rod:*
26:	em_gss_phg:*			26:	em_gss_phg:*
27:	em_gss_vrl:*			27:	em_gss_vrl:*
28:	gb_gss1:*			28:	gb_gss1:*
29:	gb_gss2:*			29:	gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	13.8	76.7	19	9 AI251781	AI251781 qu76g01.x
2	13.8	76.7	22	28 AZ876923	AZ876923 2M0192D07
3	13.4	74.4	21	9 AU254493	AU254493 AU254493
C 4	13.4	74.4	22	9 AI582080	AI582080 ar96b07.x

5	13	72.2	16	9	AA968729	AA968729 or69h11.s
6	12.8	71.1	19	28	AZ345792	AZ345792 1M0080G12
C 7	12.8	71.1	19	28	AZ447248	AZ447248 1M0244H23
C 8	12.8	71.1	19	28	AZ579189	AZ579189 1M0363I12
C 9	12.8	71.1	19	28	AZ760597	AZ760597 1M0554N21
10	12.8	71.1	19	28	AZ775540	AZ775540 2M0008H15
C 11	12.8	71.1	19	28	AZ783420	AZ783420 2M0025D07
C 12	12.8	71.1	20	28	AZ512326	AZ512326 1M0357I18
C 13	12.8	71.1	20	28	AZ645269	AZ645269 1M0510B10
C 14	12.8	71.1	20	28	AZ659755	AZ659755 1M0537F22
C 15	12.8	71.1	20	28	AZ772707	AZ772707 1M0583L18
C 16	12.8	71.1	20	28	AZ853126	AZ853126 2M0156G10
C 17	12.8	71.1	20	28	AZ969440	AZ969440 2M0242O12
18	12.8	71.1	21	28	AZ321746	AZ321746 1M0042N20
C 19	12.8	71.1	21	28	AZ476392	AZ476392 1M0295F12
C 20	12.8	71.1	21	28	AZ583408	AZ583408 1M0378N23
C 21	12.8	71.1	21	28	AZ653464	AZ653464 1M0527G11
22	12.8	71.1	21	28	AZ849030	AZ849030 2M0150I17
C 23	12.8	71.1	21	28	AZ871715	AZ871715 2M0184B13
24	12.8	71.1	22	28	AZ331988	AZ331988 1M0060B11
C 25	12.8	71.1	22	28	AZ447246	AZ447246 1M0244E23
C 26	12.8	71.1	22	28	AZ607348	AZ607348 1M0429D18
C 27	12.8	71.1	22	28	AZ645874	AZ645874 1M0511C07
C 28	12.8	71.1	22	28	AZ871408	AZ871408 2M0184E16
29	12.4	68.9	19	9	AA918795	AA918795 ol69c05.s
30	12.4	68.9	19	9	AI696833	AI696833 wc74e09.x
31	12.4	68.9	22	9	AA996014	AA996014 os26d08.s
32	12.2	67.8	18	13	BQ901245	BQ901245 hasp0002xj
33	12.2	67.8	19	28	AZ324165	AZ324165 1M0046C06
C 34	12.2	67.8	20	28	AZ666896	AZ666896 1M0549A24
C 35	12.2	67.8	21	28	AZ387199	AZ387199 1M0146P20
36	12.2	67.8	21	28	AZ967090	AZ967090 2M0237D24
37	12.2	67.8	22	9	AA911600	AA911600 od90d06.s
C 38	12.2	67.8	22	9	AI568336	AI568336 tn68h08.x
C 39	12.2	67.8	22	28	AZ766712	AZ766712 1M0564A03
C 40	12	66.7	16	9	AI075064	AI075064 ou61g11.x
C 41	11.8	65.6	19	9	AI758301	AI758301 ty06a07.x
42	11.8	65.6	20	28	AZ579495	AZ579495 1M0367C13
43	11.8	65.6	22	9	AI434548	AI434548 ti49d05.x
44	11.8	65.6	22	9	AI735392	AI735392 at10e10.x
45	11.8	65.6	22	13	BQ585098	BQ585098 E011826-0

ALIGNMENTS

RESULT 1	AI251781	19 bp	linear	EST 05-NOV-1998
AI251781/c	qu76g01.x1	NCI CGAP Brn35	Homo sapiens	CDNA clone IMAGE:1978032 3'
LOCUS	similar to	TR:Q39949	Q39949	HYDROXYPROLINE-RICH PROTEIN. ? , mRNA
DEFINITION	sequence.			
ACCESSION	AI251781			
VERSION	AI251781.1	GI:3848310		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	1 (bases 1 to 19)			
TITLE	NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGP), Tumor Gene Index			
JOURNAL	Unpublished			
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov unknown library type Trace considered overall poor quality Seq primer: -40UP from Gibco High quality sequence stop: 1. Location/Qualifiers 1. 19			
FEATURES				
source				

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1978032"  
/tissue\_type="tumor, 5 pooled (see description)"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP\_Brn35"  
/note="Organ: brain; Vector: pCMV-SPORT6; Site:1: SalI;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dr.  
Average insert size 1.33 kb. Tumor types include:  
meningioma, oligodendroglioma, astrocytoma (grade II),  
medulloblastoma, astrocytoma (grade IV). Life Technologies  
catalog #: 11544-012"  
4 a 14 c 0 g 1 t  
BASE COUNT  
ORIGIN  
Query Match 76.7%; Score 13.8; DB 9; Length 19;  
Best Local Similarity 88.2%; Pred. No. 4.8e+05;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 TTGGAGGGGGAGGAGGG 17  
Db 17 TTGGGGGGGAGGGGGG 1  
RESULT 2  
AZ876923  
LOCUS 22 bp DNA linear GSS 21-FEB-2001  
DEFINITION 2M0192D07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0192D07 F, genomic survey sequence.  
ACCESSION AZ876923  
VERSION AZ876923.1 GI:13088239  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 22)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.  
and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0192 row: D column: 07  
Seq primer: CGTTGTAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 22.  
FEATURES  
source  
1..22  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0192D07"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."  
4 a 1 c 15 g 2 t  
BASE COUNT  
ORIGIN  
Query Match 76.7%; Score 13.8; DB 28; Length 22;  
Best Local Similarity 88.2%; Pred. No. 4.8e+05;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 TTGGAGGGGGAGGAGGG 17  
Db 2 TTGGAGGGAGGAGGGGG 18  
RESULT 3  
AU254493  
LOCUS 21 bp mRNA linear EST 25-APR-2002  
DEFINITION AU254493 3'-directed mouse cDNA library Mus musculus cDNA clone  
BED0002246 3', mRNA sequence.  
ACCESSION AU254493  
VERSION AU254493.1 GI:20316325  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 21)  
AUTHORS Kato,K. and Matoba,R.  
TITLE Generation of expressed sequence tags from mouse brain  
JOURNAL Unpublished  
COMMENT Contact: Kikuya Kato  
Graduate School of Biological Sciences  
Nara Institute of Science and Technology  
8916-5 Takayama, Ikoma, Nara 630-0101, Japan  
Tel: 81-743-72-5581  
Fax: 81-743-72-5589  
Email: kkatc@bs.aist-nara.ac.jp.  
URL:http://love2.aist-nara.ac.jp/BED/index.html.  
FEATURES  
source  
1..21  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="BED0002246"  
/tissue\_type="brain"  
/clone\_lib="3'-directed mouse cDNA library"  
3 a 2 c 14 g 2 t  
BASE COUNT  
ORIGIN  
Query Match 74.4%; Score 13.4; DB 9; Length 21;  
Best Local Similarity 93.3%; Pred. No. 6.3e+05;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 4 GAGGGGGAGGAGGGGG 18  
Db 7 GTGGGGGAGGAGGGGG 21  
RESULT 4  
AI582080/c  
LOCUS AI582080 22 bp mRNA linear EST 06-APR-1999

DEFINITION ar96b07.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173429 3' similar to SW:FOR4\_MOUSE Q05859 FORMIN 4 ; contains element MSR1 repetitive element ; , mRNA sequence.

ACCESSION AI582080

VERSION AI582080.1 GI:4567977

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 22)

Hillier,L., Alian,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le.N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.

TITLE WashU-NCI human EST Project

JOURNAL Unpublished

COMMENT Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality Possible reversed clone: similarity on wrong strand Seq primer: -40UP from Gibco High quality sequence stop: 1. Location/Qualifiers 1. .22 /organism="Homo sapiens" /mol\_type="mRNA" /db\_xref="taxon:9606" /clone="IMAGE:2173429" /sex="male" /dev\_stage="adult, age 25" /lab\_host="DH10B (phage resistant)" /clone\_lib="Barstead colon HPLRB7" /note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: EcoRI; Site 2: NotI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTAGCAATCTGAGTGGAGCGCGCCCTTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors [5' AATTCAGTAGTAAT 3' and 5' ATTACTAGTG 3'], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead."

BASE COUNT 1 a 16 c 0 g 3 t 2 others

ORIGIN

Query Match 74.4%; Score 13.4; DB 9; Length 22; Best Local Similarity 87.5%; Pred. No. 6.3e+05; Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGGGAGGAGGGG 18

Db 18 GGGGGGGGAGGGGGGG 3

RESULT 5

LOCUS AA968729

DEFINITION AA968729 16 bp mRNA linear EST 27-AUG-1998 or69n11.s1 NCI CGAP GC3 Homo sapiens cDNA clone IMAGE:1601157 3' similar to SW:PRPE\_HUMAN P02811 BASIC PROLINE-RICH PEPTIDE P-E ;contains element MSR1 repetitive element ; , mRNA sequence.

ACCESSION AA968729

VERSION AA968729.1 GI:3143909

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 16)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality Insert Length: 514 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 1. Location/Qualifiers 1. .16 /organism="Homo sapiens" /mol\_type="mRNA" /db\_xref="taxon:9606" /clone="IMAGE:1601157" /tissue\_type="pooled germ cell tumors" /lab\_host="DH10B" /clone\_lib="NCI\_CGAP GC3" /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 2 a 1 c 13 g 0 t

ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 16; Best Local Similarity 100.0%; Pred. No. 8.5e+05; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGGGAGGAGGGG 18

Db 3 GGGGAGGAGGGG 15

RESULT 6

LOCUS AZ345792

DEFINITION AZ345792 19 bp DNA linear GSS 29-SEP-2000 IM0080G12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0080G12 R, genomic survey sequence.

ACCESSION AZ345792

VERSION AZ345792.1 GI:10425029

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS 1 (bases 1 to 19)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished

COMMENT Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0080 row: G column: 12  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.

FEATURES  
source

Location/Qualifiers  
1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0080G12"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 1 a 1 c 17 g 0 t  
ORIGIN

Query Match 71.1%; Score 12.8; DB 28; Length 19;  
Best Local Similarity 87.5%; Pred. No. 9.7e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGGAGGAGGGG 18  
||| ||||| |||||  
Db 2 GGGGGGGAGGAGGGG 17

RESULT 7  
AZ447248/c  
LOCUS  
DEFINITION 1M0244H23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0244H23 F, genomic survey sequence.

ACCESSION AZ447248  
VERSION GI:10599044  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

Unpublished  
JOURNAL  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0244 row: H column: 23  
Seq primer: CGTTGTAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.

FEATURES  
source

Location/Qualifiers  
1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0244H23"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 18 c 0 g 1 t  
ORIGIN

Query Match 71.1%; Score 12.8; DB 28; Length 19;  
Best Local Similarity 87.5%; Pred. No. 9.7e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGGAGGAGGGG 18  
||| ||||| |||||  
Db 16 GGGGGGGAGGAGGGG 1

RESULT 8  
AZ579189/c

LOCUS  
DEFINITION 1M0363I12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0363I12 F, genomic survey sequence.

ACCESSION AZ579189  
VERSION GI:11693534  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

Unpublished  
JOURNAL  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah

University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0363 row: 1 column: 12  
Seq primer: CGTTGTAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.

FEATURES  
source

Location/Qualifiers  
1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0363I12"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 0 a 16 c 0 g 3 t  
ORIGIN

Query Match 71.1%; Score 12.8; DB 28; Length 19;  
Best Local Similarity 87.5%; Pred. No. 9.7e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGGAGGAGGGG 18  
|||||||  
Db 16 GGAGGGGGAGGAGGGG 1

RESULT 9

AZ760597/c  
LOCUS  
DEFINITION  
AZ760597  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished  
Contact: Robert B. Weiss

AZ760597  
iM0554N21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0554N21 F, genomic survey sequence.

AZ760597.1 GI:12868613  
GSS.

Mus musculus (house mouse)  
Mus musculus

REFERENCE  
AUTHORS

1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished  
Contact: Robert B. Weiss

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished  
Contact: Robert B. Weiss

JOURNAL  
COMMENT

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished  
Contact: Robert B. Weiss

University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0554 row: N column: 21  
Seq primer: CGTTGTAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.

FEATURES  
source

Location/Qualifiers  
1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0554N21"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 0 a 18 c 0 g 1 t  
ORIGIN

Query Match 71.1%; Score 12.8; DB 28; Length 19;  
Best Local Similarity 87.5%; Pred. No. 9.7e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGGAGGAGGGG 18  
|||||||  
Db 18 GGAGGGGGGGGGGGG 3

RESULT 10

AZ775540  
LOCUS  
DEFINITION  
AZ775540  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished

AZ775540  
2M0008H15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0008H15 F, genomic survey sequence.

AZ775540.1 GI:12902183  
GSS.

Mus musculus (house mouse)  
Mus musculus

REFERENCE  
AUTHORS

1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished

JOURNAL

Unpublished





JOURNAL COMMENT

plasmid inserts  
Unpublished  
Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0357 row: I column: 18  
Seq primer: CACACAGGAACACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.

FEATURES

1. .20  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0357I18"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWP42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

0 a 18 c 0 g 2 t

ORIGIN

Query Match 71.1%; Score 12.8; DB 28; Length 20;  
Best Local Similarity 87.5%; Pred. No. 9.7e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY

3 GGAGGGGGGAGGGGG 18  
|||||

Db

18 GGAGGGGGGGGGGGG 3  
|||||

RESULT 13

AZ645269/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

AZ645269

1M0510B10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0510B10 R, genomic survey sequence.

AZ645269

1 GI:11774602

GSS.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

JOURNAL COMMENT

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished  
Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0510 row: B column: 10  
Seq primer: CACACAGGAACACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.

FEATURES

1. .20  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0510B10"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWP42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

0 a 19 c 0 g 1 t

ORIGIN

Query Match 71.1%; Score 12.8; DB 28; Length 20;  
Best Local Similarity 87.5%; Pred. No. 9.7e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY

3 GGAGGGGGGAGGGGG 18  
|||||

Db

17 GGAGGGGGGGGGGGG 2  
|||||

RESULT 14

AZ659755/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

AZ659755

1M0537F22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0537F22 F, genomic survey sequence.

AZ659755

1 GI:11796901

GSS.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.



TITLE  
JOURNAL  
COMMENT

and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0537 row: F column: 22  
Seq primer: CGTTGTAACACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 20.

FEATURES  
source

Location/Qualifiers  
1. .20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUC1M0537F22"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 0 a 18 c 0 g 2 t  
ORIGIN

Query Match 71.1%; Score 12.8; DB 28; Length 20;  
Best Local Similarity 87.5%; Pred. No. 9.7e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGGGAGGGGG 18  
|||||  
Db 20 GGAGGGGGGGGGGG 5

RESULT 15  
AZ772707/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS

AZ772707  
1M0583L18R Mouse 10kb plasmid UUC1M library Mus musculus genomic  
clone UUC1M0583L18 R, genomic survey sequence.  
AZ772707  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 20)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly

TITLE  
JOURNAL  
COMMENT

M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0583 row: L column: 18  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.

FEATURES  
source

Location/Qualifiers  
1. .20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUC1M0583L18"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 0 a 19 c 0 g 1 t  
ORIGIN

Query Match 71.1%; Score 12.8; DB 28; Length 20;  
Best Local Similarity 87.5%; Pred. No. 9.7e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGGGAGGGGG 18  
|||||  
Db 19 GGAGGGGGGAGGGGG 4

Search completed: October 27, 2003, 13:59:27  
Job time : 1582.77 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:34 ; Search time 41.3143 Seconds  
(without alignments)  
192.304 Million cell updates/sec

Title: US-09-331-204A-7

Perfect score: 18

Sequence: 1 ttggagggggaggagggg 18

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 376294

Minimum DB seq length: 0

Maximum DB seq length: 22

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:\*

- 1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*
- 2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*
- 3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*
- 4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*
- 5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*
- 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	15.4	85.6	21	3	US-09-092-077-45
2	14.8	82.2	18	2	US-08-529-878B-3
3	14.8	82.2	18	2	US-08-529-878B-44
4	14.8	82.2	21	2	US-08-529-878B-4
5	14.8	82.2	21	2	US-08-529-878B-45
6	14.4	80.0	17	2	US-08-173-489C-127
7	13.8	76.7	20	4	US-09-780-173A-93
8	13.4	74.4	20	4	US-09-661-753-30
9	12.8	71.1	17	4	US-09-495-140-26
10	12.8	71.1	18	3	US-09-344-579-9
11	12.8	71.1	20	3	US-09-490-692-153
12	12.8	71.1	21	2	US-08-256-426B-282
13	12.8	71.1	21	2	US-08-863-639A-41
14	12.8	71.1	21	2	US-08-863-639A-53
15	12.8	71.1	21	2	US-08-863-639A-59
16	12.8	71.1	21	2	US-08-863-639A-64
17	12.8	71.1	21	2	US-08-863-639A-70
18	12.8	71.1	21	2	US-08-863-639A-83
19	12.8	71.1	21	3	US-08-486-343A-5
20	12.8	71.1	21	5	PCT-US95-07349-5
21	12.4	68.9	22	1	US-08-398-613A-51
22	12.4	68.9	22	1	US-08-398-613A-54
23	12.4	68.9	22	1	US-08-398-612A-51
24	12.4	68.9	22	1	US-08-398-612A-54
25	12.4	68.9	22	1	US-08-398-611A-51
26	12.4	68.9	22	1	US-08-398-611A-54
27	12.4	68.9	22	1	US-08-396-851A-51

28	12.4	68.9	22	1	US-08-396-851A-54	Sequence 54, Appl
29	12.4	68.9	22	2	US-08-491-334A-51	Sequence 51, Appl
30	12.4	68.9	22	2	US-08-491-334A-54	Sequence 54, Appl
31	12.4	68.9	22	3	US-09-027-449-38	Sequence 38, Appl
32	12.4	68.9	22	3	US-08-804-444A-38	Sequence 38, Appl
33	12.4	68.9	22	3	US-09-026-985-38	Sequence 38, Appl
34	12.4	68.9	22	4	US-09-121-952A-38	Sequence 38, Appl
35	12.4	68.9	22	4	US-09-234-340A-38	Sequence 38, Appl
36	12.4	68.9	22	6	5256545-40	Patent No. 5256545
37	12.2	67.8	19	1	US-08-486-913-2	Sequence 2, Appl
38	12.2	67.8	19	2	US-08-486-535-2	Sequence 2, Appl
39	12.2	67.8	19	2	US-08-300-484-2	Sequence 2, Appl
40	12.2	67.8	19	3	US-08-486-885-2	Sequence 2, Appl
41	12.2	67.8	19	3	US-08-486-536-2	Sequence 2, Appl
42	12.2	67.8	19	5	PCT-US95-11234-2	Sequence 2, Appl
43	12.2	67.8	20	1	US-08-486-913-3	Sequence 3, Appl
44	12.2	67.8	20	2	US-08-486-535-3	Sequence 3, Appl
45	12.2	67.8	20	2	US-08-300-484-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1  
US-09-092-077-45  
; Sequence 45, Application US/09092077  
; Patent No. 6194142  
; GENERAL INFORMATION:  
; APPLICANT: Moncany, Maurice  
; APPLICANT: Montagnier, Luc  
; TITLE OF INVENTION: Nucleotide Sequences Derived From The  
; TITLE OF INVENTION: Genome Of Retroviruses Of The HIV-1, HIV-2 And SIV Type,  
; TITLE OF INVENTION: And Their Uses In Particular For The Amplification Of The  
; TITLE OF INVENTION: Genomes Of These Retroviruses And For The In Vitro Diagnosis  
; TITLE OF INVENTION: Of The Diseases Due To Those Viruses  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESSEE: Dunner  
; STREET: 1300 I Street, N.W., Suite 700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/092,077  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/472,928  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: US 08/160,465  
; FILING DATE: 02-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 8912371  
; FILING DATE: 20-SEP-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 8907354  
; FILING DATE: 06-FEB-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meyers, Kenneth J.  
; REGISTRATION NUMBER: 25,146  
; REFERENCE/DOCKET NUMBER: 02356.0062-02000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)408-4000  
; TELEFAX: (202)408-4400  
; INFORMATION FOR SEQ ID NO: 45:  
; SEQUENCE CHARACTERISTICS:

LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-092-077-45

Query Match  
Best Local Similarity 85.6%; Score 15.4; DB 3; Length 21;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTGAGGGGGAGGAGGGG 18  
Db 3 TGGAGGGGGAGGAGGAG 19

RESULT 2  
US-08-529-878B-3  
Sequence 3, Application US/08529878B  
Patent No. 5932556  
GENERAL INFORMATION:  
APPLICANT: Tam, Robert C.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
REGULATION OF CD28 EXPRESSION  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Crockett & Fish  
STREET: 3000 S. Augusta Court  
CITY: La Habra  
STATE: California  
COUNTRY: United States of America  
ZIP: 90631  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/529,878B  
FILING DATE: 13-SEP-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Fish, Robert D.  
REGISTRATION NUMBER: 33,880  
REFERENCE/DOCKET NUMBER: 213/003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 714-525-3433  
TELEFAX: 714-525-3303  
TELEX:

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
US-08-529-878B-3

Query Match  
Best Local Similarity 82.2%; Score 14.8; DB 2; Length 18;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGAGGGGGAGGAGGGG 18  
Db 1 TTGAGGGGGTGTGGGG 18

RESULT 3  
US-08-529-878B-4  
Sequence 44, Application US/08529878B  
Patent No. 5932556  
GENERAL INFORMATION:  
APPLICANT: Tam, Robert C.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
REGULATION OF CD28 EXPRESSION  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Crockett & Fish  
STREET: 3000 S. Augusta Court  
CITY: La Habra  
STATE: California  
COUNTRY: United States of America  
ZIP: 90631  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/529,878B  
FILING DATE: 13-SEP-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Fish, Robert D.  
REGISTRATION NUMBER: 33,880  
REFERENCE/DOCKET NUMBER: 213/003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 714-525-3433  
TELEFAX: 714-525-3303  
TELEX:

INFORMATION FOR SEQ ID NO: 44:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
US-08-529-878B-44

Query Match  
Best Local Similarity 82.2%; Score 14.8; DB 2; Length 18;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGAGGGGGAGGAGGGG 18  
Db 1 TTGAGGGGGTGTGGGG 18

RESULT 4  
US-08-529-878B-4  
Sequence 4, Application US/08529878B  
Patent No. 5932556  
GENERAL INFORMATION:  
APPLICANT: Tam, Robert C.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
REGULATION OF CD28 EXPRESSION  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Crockett & Fish  
STREET: 3000 S. Augusta Court  
CITY: La Habra  
STATE: California  
COUNTRY: United States of America  
ZIP: 90631  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/529,878B  
FILING DATE: 13-SEP-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Fish, Robert D.  
REGISTRATION NUMBER: 33,880

REFERENCE/DOCKET NUMBER: 213/003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 714-525-3433  
TELEFAX: 714-525-3303  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
US-08-529-878B-4

Query Match 82.2%; Score 14.8; DB 2; Length 21;  
Best Local Similarity 88.9%; Pred. No. 8.2e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGGAGGAGGGG 18  
Db 4 TTGGAGGGGGTGTGGGG 21

RESULT 5  
US-08-529-878B-45  
Sequence 45, Application US/08529878B  
Patent No. 5932556  
GENERAL INFORMATION:  
APPLICANT: Tam, Robert C.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Crockett & Fish  
STREET: 3000 S. Augusta Court  
CITY: La Habra  
STATE: California  
COUNTRY: United States of America  
ZIP: 90631

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/529,878B  
FILING DATE: 13-SEP-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Fish, Robert D.  
REGISTRATION NUMBER: 33,880  
REFERENCE/DOCKET NUMBER: 213/003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 714-525-3433  
TELEFAX: 714-525-3303  
TELEX:

INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
US-08-529-878B-45

Query Match 82.2%; Score 14.8; DB 2; Length 21;  
Best Local Similarity 88.9%; Pred. No. 8.2e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGGAGGAGGGG 18  
Db 4 TTGGAGGGGGTGTGGGG 21

RESULT 6  
US-08-173-489C-127/c  
Sequence 127, Application US/08173489C  
Patent No. 5861244  
GENERAL INFORMATION:  
APPLICANT: WANG, C. -G.  
APPLICANT: HEPBURN, A. G.  
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA  
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.  
NUMBER OF SEQUENCES: 365  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,  
STREET: 510 EAST 73RD STREET,  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10021.  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44Mb storage  
COMPUTER: IBM PC/XT/AT  
OPERATING SYSTEM: MS-DOS version 6.2  
SOFTWARE: Wordperfect Version 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/173,489C  
FILING DATE: 22 DEC 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/968,436  
FILING DATE: 29 OCT 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Handelman, Joseph H.  
REGISTRATION NUMBER: 26,179  
REFERENCE/DOCKET NUMBER: U9518-6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (attorney) (212) 708-1880  
TELEFAX: (attorney) (212) 246-8959  
INFORMATION FOR SEQ ID NO: 127:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double stranded  
TOPOLOGY: linear  
MOLECULE TYPE: genomic DNA  
DESCRIPTION: alpha-1-globin gene (accession #  
DESCRIPTION: V00491) nucleotides 827 to 843  
HYPOTHETICAL: no  
ANTI-SENSE: no  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
PUBLICATION INFORMATION:  
AUTHORS: Michelson, A M, Orkin, S H.  
TITLE: The 3' untranslated regions  
TITLE: of the duplicated human alpha-globin genes are  
TITLE: unexpectedly divergent  
JOURNAL: Cell  
VOLUME: 22  
PAGES: 371-377  
DATE: 1980  
RELEVANT RESIDUES IN SEQ ID NO: 127 :FROM 1 TO 17  
US-08-173-489C-127

Query Match 80.0%; Score 14.4; DB 2; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGGGGGAGGAGGGG 18  
Db 16 GGAAGGGGGAGGAGGGG 1

RESULT 7  
US-09-780-173A-93

; Sequence 93, Application US/09780173A  
; Patent No. 6455307

; GENERAL INFORMATION:

; APPLICANT: Robert McKay

; APPLICANT: Susan M. Freier

; APPLICANT: Jacqueline Wyatt

; TITLE OF INVENTION: ANTISENSE MODULATION OF CASEIN KINASE 2-ALPHA PRIME EXPRESSION

; FILE REFERENCE: RTS-0165

; CURRENT APPLICATION NUMBER: US/09/780,173A

; CURRENT FILING DATE: 2001-02-08

; NUMBER OF SEQ ID NOS: 95

; SEQ ID NO 93

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Antisense Oligonucleotide

US-09-780-173A-93

Query Match 76.7%; Score 13.8; DB 4; Length 20;

Best Local Similarity 88.2%; Pred. No. 2e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGAGGGGGAGGAGGGG 18

Db 2 TGGAGGAGGAGGAGGAG 18

RESULT 8

US-09-661-753-30/c

; Sequence 30, Application US/09661753

; Patent No. 6436909

; GENERAL INFORMATION:

; APPLICANT: Nicholas M. Dean

; APPLICANT: Susan F. Murray

; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA

; FILE REFERENCE: ISPH-0498

; CURRENT APPLICATION NUMBER: US/09/661,753

; CURRENT FILING DATE: 2000-09-14

; EARLIER APPLICATION NUMBER: 60/154,546

; EARLIER FILING DATE: 1999-09-17

; NUMBER OF SEQ ID NOS: 68

; SEQ ID NO 30

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Antisense Oligonucleotide

US-09-661-753-30

Query Match 74.4%; Score 13.4; DB 4; Length 20;

Best Local Similarity 93.3%; Pred. No. 2.8e+03;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGGGGAGGAGGGG 17

Db 20 GGAGCGGGAGGAGGG 6

RESULT 9

US-09-495-140-26

; Sequence 26, Application US/09495140

; Patent No. 6376182

; GENERAL INFORMATION:

; APPLICANT: CHAO, LEE

; APPLICANT: CHAO, JULIE

; APPLICANT: SONG, QING

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CORRELATING

; TITLE OF INVENTION: TISSUE KALLIKREIN GENE PROMOTER POLYMORPHISMS WITH TREATMENT

; TITLE OF INVENTION: OF ESSENTIAL HYPERTENSION

; FILE REFERENCE: 19113.0081

; CURRENT APPLICATION NUMBER: US/09/495,140

; CURRENT FILING DATE: 2000-01-31

; EARLIER APPLICATION NUMBER: 09/389,566

; EARLIER FILING DATE: 1999-09-03

; EARLIER APPLICATION NUMBER: 08/856,141

; EARLIER FILING DATE: 1997-05-14

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 26

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:/No. 6376182e =

; OTHER INFORMATION: synthetic construct

US-09-495-140-26

Query Match 71.1%; Score 12.8; DB 4; Length 17;

Best Local Similarity 87.5%; Pred. No. 4.7e+03;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGGAGGAGGGG 18

Db 1 GGAGGGGGGGGGGGG 16

RESULT 10

US-09-344-579-9

; Sequence 9, Application US/09344579

; Patent No. 6054316

; GENERAL INFORMATION:

; APPLICANT: Brenda F. Baker

; APPLICANT: Lex M. Cowser

; TITLE OF INVENTION: ANTISENSE MODULATION OF ETS-2 EXPRESSION

; FILE REFERENCE: RTS-0063

; CURRENT APPLICATION NUMBER: US/09/344,579

; CURRENT FILING DATE: 1999-06-25

; NUMBER OF SEQ ID NOS: 47

; SEQ ID NO 9

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Antisense Oligonucleotide

US-09-344-579-9

Query Match 71.1%; Score 12.8; DB 3; Length 18;

Best Local Similarity 87.5%; Pred. No. 4.7e+03;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGGAGGAGGGG 18

Db 2 GGAGCGGGAGGAGGAG 17

RESULT 11

US-09-490-692-153/c

; Sequence 153, Application US/09490692

; Patent No. 6180353

; GENERAL INFORMATION:

; APPLICANT: Nicholas M. Dean

; APPLICANT: Lex M. Cowser

; TITLE OF INVENTION: ANTISENSE MODULATION OF DAXX EXPRESSION

; FILE REFERENCE: RTS-0120

; CURRENT APPLICATION NUMBER: US/09/490,692

; CURRENT FILING DATE: 2000-01-24

; NUMBER OF SEQ ID NOS: 176

; SEQ ID NO 153

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Antisense Oligonucleotide

US-09-490-692-153

Query Match 71.1%; Score 12.8; DB 3; Length 20;  
Best Local Similarity 87.5%; Pred. No. 4.7e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGGGAGGAGGG 18  
||||| |||||||  
Db 16 GGAGGAGGAGGAGGAG 1

RESULT 12  
US-08-256-426B-282/c  
; Sequence 282, Application US/08256426B  
; Patent No. 5948611  
; GENERAL INFORMATION:  
; APPLICANT: Prockop, Darwin J.  
; APPLICANT: Ala-Kokko, Leena  
; APPLICANT: Williams, Charlene J.  
; APPLICANT: Ritvaniemi, Pertti  
; APPLICANT: Baldwin, Clinton  
; APPLICANT: Hopkinson, Ian  
; APPLICANT: Ahmad, Nilofar Nina  
; TITLE OF INVENTION: Methods of Detecting A Genetic  
; NUMBER OF SEQUENCES: 293  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5948611iris  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.5 INCH  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 3.1  
; SOFTWARE: WORDPERFECT 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/256,426B  
; FILING DATE: 03-FEB-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/10964  
; FILING DATE: 12-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/977,284  
; FILING DATE: 13-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mark Deluca  
; REGISTRATION NUMBER: 33,229  
; REFERENCE/DOCKET NUMBER: TJU-1082  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 568-3100  
; TELEFAX: (215) 568-3439  
; INFORMATION FOR SEQ ID NO: 282:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 21  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: SINGLE  
; TOPOLOGY: LINEAR

Query Match 71.1%; Score 12.8; DB 2; Length 21;  
Best Local Similarity 87.5%; Pred. No. 4.7e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGGAGGGGAGGAGG 16  
||||| |||||||  
Db 20 TTGGAGCAGGAGGAGG 5

RESULT 13  
US-08-863-639A-41  
; Sequence 41, Application US/08863639A  
; Patent No. 5981185

; GENERAL INFORMATION:  
; APPLICANT: Matson, Robert S.  
; APPLICANT: Coassin, Peter J.  
; APPLICANT: Rampal, Jang B.  
; APPLICANT: Caskey, C. T.  
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS  
; NUMBER OF SEQUENCES: 95  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sheldon & Mak  
; STREET: 225 South Lake Avenue, 9th Floor  
; CITY: Pasadena  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 91101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: Corel WordPerfect 8 version  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/863,639A  
; FILING DATE: May 28, 1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Joseph E. Mueth  
; REGISTRATION NUMBER: 20,532  
; REFERENCE/DOCKET NUMBER: 11859-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (626) 796-4000  
; TELEFAX: (626) 795-6321  
; INFORMATION FOR SEQ ID NO: 41:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 21 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Other nucleic acid  
; US-08-863-639A-41

Query Match 71.1%; Score 12.8; DB 2; Length 21;  
Best Local Similarity 87.5%; Pred. No. 4.7e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGGGAGGAGGG 18  
||||| |||||||  
Db 2 GGAGGAGGAGGAGGAG 17

RESULT 14  
US-08-863-639A-53/c  
; Sequence 53, Application US/08863639A  
; Patent No. 5981185  
; GENERAL INFORMATION:  
; APPLICANT: Matson, Robert S.  
; APPLICANT: Coassin, Peter J.  
; APPLICANT: Rampal, Jang B.  
; APPLICANT: Caskey, C. T.  
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS  
; NUMBER OF SEQUENCES: 95  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sheldon & Mak  
; STREET: 225 South Lake Avenue, 9th Floor  
; CITY: Pasadena  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 91101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: Corel WordPerfect 8 version  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/863,639A

;; FILING DATE: May 28, 1997  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Joseph E. Mueh  
;; REGISTRATION NUMBER: 20,532  
;; REFERENCE/DOCKET NUMBER: 11859-1  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (626) 796-4000  
;; TELEFAX: (626) 795-6321  
;; INFORMATION FOR SEQ ID NO: 53:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 21 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: Other nucleic acid  
US-08-863-639A-53

Query Match 71.1%; Score 12.8; DB 2; Length 21;  
Best Local Similarity 87.5%; Pred. No. 4.7e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGGAGGAGGGG 18  
|||||  
Db 20 GGAGGAGGAGGAGGAG 5

RESULT 15  
US-08-863-639A-59/c  
; Sequence 59, Application US/08863639A  
; Patent No. 5981185  
; GENERAL INFORMATION:  
; APPLICANT: Matson, Robert S.  
; APPLICANT: Coassin, Peter J.  
; APPLICANT: Rampal, Jang B.  
; APPLICANT: Caskey, C. T.  
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS  
; NUMBER OF SEQUENCES: 95  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sheldon & Mak  
; STREET: 225 South Lake Avenue, 9th Floor  
; CITY: Pasadena  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 91101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: Corel WordPerfect 8 version  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/863,639A  
; FILING DATE: May 28, 1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Joseph E. Mueh  
; REGISTRATION NUMBER: 20,532  
; REFERENCE/DOCKET NUMBER: 11859-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (626) 796-4000  
; TELEFAX: (626) 795-6321  
; INFORMATION FOR SEQ ID NO: 59:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 21 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Other nucleic acid  
US-08-863-639A-59

Query Match 71.1%; Score 12.8; DB 2; Length 21;  
Best Local Similarity 87.5%; Pred. No. 4.7e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGGAGGAGGGG 18  
|||||  
Db 19 GGAGGAGGAGGAGGAG 4  
  
Search completed: October 27, 2003, 14:03:35  
Job time : 42.3143 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 11:25:34 ; Search time 387.943 Seconds  
(without alignments)  
124.432 Million cell updates/sec

Title: US-09-331-204A-7  
Perfect score: 18  
Sequence: 1 ttggaggaggaggaggagg 18

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1792395 seqs, 1340900451 residues

Total number of hits satisfying chosen parameters: 408622

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*
- 16: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*
- 17: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	15	83.3	17	12	US-10-061-201-1934
C 2	15	83.3	17	12	US-10-061-201-1935
C 3	15	83.3	17	12	US-10-061-201-1936
C 4	14.8	82.2	21	9	US-09-828-034-28
C 5	14	77.8	17	12	US-10-061-201-1933
C 6	14	77.8	17	12	US-10-061-201-1937
C 7	13.4	74.4	20	11	US-09-948-002-30
C 8	13	72.2	17	11	US-09-780-533A-46
C 9	13	72.2	17	11	US-09-780-533A-47
C 10	13	72.2	17	11	US-09-780-533A-899
C 11	13	72.2	17	11	US-09-780-533A-900
C 12	13	72.2	17	11	US-09-780-533A-901
C 13	13	72.2	17	12	US-10-061-201-1932
C 14	13	72.2	17	12	US-10-061-201-1938
C 15	12.8	71.1	17	11	US-09-780-533A-45
C 16	12.8	71.1	17	11	US-09-780-533A-894

C 17	71.1	12.8	17	12	US-10-059-877-26	Sequence 26, Appl
C 18	71.1	12.8	17	12	US-10-303-109A-30	Sequence 30, Appl
C 19	71.1	12.8	17	14	US-10-059-888-26	Sequence 26, Appl
C 20	71.1	12.8	20	11	US-09-919-501-11	Sequence 11, Appl
C 21	71.1	12.8	20	12	US-10-032-585-4054	Sequence 4054, Ap
C 22	71.1	12.8	20	14	US-10-181-846-153	Sequence 153, App
C 23	71.1	12.8	21	9	US-09-828-034-9	Sequence 9, Appl
C 24	68.9	12.4	21	14	US-10-258-860-10	Sequence 10, Appl
C 25	68.9	12.4	22	11	US-09-726-258-38	Sequence 38, Appl
C 26	67.8	12.2	17	11	US-09-780-533A-902	Sequence 902, App
C 27	67.8	12.2	17	11	US-09-930-423-866	Sequence 866, App
C 28	67.8	12.2	17	12	US-09-745-237A-866	Sequence 866, App
C 29	67.8	12.2	17	14	US-10-060-756A-685	Sequence 685, App
C 30	67.8	12.2	20	9	US-09-854-883-174	Sequence 174, App
C 31	66.7	12	17	11	US-09-780-533A-898	Sequence 898, App
C 32	66.7	12	17	12	US-10-061-201-1931	Sequence 1931, Ap
C 33	66.7	12	17	12	US-10-061-201-1939	Sequence 1939, Ap
C 34	65.6	11.8	15	14	US-10-314-405-43	Sequence 43, Appl
C 35	65.6	11.8	16	12	US-10-059-877-22	Sequence 22, Appl
C 36	65.6	11.8	16	12	US-10-339-161-26	Sequence 26, Appl
C 37	65.6	11.8	16	14	US-10-059-888-22	Sequence 22, Appl
C 38	65.6	11.8	17	11	US-09-780-533A-893	Sequence 893, App
C 39	65.6	11.8	17	11	US-09-780-533A-895	Sequence 895, App
C 40	65.6	11.8	17	11	US-09-740-332-1833	Sequence 1833, Ap
C 41	65.6	11.8	17	12	US-09-817-879-1833	Sequence 1833, Ap
C 42	65.6	11.8	18	11	US-09-940-244-161	Sequence 161, App
C 43	65.6	11.8	18	11	US-09-864-536A-218	Sequence 218, App
C 44	65.6	11.8	18	12	US-10-290-386-161	Sequence 161, App
C 45	65.6	11.8	18	12	US-10-084-839-218	Sequence 218, App

ALIGNMENTS

RESULT 1

US-10-061-201-1934/c  
; Sequence 1934, Application US/10061201  
; Publication No. US20030166229A1  
; GENERAL INFORMATION:  
; APPLICANT: Shannon, Mark  
; TITLE OF INVENTION: HUWAN POSH-LIKE PROTEIN 1  
; FILE REFERENCE: PB0178  
; CURRENT APPLICATION NUMBER: US/10/061,201  
; CURRENT FILING DATE: 2002-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 09/864,761  
; PRIOR FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/328,205  
; PRIOR FILING DATE: 2001-10-10  
; NUMBER OF SEQ ID NOS: 4162  
; SOFTWARE: Aecomica Sequence Listing Engine  
; SEQ ID NO 1934  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-061-201-1934

Query Match 83.3%; Score 15; DB 12; Length 17;



```
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGGGGGAGGAGGGG 18
Db 17 GAGGGGGAGGAGGGG 3

RESULT 2
US-10-061-201-1935/c
; Sequence 1935, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1935
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-1935

Query Match 83.3%; Score 15; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGGGGGAGGAGGGG 18
Db 15 GAGGGGGAGGAGGGG 1

RESULT 4
US-09-828-034-28/c
; Sequence 28, Application US/09828034
; Patent No. US20020064771A1
; GENERAL INFORMATION:
; APPLICANT: Zhong, Weidong
; APPLICANT: Hong, Zhi
; APPLICANT: Ferraxi, Eric
; TITLE OF INVENTION: HCV REPLICASE COMPLEXES
; FILE REFERENCE: IN01165
; CURRENT APPLICATION NUMBER: US/09/828,034
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: U.S. 60/195,852
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA
US-09-828-034-28

Query Match 82.2%; Score 14.8; DB 9; Length 21;
Best Local Similarity 88.9%; Pred. No. 6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGGAGGGGAGGAGGGG 18
Db 20 TTGGAGGAGGAGGAGGAG 3

RESULT 5
US-10-061-201-1933/c
; Sequence 1933, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
```

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 1933
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-1933

Query Match 77.8%; Score 14; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AGGGGGAGGAGGGG 18
| | | | | | | | | | | | | | | | |
Db 17 AGGGGGAGGAGGGG 4

RESULT 6
US-10-061-201-1937/c
; Sequence 1937, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 1937
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-1937

Query Match 77.8%; Score 14; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGGGGGAGGAGGG 17
| | | | | | | | | | | | | | | | |
Db 14 GAGGGGGAGGAGGG 1

RESULT 7
US-09-948-002-30/c
; Sequence 30, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; TITLE OF INVENTION: FACTOR BETA EXPRESSION
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/09/948,002
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 30
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-948-002-30

Query Match 74.4%; Score 13.4; DB 11; Length 20;
Best Local Similarity 93.3%; Pred. No. 2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGGGAGGAGGG 17
| | | | | | | | | | | | | | | | |
Db 20 GGAGGGGAGGAGGG 6

RESULT 8
US-09-780-533A-46/c
; Sequence 46, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 46
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-46

Query Match 72.2%; Score 13; DB 11; Length 17;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGGGGAGGAGGGG 18

Db 16 GGGGGAGGAGGGG 4

RESULT 9

US-09-780-533A-47/c  
; Sequence 47, Application US/09780533A  
; Publication No. US20030060611A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Chowrira, Bharat  
; APPLICANT: Haerberli, Pete  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene  
; FILE REFERENCE: MBHB00,878-A (400/011)  
; CURRENT APPLICATION NUMBER: US/09/780,533A  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,797  
; PRIOR FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 6679  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 47  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-780-533A-47

Query Match 72.2%; Score 13; DB 11; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3e+04;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGGGGAGGAGGGG 18  
Db 13 GGGGGAGGAGGGG 1

RESULT 10

US-09-780-533A-899/c  
; Sequence 899, Application US/09780533A  
; Publication No. US20030060611A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Chowrira, Bharat  
; APPLICANT: Haerberli, Pete  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene  
; FILE REFERENCE: MBHB00,878-A (400/011)  
; CURRENT APPLICATION NUMBER: US/09/780,533A  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,797  
; PRIOR FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 6679  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 899  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-780-533A-899

Query Match 72.2%; Score 13; DB 11; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3e+04;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGGGGAGGAGGGG 18  
Db 17 GGGGGAGGAGGGG 5

RESULT 11

US-09-780-533A-900/c  
; Sequence 900, Application US/09780533A

; Publication No. US20030060611A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Chowrira, Bharat  
; APPLICANT: Haerberli, Pete  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene  
; FILE REFERENCE: MBHB00,878-A (400/011)  
; CURRENT APPLICATION NUMBER: US/09/780,533A  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,797  
; PRIOR FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 6679  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 900  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-780-533A-900

Query Match 72.2%; Score 13; DB 11; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3e+04;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGGGGAGGAGGGG 18  
Db 15 GGGGGAGGAGGGG 3

RESULT 12

US-09-780-533A-901/c  
; Sequence 901, Application US/09780533A  
; Publication No. US20030060611A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Chowrira, Bharat  
; APPLICANT: Haerberli, Pete  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene  
; FILE REFERENCE: MBHB00,878-A (400/011)  
; CURRENT APPLICATION NUMBER: US/09/780,533A  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,797  
; PRIOR FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 6679  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 901  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-780-533A-901

Query Match 72.2%; Score 13; DB 11; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3e+04;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGGGGAGGAGGGG 18  
Db 14 GGGGGAGGAGGGG 2

RESULT 13

US-10-061-201-1932/c  
; Sequence 1932, Application US/10061201  
; Publication No. US20030166229A1  
; GENERAL INFORMATION:  
; APPLICANT: Shannon, Mark  
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1  
; FILE REFERENCE: PB0178  
; CURRENT APPLICATION NUMBER: US/10/061,201  
; CURRENT FILING DATE: 2002-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1932
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-1932

Query Match 72.2%; Score 13; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGGGGAGGAGGGG 18
Db 17 GGGGGAGGAGGGG 5

RESULT 14
US-10-061-201-1938/c
; Sequence 1938, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1938
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-061-201-1938

Query Match 72.2%; Score 13; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAGGGGAGGAGG 16
Db 13 GAGGGGAGGAGG 1

RESULT 15
US-09-780-533A-45/c
; Sequence 45, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haeberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MEHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-45

Query Match 71.1%; Score 12.8; DB 11; Length 17;
Best Local Similarity 87.5%; Pred. No. 3.6e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGAGGGGAGGAGGGG 18
Db 16 GGAGGGGAGGAGGGG 1

Search completed: October 27, 2003, 19:00:53
Job time : 387.943 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:35 ; Search time 2356.29 Seconds  
(without alignments)  
253.343 Million cell updates/sec

Title: US-09-331-204A-7  
Perfect score: 18  
Sequence: 1 ttggaggaggaggagg 18

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 33363688 seqs, 16581889874 residues

Total number of hits satisfying chosen parameters: 2938060

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents NA Main:\*

- 1: /cgn2\_6/ptodata/1/pna/PCTUS\_COMB.seq.\*
- 2: /cgn2\_6/ptodata/1/pna/PCTUS\_COMB.seq.oid.\*
- 3: /cgn2\_6/ptodata/1/pna/US06\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/pna/US07\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pna/US080\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/pna/US081\_COMB.seq.\*
- 7: /cgn2\_6/ptodata/1/pna/US082\_COMB.seq.\*
- 8: /cgn2\_6/ptodata/1/pna/US083\_COMB.seq.\*
- 9: /cgn2\_6/ptodata/1/pna/US084\_COMB.seq.\*
- 10: /cgn2\_6/ptodata/1/pna/US085\_COMB.seq.\*
- 11: /cgn2\_6/ptodata/1/pna/US086\_COMB.seq.\*
- 12: /cgn2\_6/ptodata/1/pna/US087\_COMB.seq.\*
- 13: /cgn2\_6/ptodata/1/pna/US088\_COMB.seq.\*
- 14: /cgn2\_6/ptodata/1/pna/US089\_COMB.seq.\*
- 15: /cgn2\_6/ptodata/1/pna/US090\_COMB.seq.\*
- 16: /cgn2\_6/ptodata/1/pna/US091\_COMB.seq.\*
- 17: /cgn2\_6/ptodata/1/pna/US092A\_COMB.seq.\*
- 18: /cgn2\_6/ptodata/1/pna/US092B\_COMB.seq.\*
- 19: /cgn2\_6/ptodata/1/pna/US093A\_COMB.seq.\*
- 20: /cgn2\_6/ptodata/1/pna/US093B\_COMB.seq.\*
- 21: /cgn2\_6/ptodata/1/pna/US094\_COMB.seq.\*
- 22: /cgn2\_6/ptodata/1/pna/US095A\_COMB.seq.\*
- 23: /cgn2\_6/ptodata/1/pna/US095B\_COMB.seq.\*
- 24: /cgn2\_6/ptodata/1/pna/US095C\_COMB.seq.\*
- 25: /cgn2\_6/ptodata/1/pna/US095D\_COMB.seq.\*
- 26: /cgn2\_6/ptodata/1/pna/US096A\_COMB.seq.\*
- 27: /cgn2\_6/ptodata/1/pna/US096B\_COMB.seq.\*
- 28: /cgn2\_6/ptodata/1/pna/US096C\_COMB.seq.\*
- 29: /cgn2\_6/ptodata/1/pna/US096D\_COMB.seq.\*
- 30: /cgn2\_6/ptodata/1/pna/US096E\_COMB.seq.\*
- 31: /cgn2\_6/ptodata/1/pna/US097A\_COMB.seq.\*
- 32: /cgn2\_6/ptodata/1/pna/US097B\_COMB.seq.\*
- 33: /cgn2\_6/ptodata/1/pna/US097C\_COMB.seq.\*
- 34: /cgn2\_6/ptodata/1/pna/US098A\_COMB.seq.\*
- 35: /cgn2\_6/ptodata/1/pna/US098B\_COMB.seq.\*
- 36: /cgn2\_6/ptodata/1/pna/US098C\_COMB.seq.\*
- 37: /cgn2\_6/ptodata/1/pna/US098D\_COMB.seq.\*
- 38: /cgn2\_6/ptodata/1/pna/US099A\_COMB.seq.\*
- 39: /cgn2\_6/ptodata/1/pna/US099B\_COMB.seq.\*
- 40: /cgn2\_6/ptodata/1/pna/US099C\_COMB.seq.\*
- 41: /cgn2\_6/ptodata/1/pna/US099D\_COMB.seq.\*
- 42: /cgn2\_6/ptodata/1/pna/US099E\_COMB.seq.\*
- 43: /cgn2\_6/ptodata/1/pna/US099F\_COMB.seq.\*

- 44: /cgn2\_6/ptodata/1/pna/US100A\_COMB.seq.\*
- 45: /cgn2\_6/ptodata/1/pna/US100B\_COMB.seq.\*
- 46: /cgn2\_6/ptodata/1/pna/US101A\_COMB.seq.\*
- 47: /cgn2\_6/ptodata/1/pna/US101B\_COMB.seq.\*
- 48: /cgn2\_6/ptodata/1/pna/US102A\_COMB.seq.\*
- 49: /cgn2\_6/ptodata/1/pna/US102B\_COMB.seq.\*
- 50: /cgn2\_6/ptodata/1/pna/US103A\_COMB.seq.\*
- 51: /cgn2\_6/ptodata/1/pna/US103B\_COMB.seq.\*
- 52: /cgn2\_6/ptodata/1/pna/US104A\_COMB.seq.\*
- 53: /cgn2\_6/ptodata/1/pna/US104B\_COMB.seq.\*
- 54: /cgn2\_6/ptodata/1/pna/US6000\_COMB.seq.\*
- 55: /cgn2\_6/ptodata/1/pna/US6001\_COMB.seq.\*
- 56: /cgn2\_6/ptodata/1/pna/US6002\_COMB.seq.\*
- 57: /cgn2\_6/ptodata/1/pna/US6003\_COMB.seq.\*
- 58: /cgn2\_6/ptodata/1/pna/US6004\_COMB.seq.\*
- 59: /cgn2\_6/ptodata/1/pna/US6005\_COMB.seq.\*
- 60: /cgn2\_6/ptodata/1/pna/US6006\_COMB.seq.\*
- 61: /cgn2\_6/ptodata/1/pna/US6007\_COMB.seq.\*
- 62: /cgn2\_6/ptodata/1/pna/US6008\_COMB.seq.\*
- 63: /cgn2\_6/ptodata/1/pna/US6009\_COMB.seq.\*
- 64: /cgn2\_6/ptodata/1/pna/US6010\_COMB.seq.\*
- 65: /cgn2\_6/ptodata/1/pna/US6011\_COMB.seq.\*
- 66: /cgn2\_6/ptodata/1/pna/US6012\_COMB.seq.\*
- 67: /cgn2\_6/ptodata/1/pna/US6013\_COMB.seq.\*
- 68: /cgn2\_6/ptodata/1/pna/US6014\_COMB.seq.\*
- 69: /cgn2\_6/ptodata/1/pna/US6015\_COMB.seq.\*
- 70: /cgn2\_6/ptodata/1/pna/US6016\_COMB.seq.\*
- 71: /cgn2\_6/ptodata/1/pna/US6017\_COMB.seq.\*
- 72: /cgn2\_6/ptodata/1/pna/US6018\_COMB.seq.\*
- 73: /cgn2\_6/ptodata/1/pna/US6019\_COMB.seq.\*
- 74: /cgn2\_6/ptodata/1/pna/US6020\_COMB.seq.\*
- 75: /cgn2\_6/ptodata/1/pna/US6021\_COMB.seq.\*
- 76: /cgn2\_6/ptodata/1/pna/US6022\_COMB.seq.\*
- 77: /cgn2\_6/ptodata/1/pna/US6023A\_COMB.seq.\*
- 78: /cgn2\_6/ptodata/1/pna/US6023B\_COMB.seq.\*
- 79: /cgn2\_6/ptodata/1/pna/US6024\_COMB.seq.\*
- 80: /cgn2\_6/ptodata/1/pna/US6025\_COMB.seq.\*
- 81: /cgn2\_6/ptodata/1/pna/US6026\_COMB.seq.\*
- 82: /cgn2\_6/ptodata/1/pna/US6027\_COMB.seq.\*
- 83: /cgn2\_6/ptodata/1/pna/US6028\_COMB.seq.\*
- 84: /cgn2\_6/ptodata/1/pna/US6029\_COMB.seq.\*
- 85: /cgn2\_6/ptodata/1/pna/US6030\_COMB.seq.\*
- 86: /cgn2\_6/ptodata/1/pna/US6031\_COMB.seq.\*
- 87: /cgn2\_6/ptodata/1/pna/US6032\_COMB.seq.\*
- 88: /cgn2\_6/ptodata/1/pna/US6033\_COMB.seq.\*
- 89: /cgn2\_6/ptodata/1/pna/US6034\_COMB.seq.\*
- 90: /cgn2\_6/ptodata/1/pna/US6035\_COMB.seq.\*
- 91: /cgn2\_6/ptodata/1/pna/US6036\_COMB.seq.\*
- 92: /cgn2\_6/ptodata/1/pna/US6037\_COMB.seq.\*
- 93: /cgn2\_6/ptodata/1/pna/US6038\_COMB.seq.\*
- 94: /cgn2\_6/ptodata/1/pna/US6039\_COMB.seq.\*
- 95: /cgn2\_6/ptodata/1/pna/US6040\_COMB.seq.\*
- 96: /cgn2\_6/ptodata/1/pna/US6041\_COMB.seq.\*
- 97: /cgn2\_6/ptodata/1/pna/US6042\_COMB.seq.\*
- 98: /cgn2\_6/ptodata/1/pna/US6043\_COMB.seq.\*
- 99: /cgn2\_6/ptodata/1/pna/US6044\_COMB.seq.\*
- 100: /cgn2\_6/ptodata/1/pna/US6045\_COMB.seq.\*
- 101: /cgn2\_6/ptodata/1/pna/US6046\_COMB.seq.\*
- 102: /cgn2\_6/ptodata/1/pna/US6047\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query Match			Length DB	ID	Description
	No.	Score	Match			
1	18	100.0	18	19	US-09-331-204A-7	Sequence 7, Appli
2	18	100.0	19	19	US-09-331-204-4	Sequence 4, Appli
3	17	94.4	19	50	US-10-310-188-47426	Sequence 47426, A
4	16.4	91.1	18	19	US-09-331-204-5	Sequence 5, Appli

```

5 16.4 91.1 18 19 US-09-331-204A-8
6 15.4 85.6 21 9 US-08-472-928B-45
7 15.4 85.6 21 29 US-09-670-105-45
8 15 83.3 17 45 US-10-061-201-1934
9 15 83.3 17 45 US-10-061-201-1935
10 15 83.3 17 45 US-10-061-201-1936
11 15 83.3 17 87 US-60-328-205-1934
12 15 83.3 17 87 US-60-328-205-1935
13 15 83.3 17 87 US-60-328-205-1936
14 15 83.3 18 50 US-10-310-188-6227
15 15 83.3 19 50 US-10-303-778-16894
16 14.8 82.2 18 8 US-08-387-041A-3
17 14.8 82.2 18 19 US-09-331-204-1
18 14.8 82.2 18 19 US-09-331-204A-4
19 14.8 82.2 18 33 US-09-786-436-17
20 14.8 82.2 18 33 US-09-786-436-42
21 14.8 82.2 21 8 US-08-387-041A-4
22 14.8 82.2 21 19 US-09-331-204-6
23 14.8 82.2 21 19 US-09-331-204A-6
24 14.8 82.2 21 34 US-09-828-034-28
25 14.8 82.2 21 73 US-60-195-852-28
26 14.8 82.2 22 50 US-10-310-188-18159
27 14.4 80.0 16 50 US-10-310-188-39032
28 14.4 80.0 17 50 US-10-310-188-38911
29 14.4 80.0 18 50 US-10-310-188-6229
30 14.4 80.0 18 50 US-10-310-188-39031
31 14.4 80.0 18 50 US-10-310-188-41647
32 14.4 80.0 19 50 US-10-310-188-38912
33 14.4 80.0 20 49 US-10-266-090-49542
34 14.4 80.0 21 50 US-10-303-778-5120
35 14.4 80.0 21 52 US-10-418-182-126
36 14 77.8 17 45 US-10-061-201-1933
37 14 77.8 17 45 US-10-061-201-1937
38 14 77.8 17 50 US-10-303-778-3706
39 14 77.8 17 50 US-10-310-188-6220
40 14 77.8 17 50 US-10-310-188-38954
41 14 77.8 17 87 US-60-328-205-1933
42 14 77.8 17 87 US-60-328-205-1937
43 14 77.8 19 50 US-10-310-188-26652
44 13.8 76.7 17 50 US-10-310-188-18314
45 13.8 76.7 18 50 US-10-303-778-8260

```

ALIGNMENTS

```

RESULT 1
US-09-331-204A-7
; Sequence 7, Application US/09331204A
; GENERAL INFORMATION:
; APPLICANT: ICN Pharmaceuticals, Inc.
; APPLICANT: Tam, Robert
; TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Respo
; FILE REFERENCE: 216/013-US1
; CURRENT APPLICATION NUMBER: US/09/331,204A
; CURRENT FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: PCT/US97/23927
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 18
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-331-204A-7

```

```

Query Match 100.0%; Score 18; DB 19; Length 18;
Best Local Similarity 100.0%; Pred.No. 7.1e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGAGGAGGGG 18
   |||||
Db 1 TTGGAGGGGGAGGAGGGG 18

```

```

Sequence 8, Appli
Sequence 45, Appl
Sequence 45, Appl
Sequence 1934, Ap
Sequence 1935, Ap
Sequence 1936, Ap
Sequence 1934, Ap
Sequence 1935, Ap
Sequence 1936, Ap
Sequence 1934, A
Sequence 16894, A
Sequence 3, Appli
Sequence 1, Appli
Sequence 4, Appli
Sequence 17, Appl
Sequence 42, Appl
Sequence 4, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 28, Appl
Sequence 18159, A
Sequence 39032, A
Sequence 38911, A
Sequence 6229, Ap
Sequence 39031, A
Sequence 41647, A
Sequence 38912, A
Sequence 49542, A
Sequence 5120, Ap
Sequence 126, App
Sequence 1933, Ap
Sequence 1937, Ap
Sequence 3706, Ap
Sequence 6220, Ap
Sequence 38954, A
Sequence 1933, Ap
Sequence 1937, Ap
Sequence 26652, A
Sequence 18314, A
Sequence 8260, Ap

```

```

RESULT 2
US-09-331-204-4
; Sequence 4, Application US/09331204
; GENERAL INFORMATION:
; APPLICANT: Tam, Robert
; TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN
; FILE REFERENCE: ICNSequence
; CURRENT APPLICATION NUMBER: US/09/331,204
; CURRENT FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: PCT/US97/23927
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: An oligomer
; OTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic
; OTHER INFORMATION: acid. This term includes oligomers consisting of
; OTHER INFORMATION: naturally occurring bases, sugars and intersugar (
US-09-331-204-4

```

```

Query Match 100.0%; Score 18; DB 19; Length 19;
Best Local Similarity 100.0%; Pred.No. 7.1e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGAGGAGGGG 18
   |||||
Db 1 TTGGAGGGGGAGGAGGGG 18

```

```

RESULT 3
US-10-310-188-47426
; Sequence 47426, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEI
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47426
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-47426

```

```

Query Match 94.4%; Score 17; DB 50; Length 19;
Best Local Similarity 100.0%; Pred.No. 1.7e+04;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGAGGGGGAGGAGGGG 18
   |||||
Db 3 TGGAGGGGGAGGAGGGG 19

```

```

RESULT 4
US-09-331-204-5
; Sequence 5, Application US/09331204
; GENERAL INFORMATION:
; APPLICANT: Tam, Robert
; TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN
; FILE REFERENCE: ICNSequence
; CURRENT APPLICATION NUMBER: US/09/331,204
; CURRENT FILING DATE: 1999-08-20

```

;; PRIOR APPLICATION NUMBER: PCT/US97/23927  
;; PRIOR FILING DATE: 1997-12-19  
;; NUMBER OF SEQ ID NOS: 6  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 5  
;; LENGTH: 18  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: An oligomer  
;; OTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic  
;; OTHER INFORMATION: acid. This term includes oligomers consisting of  
;; OTHER INFORMATION: naturally occurring bases, sugars and intersugar (

US-09-331-204-5

Query Match 91.1%; Score 16.4; DB 19; Length 18;  
Best Local Similarity 94.4%; Pred. No. 2.7e+04;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTGAGGGGGGAGGGG 18  
| | | | | | | | | | | | | | | | | | | |  
Db 1 TTGAGGGGGGAGGTGGG 18

RESULT 5  
US-09-331-204A-8  
;; GENERAL INFORMATION:  
;; APPLICANT: ICN Pharmaceuticals, Inc.  
;; APPLICANT: Tam, Robert  
;; TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Respo  
;; FILE REFERENCE: 216/013-US1  
;; CURRENT APPLICATION NUMBER: US/09/331.204A  
;; CURRENT FILING DATE: 1999-08-20  
;; PRIOR APPLICATION NUMBER: PCT/US97/23927  
;; PRIOR FILING DATE: 1997-12-19  
;; NUMBER OF SEQ ID NOS: 28  
;; SOFTWARE: PatentIn version 3.0  
;; SEQ ID NO 8  
;; LENGTH: 18  
;; TYPE: DNA  
;; ORGANISM: synthetic construct

US-09-331-204A-8

Query Match 91.1%; Score 16.4; DB 19; Length 18;  
Best Local Similarity 94.4%; Pred. No. 2.7e+04;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTGAGGGGGGAGGGG 18  
| | | | | | | | | | | | | | | | | | | |  
Db 1 TTGAGGGGGGAGGTGGG 18

RESULT 6  
US-08-472-928B-45  
;; Sequence 45, Application US/08472928B  
;; GENERAL INFORMATION:  
;; APPLICANT: Moncany, Maurice  
;; APPLICANT: Montagnier, Luc  
;; TITLE OF INVENTION: Nucleotide Sequences Derived From The  
;; TITLE OF INVENTION: Genome Of Retroviruses Of The HIV-1, HIV-2 And SIV Type,  
;; TITLE OF INVENTION: And Their Uses In Particular For The Amplification Of The  
;; TITLE OF INVENTION: Genomes Of These Retroviruses And For The In Vitro Diagnosis  
;; TITLE OF INVENTION: Of The Diseases Due To Those Viruses  
;; NUMBER OF SEQUENCES: 68  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
;; ADDRESSEE: Dunner  
;; STREET: 1300 I Street, N.W., Suite 700  
;; CITY: Washington  
;; STATE: D.C.  
;; COUNTRY: USA  
;; ZIP: 20005-3315

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/472,928B  
;; FILING DATE: 07-JUN-1995  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/160,465  
;; FILING DATE: 02-DEC-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: FR 8912371  
;; FILING DATE: 20-SEP-1989  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: FR 8907354  
;; FILING DATE: 06-FEB-1989  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Meyers, Kenneth J.  
;; REGISTRATION NUMBER: 25,146  
;; REFERENCE/DOCKET NUMBER: 02356.0062-02000  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202)408-4000  
;; TELEFAX: (202)408-4400  
;; INFORMATION FOR SEQ ID NO: 45:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 21 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
US-08-472-928B-45

Query Match 85.6%; Score 15.4; DB 9; Length 21;  
Best Local Similarity 94.1%; Pred. No. 6.4e+04;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGGAGGGGGGAGGGG 18  
| | | | | | | | | | | | | | | | | | | |  
Db 3 TGGAGGGGGGAGGAGG 19

RESULT 7  
US-09-670-105-45  
;; Sequence 45, Application US/09670105  
;; GENERAL INFORMATION:  
;; APPLICANT: Moncany, Maurice  
;; APPLICANT: Montagnier, Luc  
;; TITLE OF INVENTION: Nucleotide Sequences Derived From The  
;; TITLE OF INVENTION: Genome Of Retroviruses Of The HIV-1, HIV-2 And SIV Type,  
;; TITLE OF INVENTION: And Their Uses In Particular For The Amplification Of The  
;; TITLE OF INVENTION: Genomes Of These Retroviruses And For The In Vitro Diagnosis  
;; NUMBER OF SEQUENCES: 68  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
;; ADDRESSEE: Dunner  
;; STREET: 1300 I Street, N.W., Suite 700  
;; CITY: Washington  
;; STATE: D.C.  
;; COUNTRY: USA  
;; ZIP: 20005-3315  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/670,105  
;; FILING DATE: 26-Sep-2000  
;; CLASSIFICATION: <Unknown>  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 09/092,077



; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US/08/472,928  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: US 08/160,465  
; FILING DATE: 02-DEC-1993  
; APPLICATION NUMBER: FR 8912371  
; FILING DATE: 20-SEP-1989  
; APPLICATION NUMBER: FR 8907354  
; FILING DATE: 06-FEB-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meyers, Kenneth J.  
; REGISTRATION NUMBER: 25,146  
; REFERENCE/DOCKET NUMBER: 023356.0062-02000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)408-4000  
; TELEFAX: (202)408-4400  
; INFORMATION FOR SEQ ID NO: 45:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 21 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:  
US-09-670-105-45

Query Match 85.6%; Score 15.4; DB 29; Length 21;  
Best Local Similarity 94.1%; Pred. No. 6.4e+04;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TCGAGGGGAGGAGGGG 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 3 TCGAGGGGAGGAGGAG 19

RESULT 8  
US-10-061-201-1934/c  
; Sequence 1934, Application US/10061201  
; GENERAL INFORMATION:  
; APPLICANT: Shannon, Mark  
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1  
; FILE REFERENCE: PB0178  
; CURRENT APPLICATION NUMBER: US/10/061,201  
; CURRENT FILING DATE: 2002-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 09/864,761  
; PRIOR FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/328,205  
; PRIOR FILING DATE: 2001-10-10  
; NUMBER OF SEQ ID NOS: 4162  
; SOFTWARE: Acomica Sequence Listing Engine  
; SEQ ID NO 1934  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-061-201-1934

Query Match 83.3%; Score 15; DB 45; Length 17;

Best Local Similarity 100.0%; Pred. No. 8.9e+04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 GAGGGGAGGAGGGG 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 17 GAGGGGAGGAGGGG 3

RESULT 9  
US-10-061-201-1935/c  
; Sequence 1935, Application US/10061201  
; GENERAL INFORMATION:  
; APPLICANT: Shannon, Mark  
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1  
; FILE REFERENCE: PB0178  
; CURRENT APPLICATION NUMBER: US/10/061,201  
; CURRENT FILING DATE: 2002-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 09/864,761  
; PRIOR FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/328,205  
; PRIOR FILING DATE: 2001-10-10  
; NUMBER OF SEQ ID NOS: 4162  
; SOFTWARE: Acomica Sequence Listing Engine  
; SEQ ID NO 1935  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-061-201-1935

Query Match 83.3%; Score 15; DB 45; Length 17;  
Best Local Similarity 100.0%; Pred. No. 8.9e+04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGGGGAGGAGGGG 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 16 GAGGGGAGGAGGGG 2

RESULT 10  
US-10-061-201-1936/c  
; Sequence 1936, Application US/10061201  
; GENERAL INFORMATION:  
; APPLICANT: Shannon, Mark  
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1  
; FILE REFERENCE: PB0178  
; CURRENT APPLICATION NUMBER: US/10/061,201  
; CURRENT FILING DATE: 2002-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30



; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 09/864,761  
; PRIOR FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/328,205  
; PRIOR FILING DATE: 2001-10-10  
; NUMBER OF SEQ ID NOS: 4162  
; SOFTWARE: Aecmica Sequence Listing Engine  
; SEQ ID NO 1936  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-061-201-1936

Query Match 83.3%; Score 15; DB 45; Length 17;  
Best Local Similarity 100.0%; Pred. No. 8.9e+04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGGGGGAGGAGGGG 18  
|||  
Db 15 GAGGGGGAGGAGGGG 1

RESULT 11  
US-60-328-205-1934/c  
; Sequence 1934, Application US/60328205  
; GENERAL INFORMATION:  
; APPLICANT: Shannon, Mark  
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1  
; FILE REFERENCE: AEOMICA-26  
; CURRENT APPLICATION NUMBER: US/60/328,205  
; CURRENT FILING DATE: 2001-10-10  
; NUMBER OF SEQ ID NOS: 4162  
; SOFTWARE: Aecmica Sequence Listing Engine  
; SEQ ID NO 1934  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-60-328-205-1934

Query Match 83.3%; Score 15; DB 87; Length 17;  
Best Local Similarity 100.0%; Pred. No. 8.9e+04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGGGGGAGGAGGGG 18  
|||  
Db 17 GAGGGGGAGGAGGGG 3

RESULT 12  
US-60-328-205-1935/c  
; Sequence 1935, Application US/60328205  
; GENERAL INFORMATION:  
; APPLICANT: Shannon, Mark  
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1  
; FILE REFERENCE: AEOMICA-26  
; CURRENT APPLICATION NUMBER: US/60/328,205  
; CURRENT FILING DATE: 2001-10-10  
; NUMBER OF SEQ ID NOS: 4162  
; SOFTWARE: Aecmica Sequence Listing Engine  
; SEQ ID NO 1935  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-60-328-205-1935

Query Match 83.3%; Score 15; DB 87; Length 17;  
Best Local Similarity 100.0%; Pred. No. 8.9e+04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGGGGGAGGAGGGG 18  
|||  
Db 16 GAGGGGGAGGAGGGG 2

RESULT 13  
US-60-328-205-1936/c  
; Sequence 1936, Application US/60328205  
; GENERAL INFORMATION:  
; APPLICANT: Shannon, Mark  
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1  
; FILE REFERENCE: AEOMICA-26  
; CURRENT APPLICATION NUMBER: US/60/328,205  
; CURRENT FILING DATE: 2001-10-10  
; NUMBER OF SEQ ID NOS: 4162  
; SOFTWARE: Aecmica Sequence Listing Engine  
; SEQ ID NO 1936  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-60-328-205-1936

Query Match 83.3%; Score 15; DB 87; Length 17;  
Best Local Similarity 100.0%; Pred. No. 8.9e+04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGGGGGAGGAGGGG 18  
|||  
Db 15 GAGGGGGAGGAGGGG 1

RESULT 14  
US-10-310-188-6227/c  
; Sequence 6227, Application US/10310188  
; GENERAL INFORMATION:  
; APPLICANT: RosettaGenomics  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: 47487  
; CURRENT APPLICATION NUMBER: US/10/310,188  
; CURRENT FILING DATE: 2002-12-19  
; NUMBER OF SEQ ID NOS: 86841  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6227  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-310-188-6227

Query Match 83.3%; Score 15; DB 50; Length 18;  
Best Local Similarity 100.0%; Pred. No. 8.9e+04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGAGGGGGAGGAGGGG 17  
|||  
Db 15 GGAGGGGGAGGAGGGG 1

RESULT 15  
US-10-303-778-16894  
; Sequence 16894, Application US/10303778  
; GENERAL INFORMATION:  
; APPLICANT: RosettaGenomics  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL  
; TITLE OF INVENTION: REGULATORY GENES AND USES THEREOF  
; FILE REFERENCE: 47416  
; CURRENT APPLICATION NUMBER: US/10/303,778  
; CURRENT FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 17608  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 16894  
; LENGTH: 19

; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-303-778-16894

Query Match 83.3%; Score 15; DB 50; Length 19;  
Best Local Similarity 100.0%; Pred. No. 8.9e+04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGAGGGGGGAGGAGGG 17  
| | | | | | | | | |  
Db 4 GGAGGGGGGAGGAGGG 18

Search completed: October 27, 2003, 17:52:53  
Job time : 2356.29 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:29 ; Search time 162 Seconds  
(without alignments)  
299,938 Million cell updates/sec

Title: US-09-331-204A-7

Perfect score: 18

Sequence: 1 ttggaggaggaggagg 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 1643890

Minimum DB seq length: 0

Maximum DB seq length: 22

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_19Jun03:\*

1: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:\*

2: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:\*

3: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:\*

4: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:\*

5: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:\*

6: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:\*

7: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:\*

8: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:\*

9: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:\*

10: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:\*

11: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:\*

12: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:\*

13: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:\*

14: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:\*

15: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:\*

16: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:\*

17: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:\*

18: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:\*

19: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:\*

20: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:\*

21: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:\*

22: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:\*

23: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*

24: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

25: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	17 AAT36242	CD28 expression in
2	18	100.0	18	20 AAX90335	CD28 inhibiting ph
3	16.4	91.1	18	17 AAT36243	CD28 expression in
4	16.4	91.1	18	20 AAX90336	CD28 inhibiting ph
5	15.4	85.6	21	11 AAQ06932	NMy24 nucleotide c
6	15.4	85.6	21	18 AAT98040	Human or simian im
C 7	15	83.3	17	24 ABV91221	Human POSHL1 scann
C 8	15	83.3	17	24 ABV91222	Human POSHL1 scann

C	9	15	83.3	17	24	ABV91223	Human POSHL1 scann
	10	14.8	82.2	18	17	AAT36196	Triplex forming ol
	11	14.8	82.2	18	20	AAX90328	CD28 inhibiting ph
	12	14.8	82.2	18	20	AAX90290	CD28 inhibition ol
	13	14.8	82.2	18	21	AAZ99625	Nucleotide sequenc
C	14	14.8	82.2	18	21	AAZ99650	Triplex forming ol
	15	14.8	82.2	21	17	AAT36197	CD28 inhibiting ph
	16	14.8	82.2	21	20	AAX90329	CD28 inhibition ol
C	18	14.8	82.2	21	20	AAX90291	Hepatitis C virus
	17	14.8	82.2	21	24	ABK99294	Triple helix formi
C	19	14.4	80.0	17	20	AAX14740	Human POSHL1 scann
C	20	14	77.8	17	24	ABV91220	Human POSHL1 scann
C	21	14	77.8	17	24	ABV91224	Human casein kinas
	22	13.8	76.7	20	24	ABSG7915	Gastric acid produ
	23	13.6	75.6	22	22	AAF16593	TPO B13 sequence.
	24	13.4	74.4	21	20	AAX32871	Human tumour assoc
C	25	13.2	73.3	20	22	AAH50875	RNL primer used to
C	26	13.2	73.3	20	22	AAD03330	Human NOGO Hammerh
C	27	13	72.2	17	23	ABK00046	Human NOGO Hammerh
C	28	13	72.2	17	23	ABK00047	Human NOGO Inozyme
C	29	13	72.2	17	23	ABK00899	Human NOGO Inozyme
C	30	13	72.2	17	23	ABK00900	Human NOGO Inozyme
C	31	13	72.2	17	23	ABK00901	Human POSHL1 scann
C	32	13	72.2	17	24	ABV91219	Human POSHL1 scann
C	33	13	72.2	17	24	ABV91225	Human tissue kalli
	34	12.8	71.1	17	20	AAV55680	Hammerhead ribozym
C	35	12.8	71.1	17	21	AAF01954	Oestrogen receptor
C	36	12.8	71.1	17	21	AAF05272	Human NOGO Hammerh
C	37	12.8	71.1	17	21	AAA25277	Human NOGO Inozyme
C	38	12.8	71.1	17	23	ABK00045	Human tissue kalli
C	39	12.8	71.1	17	23	ABK00894	Human Ets-2 phosph
	40	12.8	71.1	17	24	AAAL43484	3' flanking sequen
	41	12.8	71.1	18	21	AAA38350	Human psoriasis-li
	42	12.8	71.1	20	15	AAQ55605	Human psoriasis-li
C	43	12.8	71.1	20	21	AAC60760	Human psoriasis-li
C	44	12.8	71.1	20	21	AAC62403	Feline immunodefec
C	45	12.8	71.1	20	21	AAA88033	

ALIGNMENTS

RESULT 1

AAT36242

ID AAT36242 standard; DNA; 18 BP.

XX AAT36242;

XX 25-MAR-2003 (updated)

DT 16-APR-1997 (first entry)

XX CD28 expression inhibiting oligonucleotide, RT05s.

XX Reduction; T cell; CD28; Gene expression; treatment; immune system;  
KW disorder; graft versus host disease; septic shock; viral disease;  
KW psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;  
KW multiple sclerosis; uveitis; rheumatoid arthritis; interleukin 2;  
KW systemic lupus erythematosus; inflammatory bowel disease;  
KW IL-2; production; antisense; inhibition; ss

XX Synthetic.

XX WO9624380-A1.

XX 15-AUG-1996.

XX 05-FEB-1996; 96WO-US01507.

XX 09-FEB-1995; 95US-0387041.

PR 18-SEP-1995; 95US-0529878.

PR 09-FEB-1995; 95US-0387041.

PR 18-SEP-1995; 95US-0529878.

XX

PA (ICNC ) ICN PHARM INC.  
XX Tam RC;  
PI  
XX WPI; 1996-384228/38.  
DR  
XX  
PT Oligo:nucleotide which reduces CD28 gene expression in T cells -  
PT for treating immune system diseases, e.g. graft vs. host disease,  
PT septic shock, psoriasis, etc.  
XX  
PS Example 2; Page 45; 77pp; English.  
XX  
CC The present oligonucleotide reduces CD28 dependent interleukin-2  
CC (IL-2) production and T cell CD28 gene expression, useful in the  
CC treatment of CD28 mediated diseases, particularly immune system  
CC disorders, e.g. graft versus host disease, septic shock, viral  
CC disease, psoriasis, type I diabetes mellitus, thyroiditis,  
CC sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis,  
CC systemic lupus erythematosus, inflammatory bowel disease, etc..  
CC Reducing CD28 expression may reduce the effects of antigenic  
CC stimulation of CD28 positive T cells, with a consequent reduction  
CC in cytokine release.  
CC (Updated on 25-MAR-2003 to correct PR field.)  
XX  
XX Sequence 18 BP; 3 A; 0 C; 13 G; 2 T; 0 other;  
SQ Query Match 100.0%; Score 18; DB 17; Length 18;  
Best Local Similarity 100.0%; Pred.No. 5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 TTGGAGGGGGAGGAGGGG 18  
Db 1 TTGGAGGGGGAGGAGGGG 18  
  
RESULT 2  
AAX90335  
ID AAX90335 standard; DNA; 18 BP.  
XX  
AC AAX90335;  
XX  
DT 24-SEP-1999 (first entry)  
XX  
DE CD28 inhibiting phosphorothioate oligonucleotide RT05S.  
XX  
XX CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;  
KW immune system mediated disease; gamma-interferon; IL-8;  
KW phosphorothioate; ss.  
XX  
OS Synthetic.  
XX  
XX US5932556-A.  
PN  
XX  
PD 03-AUG-1999.  
XX  
PF 18-SEP-1995; 95US-0529878.  
XX  
PR 18-SEP-1995; 95US-0529878.  
XX  
PA (TAMR/) TAM R C.  
XX  
PI Tam RC;  
XX  
XX WPI; 1999-443609/37.  
DR  
XX Treatment of immune system-mediated diseases by inhibiting  
PT expression of CD28, IL-2, gamma-interferon or IL-8  
XX  
PS Example; Column 24; 45pp; English.  
XX  
CC The present invention describes a method for inhibiting the expression  
CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method  
CC comprises subcutaneous administration of an oligonucleotide (OGN).

CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the  
CC method. The OGNs are used for the treatment of immune system-mediated  
CC diseases. The present sequence represents a CD28 inhibiting  
CC phosphorothioate oligonucleotide used in the exemplification of the  
CC present invention.  
XX  
SQ Sequence 18 BP; 3 A; 0 C; 13 G; 2 T; 0 other;  
  
Query Match 100.0%; Score 18; DB 20; Length 18;  
Best Local Similarity 100.0%; Pred.No. 5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 TTGGAGGGGGAGGAGGGG 18  
Db 1 TTGGAGGGGGAGGAGGGG 18  
  
RESULT 3  
AAT36243  
ID AAT36243 standard; DNA; 18 BP.  
XX  
AC AAT36243;  
XX  
DT 25-MAR-2003 (updated)  
DT 16-APR-1997 (first entry)  
XX  
DE CD28 expression inhibiting oligonucleotide, RT09S.  
XX  
XX Reduction; T cell; CD28; gene expression; treatment; immune system;  
KW disorder; graft versus host disease; septic shock; viral disease;  
KW psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;  
KW multiple sclerosis; uveitis; rheumatoid arthritis; interleukin 2;  
KW systemic lupus erythematosus; inflammatory bowel disease;  
KW IL-2; production; antisense; inhibition; ss  
XX  
OS Synthetic.  
XX  
XX WO9624380-A1.  
PN  
XX  
PD 15-AUG-1996.  
XX  
XX 05-FEB-1996; 96WO-US01507.  
PF  
XX  
PR 09-FEB-1995; 95US-0387041.  
PR 18-SEP-1995; 95US-0529878.  
PR 09-FEB-1995; 95US-0387041.  
PR 18-SEP-1995; 95US-0529878.  
XX  
PA (ICNC ) ICN PHARM INC.  
XX  
XX Tam RC;  
PI  
XX  
XX WPI; 1996-384228/38.  
DR  
XX Oligo:nucleotide which reduces CD28 gene expression in T cells -  
PT for treating immune system diseases, e.g. graft vs. host disease,  
PT septic shock, psoriasis, etc.  
XX  
PS Example 2; Page 45; 77pp; English.  
XX  
CC The present oligonucleotide reduces CD28 dependent interleukin-2  
CC (IL-2) production and T cell CD28 gene expression, useful in the  
CC treatment of CD28 mediated diseases, particularly immune system  
CC disorders, e.g. graft versus host disease, septic shock, viral  
CC disease, psoriasis, type I diabetes mellitus, thyroiditis,  
CC sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis,  
CC systemic lupus erythematosus, inflammatory bowel disease, etc..  
CC Reducing CD28 expression may reduce the effects of antigenic  
CC stimulation of CD28 positive T cells, with a consequent reduction  
CC in cytokine release.  
CC (Updated on 25-MAR-2003 to correct PR field.)  
XX  
XX Sequence 18 BP; 2 A; 0 C; 13 G; 3 T; 0 other;

Query Match 91.1%; Score 16.4; DB 17; Length 18;  
Best Local Similarity 94.4%; Pred. No. 2e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGGAGGGG 18  
| | | | | | | | | | | | | | | |  
DB 1 TTGGAGGGGGGAGGTGGG 18

RESULT 4  
AAX90336  
ID AAX90336 standard; DNA; 18 BP.  
XX  
AC AAX90336;  
XX  
DT 24-SEP-1999 (first entry)  
XX  
DE CD28 inhibiting phosphorothioate oligonucleotide RT09S.  
XX  
KW CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;  
KW immune system mediated disease; gamma-interferon; IL-8;  
KW phosphorothioate; ss.  
XX  
OS Synthetic.  
XX  
PN US5932556-A.  
XX  
PD 03-AUG-1999.  
XX  
PF 18-SEP-1995; 95US-0529878.  
XX  
PR 18-SEP-1995; 95US-0529878.  
XX  
PA (TAMR/) TAM R C.  
XX  
PI Tam RC;  
XX  
DR WPI; 1999-443609/37.  
XX  
PT Treatment of immune system-mediated diseases by inhibiting  
PT expression of CD28, IL-2, gamma-interferon or IL-8  
XX  
PS Example; Column 24; 45pp; English.  
XX

CC The present invention describes a method for inhibiting the expression  
CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method  
CC comprises subcutaneous administration of an oligonucleotide (OGN).  
CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the  
CC method. The OGNs are used for the treatment of immune system-mediated  
CC diseases. The present sequence represents a CD28 inhibiting  
CC phosphorothioate oligonucleotide used in the exemplification of the  
CC present invention.  
XX  
SQ Sequence 18 BP; 2 A; 0 C; 13 G; 3 T; 0 other;

Query Match 91.1%; Score 16.4; DB 20; Length 18;  
Best Local Similarity 94.4%; Pred. No. 2e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGGAGGGG 18  
| | | | | | | | | | | | | | | |  
DB 1 TTGGAGGGGGGAGGTGGG 18

RESULT 5  
AAQ06932  
ID AAQ06932 standard; DNA; 21 BP.  
XX  
AC AAQ06932;  
XX  
DT 09-JAN-2003 (updated)  
DT 05-MAR-1991 (first entry)

XX MMy24 nucleotide constituent of vpx gene of HIV-2 ROD  
DE and SIV-MAC.  
XX HIV-2; SIV; AIDS; anti-sense nucleotide; ss.  
XX Human immunodeficiency virus.  
OS Simian immunodeficiency virus.  
XX EP403333-A.  
XX 19-DEC-1990.  
PD 05-JUN-1990; 90EP-0401520.  
PF 20-SEP-1989; 89FR-0012371.  
XX (INSP ) INST PASTEUR.  
PA (INRM ) INSERM INST NAT SANTE RE.  
XX Moncany M, Montagnier L;  
PI WPI; 1990-378039/51.  
DR  
XX New nucleotide sequences derived from genome of HIV-1, HIV-2 and  
PT SIV - useful as primers for amplification of immuno-deficiency  
PT viruses in diagnosis and for raising antibodies in treatment of  
PT HIV infections  
XX  
PS Claim 7; page 20; 24pp; French.  
XX  
CC This nucleotide sequence is found in posn. 6228-6208 of HIV-2 ROD  
CC and 6141-6121 of SIV-MAC. It is the anti-sense strand of a primer  
CC pair used to amplify these HIV-1, HIV-2 and SIV viral sequences,  
CC esp. in conjunction with in vitro diagnosis of infection. It is  
CC useful for treating viral diseases, eg. AIDS.  
CC See also AAQ06905-31 and AAQ06933-54.  
CC (Updated on 09-JAN-2003 to add missing OS field.)  
XX  
SQ Sequence 21 BP; 5 A; 2 C; 13 G; 1 T; 0 other;

Query Match 85.6%; Score 15.4; DB 11; Length 21;  
Best Local Similarity 94.1%; Pred. No. 4.5e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGGAGGGGGAGGGGG 18  
| | | | | | | | | | | | | | | |  
DB 3 TGGAGGGGGAGGGAGG 19

RESULT 6  
AAT98040  
ID AAT98040 standard; DNA; 21 BP.  
XX  
AC AAT98040;  
XX  
DT 25-MAR-2003 (updated)  
DT 08-SEP-1998 (first entry)  
XX  
DE Human or simian immunodeficiency virus detection primer MMy24.  
XX  
KW Primer; PCR; amplification; gag; vpr; pol; vpu; HIV-1; HIV-2; SIV; nef2;  
KW vif2; vpx; detection; ss.  
XX  
OS Synthetic.  
OS Human immunodeficiency virus.  
OS Simian immunodeficiency virus.  
XX  
PN EP806484-A2.  
XX  
PD 12-NOV-1997.  
XX  
PF 05-JUN-1990; 97EP-0110543.

```
XX 02-JUN-1989; 89FR-0007354.
PR 20-SEP-1989; 89FR-0012371.
PR 05-JUN-1990; 90EP-0401520.
XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA (INSP ) INST PASTEUR.
XX Moncany M, Montagnier L;
PI WPI; 1997-538622/50.
DR Oligo-nucleotide primers for amplifying retroviral nucleic acids -
XX comprising conserved sequences of human immunodeficiency virus and
PT simian immunodeficiency virus genes
PT Claim 10; Page 21; 23pp; French.
XX The oligonucleotides AAT98010-T98059 are useful as primers for nucleic
CC acid amplification of conserved sequences of the gag, vpr, pol or vpu
CC genes of the HIV-1 strains Bru, Mal, Eli, HIV-2 ROD or simian
CC immunodeficiency virus (SIV) MAC or the nef2, vif2 or vpx genes of HIV-2
CC ROD and SIV MAC. This primer is targetted to sequences in the vpx gene of
CC the viral strains. The sequences are therefore used to detect HIV-1,
CC HIV-2 or SIV infections.
CC (Updated on 25-MAR-2003 to correct PF field.)
CC (Updated on 25-MAR-2003 to correct PR field.)
XX Sequence 21 BP; 5 A; 2 C; 13 G; 1 T; 0 other;
SQ Query Match 85.6%; Score 15.4; DB 18; Length 21;
Best Local Similarity 94.1%; Pred. No. 4.5e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 TGGAGGGGGAGGAGGGG 18
DB 3 TGGAGGGGGAGGAGGAG 19
RESULT 7
ABV91221/c
ID ABV91221 standard; DNA; 17 BP.
XX AC ABV91221;
XX DT 23-DEC-2002 (first entry)
XX DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1934.
XX KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW gene therapy; transgenic; ss.
XX OS Homo sapiens.
XX PN EP1239051-A2.
XX PD 11-SEP-2002.
XX PF 28-JAN-2002; 2002EP-0001165.
XX PR 30-JAN-2001; 2001WO-US00663.
PR 30-JAN-2001; 2001WO-US00664.
PR 30-JAN-2001; 2001WO-US00665.
PR 30-JAN-2001; 2001WO-US00666.
PR 30-JAN-2001; 2001WO-US00667.
PR 30-JAN-2001; 2001WO-US00668.
PR 30-JAN-2001; 2001WO-US00669.
PR 30-JAN-2001; 2001WO-US00670.
PR 23-MAY-2001; 2001US-0864761.
PR 10-OCT-2001; 2001US-0328205.
XX (AEOM-) AEOMICA INC.
XX Shannon M;
XX WPI; 2002-684061/74.
XX Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide,
PT POSHL-1, useful for treating disorders associated with decreased
PT expression or activity of human POSHL1 -
XX Example 2; SEQ ID NO 1934; 60pp + Sequence Listing; English.
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC acids (Sl, ABB83999), a sequence having 65% sequence identity to (S1),
CC (S1) having 95% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (I) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC caused by altered expression of human POSHL1 including diagnosing and
CC treating cancer, they are useful in the development of vaccines and (II) is
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention.
CC Note: The present sequence did not form part of the printed
CC specification, but is based on sequence information supplied to Derwent
CC by the European Patent Office.
XX Sequence 17 BP; 1 A; 12 C; 0 G; 4 T; 0 other;
SQ Query Match 83.3%; Score 15; DB 24; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GAGGGGGAGGAGGGG 18
DB 17 GAGGGGGAGGAGGGG 3
RESULT 8
ABV91222/c
ID ABV91222 standard; DNA; 17 BP.
XX AC ABV91222;
XX DT 23-DEC-2002 (first entry)
XX DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1935.
XX KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW gene therapy; transgenic; ss.
XX OS Homo sapiens.
XX PN EP1239051-A2.
XX PD 11-SEP-2002.
XX PF 28-JAN-2002; 2002EP-0001165.
XX PR 30-JAN-2001; 2001WO-US00663.
PR 30-JAN-2001; 2001WO-US00664.
PR 30-JAN-2001; 2001WO-US00665.
PR 30-JAN-2001; 2001WO-US00666.
PR 30-JAN-2001; 2001WO-US00667.
PR 30-JAN-2001; 2001WO-US00668.
PR 30-JAN-2001; 2001WO-US00669.
PR 30-JAN-2001; 2001WO-US00670.
```

PR 23-MAY-2001; 2001US-0864761.  
PR 10-OCT-2001; 2001US-0328205.  
XX  
PA (AEOM-) AEOMICA INC.  
XX Shannon M;  
PI  
XX WPI; 2002-684061/74.  
DR  
XX Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide,  
PT POSHL-1, useful for treating disorders associated with decreased  
PT expression or activity of human POSHL1 -  
XX  
XX Example 2; SEQ ID NO 1935; 60pp + Sequence Listing; English.  
PS The invention relates to an isolated SH3 domain (POSH)-like signalling  
XX protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino  
CC acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),  
CC (S1) having 95% deviations, especially conservative substitutions or a  
CC fragment of the sequences comprising at least 8 contiguous amino acids.  
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an  
CC adaptor protein that interacts with Rho family small GTPases as well as  
CC downstream components of the signal transduction pathway. (I) is useful  
CC for identifying a specific binding partner. (I) and nucleic acids (II)  
CC encoding (I) are useful for diagnosing, monitoring disease and treating  
CC caused by altered expression of human POSHL1 including diagnosing and  
CC treating cancer, they useful in the development of vaccines and (II) is  
CC useful in gene therapy. (II) is useful for constructing microarrays which  
CC are useful for measuring and for surveying gene expression and creating  
CC transgenic non-human animals capable of producing the proteins. The  
CC present sequence is that of a scanning oligonucleotide useful in examples  
CC of the invention.  
CC Note: The present sequence did not form part of the printed  
CC specification, but is based on sequence information supplied to Derwent  
CC by the European Patent Office.  
XX  
SQ Sequence 17 BP; 1 A; 12 C; 0 G; 4 T; 0 other;  
Query Match 83.3%; Score 15; DB 24; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 GAGGGGGAGGAGGGG 18  
DB 16 GAGGGGGAGGAGGGG 2  
RESULT 9  
ABV91223/c  
ID ABV91223 standard; DNA; 17 BP.  
XX  
AC ABV91223;  
XX  
DT 23-DEC-2002 (first entry)  
XX  
DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1936.  
XX  
KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;  
KW Rho GTPase; signal transduction; Gene expression; cancer; vaccine;  
KW gene therapy; transgenic; ss.  
XX  
OS Homo sapiens.  
XX  
PN EP1239051-A2.  
XX  
PD 11-SEP-2002.  
XX  
PF 28-JAN-2002; 2002EP-0001165.  
XX  
PR 30-JAN-2001; 2001WO-US00663.  
PR 30-JAN-2001; 2001WO-US00664.  
PR 30-JAN-2001; 2001WO-US00665.  
PR 30-JAN-2001; 2001WO-US00666.

PR 30-JAN-2001; 2001WO-US00667.  
PR 30-JAN-2001; 2001WO-US00668.  
PR 30-JAN-2001; 2001WO-US00669.  
PR 30-JAN-2001; 2001WO-US00670.  
PR 23-MAY-2001; 2001US-0864761.  
PR 10-OCT-2001; 2001US-0328205.  
XX  
XX (AEOM-) AEOMICA INC.  
PA  
XX Shannon M;  
PI  
XX WPI; 2002-684061/74.  
DR  
XX Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide,  
PT POSHL-1, useful for treating disorders associated with decreased  
PT expression or activity of human POSHL1 -  
XX  
XX Example 2; SEQ ID NO 1936; 60pp + Sequence Listing; English.  
PS The invention relates to an isolated SH3 domain (POSH)-like signalling  
XX protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino  
CC acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),  
CC (S1) having 95% deviations, especially conservative substitutions or a  
CC fragment of the sequences comprising at least 8 contiguous amino acids.  
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an  
CC adaptor protein that interacts with Rho family small GTPases as well as  
CC downstream components of the signal transduction pathway. (I) is useful  
CC for identifying a specific binding partner. (I) and nucleic acids (II)  
CC encoding (I) are useful for diagnosing, monitoring disease and treating  
CC caused by altered expression of human POSHL1 including diagnosing and  
CC treating cancer, they useful in the development of vaccines and (II) is  
CC useful in gene therapy. (II) is useful for constructing microarrays which  
CC are useful for measuring and for surveying gene expression and creating  
CC transgenic non-human animals capable of producing the proteins. The  
CC present sequence is that of a scanning oligonucleotide useful in examples  
CC of the invention.  
CC Note: The present sequence did not form part of the printed  
CC specification, but is based on sequence information supplied to Derwent  
CC by the European Patent Office.  
XX  
SQ Sequence 17 BP; 1 A; 12 C; 1 G; 3 T; 0 other;  
Query Match 83.3%; Score 15; DB 24; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 GAGGGGGAGGAGGGG 18  
DB 15 GAGGGGGAGGAGGGG 1  
RESULT 10  
AAT36196  
ID AAT36196 standard; DNA; 18 BP.  
XX  
AC AAT36196;  
XX  
DT 25-MAR-2003 (updated)  
DT 15-APR-1997 (first entry)  
XX  
DE Triplex forming oligo targetting CD28 5'-UTR (nt 58-75).  
XX  
KW Reduction; T cell; CD28; gene expression; treatment; immune system;  
KW disorder; graft versus host disease; septic shock; viral disease;  
KW psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;  
KW multiple sclerosis; uveitis; rheumatoid arthritis; 5'-UTR;  
KW systemic lupus erythematosus; inflammatory bowel disease;  
KW triplex forming; oligonucleotide; 5'-untranslated region; ss  
XX  
OS Synthetic.  
XX  
PN WO9624380-A1.  
XX

PD 15-AUG-1996.  
XX  
PF 05-FEB-1996; 96WO-US01507.  
XX  
PR 09-FEB-1995; 95US-0387041.  
PR 18-SEP-1995; 95US-0529878.  
PR 09-FEB-1995; 95US-0387041.  
PR 18-SEP-1995; 95US-0529878.  
XX  
PA (ICNC ) ICN PHARM INC.  
XX  
PI Tam RC;  
XX  
DR WPI; 1996-384228/38.  
XX  
PT Oligo:nucleotide which reduces CD28 gene expression in T cells -  
PT for treating immune system diseases, e.g. graft vs. host disease,  
PT septic shock, psoriasis, etc.  
XX  
PS Claim 9; Page 54; 77pp; English.  
XX  
CC The present oligonucleotide reduces T cell CD28 gene expression,  
CC useful in the treatment of CD28 mediated diseases, particularly  
CC immune system disorders, e.g. graft versus host disease, septic  
CC shock, viral disease, psoriasis, type I diabetes mellitus,  
CC thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid  
CC arthritis, systemic lupus erythematosus, inflammatory bowel  
CC disease, etc.. Reducing CD28 expression may reduce the effects of  
CC antigenic stimulation of CD28 positive T cells, with a consequent  
CC reduction in cytokine release.  
CC (Updated on 25-MAR-2003 to correct PR field.)  
XX  
SQ Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;  
Query Match 82.2%; Score 14.8; DB 17; Length 18;  
Best Local Similarity 88.9%; Pred. No. 7.6e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 TTGGAGGGGGGAGGGG 18  
Db 1 TTGGAGGGGGTGGTGGG 18  
RESULT 11  
AAX90328  
ID AAX90328 standard; DNA; 18 BP.  
AC AAX90328;  
XX  
DT 24-SEP-1999 (first entry)  
XX  
DE CD28 inhibiting phosphorothioate oligonucleotide RT03S.  
XX  
KW CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;  
KW immune system mediated disease; gamma-interferon; IL-8;  
KW phosphorothioate; ss.  
XX  
OS Synthetic.  
XX  
PN US5932556-A.  
XX  
PD 03-AUG-1999.  
XX  
PF 18-SEP-1995; 95US-0529878.  
XX  
PR 18-SEP-1995; 95US-0529878.  
XX  
PA (TAMR/) TAM R C.  
XX  
PI Tam RC;  
XX  
DR WPI; 1999-443609/37.  
XX

PT Treatment of immune system-mediated diseases by inhibiting  
PT expression of CD28, IL-2, gamma-interferon or IL-8  
XX  
PS Example; Column 21; 45pp; English.  
XX  
CC The present invention describes a method for inhibiting the expression  
CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method  
CC comprises subcutaneous administration of an oligonucleotide (OGN).  
CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the  
CC method. The OGNs are used for the treatment of immune system-mediated  
CC diseases. The present sequence represents a CD28 inhibiting  
CC phosphorothioate oligonucleotide used in the exemplification of the  
CC present invention.  
XX  
SQ Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;  
Query Match 82.2%; Score 14.8; DB 20; Length 18;  
Best Local Similarity 88.9%; Pred. No. 7.6e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 TTGGAGGGGGGAGGGG 18  
Db 1 TTGGAGGGGGTGGTGGG 18  
RESULT 12  
AAX90290  
ID AAX90290 standard; DNA; 18 BP.  
XX  
AC AAX90290;  
XX  
DT 24-SEP-1999 (first entry)  
XX  
DE CD28 inhibition oligonucleotide RT03.  
XX  
KW CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;  
KW immune system mediated disease; gamma-interferon; IL-8; ss.  
XX  
OS Synthetic.  
XX  
PN US5932556-A.  
XX  
PD 03-AUG-1999.  
XX  
PF 18-SEP-1995; 95US-0529878.  
XX  
PR 18-SEP-1995; 95US-0529878.  
XX  
PA (TAMR/) TAM R C.  
XX  
PI Tam RC;  
XX  
DR WPI; 1999-443609/37.  
XX  
PT Treatment of immune system-mediated diseases by inhibiting  
PT expression of CD28, IL-2, gamma-interferon or IL-8  
XX  
PS Claim 5; Column 29; 45pp; English.  
XX  
CC The present invention describes a method for inhibiting the expression  
CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method  
CC comprises subcutaneous administration of an oligonucleotide (OGN).  
CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the  
CC method. The OGNs are used for the treatment of immune system-mediated  
CC diseases.  
XX  
SQ Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;  
Query Match 82.2%; Score 14.8; DB 20; Length 18;  
Best Local Similarity 88.9%; Pred. No. 7.6e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 TTGGAGGGGGGAGGGG 18



Db 1 TTGGAGGGGGTGGTGGG 18

RESULT 13  
AAZ99625  
ID AAZ99625 standard; DNA; 18 BP.

XX AC AAZ99625;

XX DT 12-JUL-2000 (first entry)

XX DE Nucleotide sequence of G-motif oligonucleotide GRI.

XX KW G-motif oligonucleotide; vaccine; Toxoplasmosis; viral infection;  
KW antigen presenting cell activation; natural killer cell; septic shock;  
KW cytotoxic T-lymphocyte; inflammation; autoimmune disease;  
KW rheumatoid arthritis; Crohn's disease; sarcoidosis; multiple sclerosis;  
KW Kawasaki syndrome; graft-versus-host disease; transplant rejection;  
KW helper T cell response 1-mediated disease; Lyme arthritis;  
KW Streptococcal induced arthritis; chronic inflammatory bowel disease;  
KW psoriasis vulgaris; experimental allergic encephalomyelitis;  
KW insulin-dependent diabetes mellitus; bacterial infection;  
KW parasitic infection; Leishmaniasis; spontaneous abortion; tumour; ss.

XX OS Synthetic.

XX PN WO200014217-A2.

XX PD 16-MAR-2000.

XX PF 03-SEP-1999; 99WO-EP06502.

XX PR 03-SEP-1998; 98EP-0116652.

XX PA (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.

XX PI Wagner H, Lipford GB, Heeg K;

XX DR WPI; 2000-256970/22.

XX PT Compositions comprising G-motif oligonucleotides useful for treating  
PT e.g. septic shock, rheumatoid arthritis, diabetes and human  
PT immunodeficiency virus infections -

XX PS Example 14; Page 32; 75pp; English.

XX CC The present sequence represents a G-motif oligonucleotide of the  
CC invention. The specification describes compositions comprising G-motif  
CC oligonucleotides. The G-motif oligonucleotides inhibit activation of  
CC antigen presenting cells by inhibiting the uptake of DNA by a cell, by  
CC stimulating natural killer cells, or by co-stimulating cytotoxic  
CC T-lymphocytes. The G-motif oligonucleotides may be used for the  
CC productions of vaccines for treating septic shock, inflammation,  
CC autoimmune diseases (e.g. rheumatoid arthritis, Crohn's disease,  
CC sarcoidosis, multiple sclerosis, Kawasaki syndrome, graft-versus-host  
CC disease and transplant rejection), helper T cell response 1-mediated  
CC diseases (e.g. Streptococcal induced arthritis, Lyme arthritis, chronic  
CC inflammatory bowel disease, psoriasis vulgaris, experimental allergic  
CC encephalomyelitis, and insulin-dependent diabetes mellitus), bacterial  
CC infections, parasitic infections (e.g. Leishmaniasis or Toxoplasmosis),  
CC viral infections (e.g. Cytomegalovirus and human immunodeficiency virus  
CC (HIV)-infections), spontaneous abortions and tumours. They may also be  
CC used to induce proliferation of bone marrow cells, especially macrophage  
CC precursor cells.

XX SQ Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;

Query Match 82.2%; Score 14.8; DB 21; Length 18;  
Best Local Similarity 88.9%; Pred. No. 7.6e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGAGGAGGGG 18

Db 1 TTGGAGGGGGTGGTGGG 18

RESULT 14  
AAZ99650/C  
ID AAZ99650 standard; DNA; 18 BP.

XX AC AAZ99650;

XX DT 12-JUL-2000 (first entry)

XX DE Nucleotide sequence of non-G-motif oligonucleotide GRFlcomp.

XX KW G-motif oligonucleotide; vaccine; Toxoplasmosis; viral infection;  
KW antigen presenting cell activation; natural killer cell; septic shock;  
KW cytotoxic T-lymphocyte; inflammation; autoimmune disease;  
KW rheumatoid arthritis; Crohn's disease; sarcoidosis; multiple sclerosis;  
KW Kawasaki syndrome; graft-versus-host disease; transplant rejection;  
KW helper T cell response 1-mediated disease; Lyme arthritis;  
KW Streptococcal induced arthritis; chronic inflammatory bowel disease;  
KW psoriasis vulgaris; experimental allergic encephalomyelitis;  
KW insulin-dependent diabetes mellitus; bacterial infection;  
KW parasitic infection; Leishmaniasis; spontaneous abortion; tumour; ss.

XX OS Synthetic.

XX PN WO200014217-A2.

XX PD 16-MAR-2000.

XX PF 03-SEP-1999; 99WO-EP06502.

XX PR 03-SEP-1998; 98EP-0116652.

XX PA (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.

XX PI Wagner H, Lipford GB, Heeg K;

XX DR WPI; 2000-256970/22.

XX PT Compositions comprising G-motif oligonucleotides useful for treating  
PT e.g. septic shock, rheumatoid arthritis, diabetes and human  
PT immunodeficiency virus infections -

XX PS Example 14; Page 32; 75pp; English.

XX CC The present sequence represents a non-G-motif oligonucleotide of the  
CC invention. The specification describes compositions comprising G-motif  
CC oligonucleotides. The G-motif oligonucleotides inhibit activation of  
CC antigen presenting cells by inhibiting the uptake of DNA by a cell, by  
CC stimulating natural killer cells, or by co-stimulating cytotoxic  
CC T-lymphocytes. The G-motif oligonucleotides may be used for the  
CC productions of vaccines for treating septic shock, inflammation,  
CC autoimmune diseases (e.g. rheumatoid arthritis, Crohn's disease,  
CC sarcoidosis, multiple sclerosis, Kawasaki syndrome, graft-versus-host  
CC disease and transplant rejection), helper T cell response 1-mediated  
CC diseases (e.g. Streptococcal induced arthritis, Lyme arthritis, chronic  
CC inflammatory bowel disease, psoriasis vulgaris, experimental allergic  
CC encephalomyelitis, and insulin-dependent diabetes mellitus), bacterial  
CC infections, parasitic infections (e.g. Leishmaniasis or Toxoplasmosis),  
CC viral infections (e.g. Cytomegalovirus and human immunodeficiency virus  
CC (HIV)-infections), spontaneous abortions and tumours. They may also be  
CC used to induce proliferation of bone marrow cells, especially macrophage  
CC precursor cells.

XX SQ Sequence 18 BP; 4 A; 13 C; 0 G; 1 T; 0 other;

Query Match 82.2%; Score 14.8; DB 21; Length 18;  
Best Local Similarity 88.9%; Pred. No. 7.6e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGAGGAGGGG 18

Db 18 TTGGAGGGGTGGTGGG 1

RESULT 15  
AAT36197  
ID AAT36197 standard; DNA; 21 BP.  
XX AC AAT36197;  
XX AC AAT36197;  
DT 25-MAR-2003 (updated)  
DT 15-APR-1997 (first entry)  
XX DE Triplex forming oligo targetting CD28 5'-UTR (nt 58-78).  
XX KW Reduction; T cell; CD28; gene expression; treatment; immune system;  
KW disorder; graft versus host disease; septic shock; viral disease;  
KW psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;  
KW multiple sclerosis; uveitis; rheumatoid arthritis; 5'-UTR;  
KW systemic lupus erythematosus; inflammatory bowel disease;  
KW triplex forming; oligonucleotide; 5'-untranslated region; ss  
XX OS Synthetic.  
XX PN WO9624380-A1.  
XX PD 15-AUG-1996.  
XX PF 05-FEB-1996; 96WO-US01507.  
XX PR 09-FEB-1995; 95US-0387041.  
PR 18-SEP-1995; 95US-0529878.  
PR 09-FEB-1995; 95US-0387041.  
PR 18-SEP-1995; 95US-0529878.  
XX PA (ICNC ) ICN PHARM INC.  
XX PI Tam RC;  
XX DR WPI; 1996-384228/38.  
XX PT Oligo:nucleotide which reduces CD28 gene expression in T cells -  
PT for treating immune system diseases, e.g. graft vs. host disease,  
PT septic shock, psoriasis, etc.  
XX PS Claim 10; Page 54; 77pp; English.  
XX CC The present oligonucleotide reduces T cell CD28 gene expression,  
CC useful in the treatment of CD28 mediated diseases, particularly  
CC immune system disorders, e.g. graft versus host disease, septic  
CC shock, viral disease, psoriasis, type I diabetes mellitus,  
CC thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid  
CC arthritis, systemic lupus erythematosus, inflammatory bowel  
CC disease, etc.. Reducing CD28 expression may reduce the effects of  
CC antigenic stimulation of CD28 positive T cells, with a consequent  
CC reduction in cytokine release.  
CC (Updated on 25-MAR-2003 to correct PR field.)  
XX SQ Sequence 21 BP; 1 A; 0 C; 16 G; 4 T; 0 other;  
Query Match 82.2%; Score 14.8; DB 17; Length 21;  
Best Local Similarity 88.9%; Pred. No. 7.6e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGAGGAGGGG 18  
Db 4 TTGGAGGGGGTGGTGGG 21

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: October 27, 2003, 10:32:29 ; Search time 376.114 Seconds  
(without alignments)  
1957.844 Million cell updates/sec

Title: US-09-331-204A-8  
Perfect score: 18  
Sequence: 1 ttggagggggaggtggg 18

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues  
Total number of hits satisfying chosen parameters: 681044

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:

- 1: gb\_ba:\*
- 2: gb\_htg:\*
- 3: gb\_in:\*
- 4: gb\_om:\*
- 5: gb\_ov:\*
- 6: gb\_pat:\*
- 7: gb\_ph:\*
- 8: gb\_pl:\*
- 9: gb\_pr:\*
- 10: gb\_ro:\*
- 11: gb\_sts:\*
- 12: gb\_sy:\*
- 13: gb\_un:\*
- 14: gb\_vi:\*
- 15: em\_ba:\*
- 16: em\_fun:\*
- 17: em\_hum:\*
- 18: em\_in:\*
- 19: em\_mu:\*
- 20: em\_om:\*
- 21: em\_or:\*
- 22: em\_ov:\*
- 23: em\_pat:\*
- 24: em\_ph:\*
- 25: em\_pl:\*
- 26: em\_ro:\*
- 27: em\_sts:\*
- 28: em\_un:\*
- 29: em\_vi:\*
- 30: em\_htg\_hum:\*
- 31: em\_htg\_inv:\*
- 32: em\_htg\_other:\*
- 33: em\_htg\_mus:\*
- 34: em\_htg\_pln:\*
- 35: em\_htg\_rod:\*
- 36: em\_htg\_mam:\*
- 37: em\_htg\_vrt:\*
- 38: em\_sy:\*
- 39: em\_htgo\_hum:\*
- 40: em\_htgo\_mus:\*
- 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	16.4	91.1	18	6	AX023402	AX023402 Sequence
2	16.4	91.1	18	6	AX023427	AX023427 Sequence
3	13.8	76.7	20	6	AX418779	AX418779 Sequence
4	13.8	76.7	21	6	A31974	A31974 Synthetic H
5	13.8	76.7	21	6	AR131393	AR131393 Sequence
6	13.8	76.7	21	6	BD001798	BD001798 Immunogen
7	13.4	74.4	17	6	AX532425	AX532425 Sequence
8	13.4	74.4	17	6	AX532426	AX532426 Sequence
9	13.4	74.4	17	6	AX532427	AX532427 Sequence
10	13.4	74.4	19	6	AX477615	AX477615 Sequence
11	13.4	74.4	19	6	AX505035	AX505035 Sequence
12	13.4	74.4	19	6	I28584	I28584 Sequence 37
13	13.4	74.4	19	6	I58746	I58746 Sequence 37
14	13.4	74.4	20	6	AR297674	AR297674 Sequence
15	13	72.2	20	6	AX662935	AX662935 Sequence
16	12.8	71.1	17	6	AR029938	AR029938 Sequence
17	12.8	71.1	17	6	AX214603	AX214603 Sequence
18	12.8	71.1	17	6	AX215452	AX215452 Sequence
19	12.8	71.1	18	6	AR055448	AR055448 Sequence
20	12.8	71.1	18	6	AX600765	AX600765 Sequence
21	12.8	71.1	18	6	E04543	E04543 linker. 9/1
22	12.8	71.1	20	6	AR212973	AR212973 Sequence
23	12.8	71.1	20	6	AX418780	AX418780 Sequence
24	12.8	71.1	20	6	BD177744	BD177744 A method
25	12.8	71.1	21	6	AR061827	AR061827 Sequence
26	12.8	71.1	21	6	AR252818	AR252818 Sequence
27	12.4	68.9	17	6	AX532424	AX532424 Sequence
28	12.4	68.9	17	6	AX532428	AX532428 Sequence
29	12.4	68.9	22	6	AX188499	AX188499 Sequence
30	12.2	67.8	17	6	AX235037	AX235037 Sequence
31	12.2	67.8	17	6	AX532447	AX532447 Sequence
32	12.2	67.8	18	6	A02165	A02165 Nucleotide
33	12.2	67.8	18	6	A04686	A04686 Nucleotide
34	12.2	67.8	19	6	AR012711	AR012711 Sequence
35	12.2	67.8	19	6	AR036657	AR036657 Sequence
36	12.2	67.8	19	6	AR088921	AR088921 Sequence
37	12.2	67.8	19	6	AR152368	AR152368 Sequence
38	12.2	67.8	20	6	AR012712	AR012712 Sequence
39	12.2	67.8	20	6	AR036658	AR036658 Sequence
40	12.2	67.8	20	6	AR088922	AR088922 Sequence
41	12.2	67.8	20	6	AR152369	AR152369 Sequence
42	12.2	67.8	20	6	AR232303	AR232303 Sequence
43	12.2	67.8	20	6	AX488033	AX488033 Sequence
44	12.2	67.8	20	6	BD138339	BD138339 Antisense
45	12.2	67.8	21	6	AX023422	AX023422 Sequence

ALIGNMENTS

RESULT 1  
AX023402  
LOCUS AX023402 18 bp DNA linear PAT 15-SEP-2000  
DEFINITION Sequence 17 from Patent WO0014217.  
ACCESSION AX023402  
VERSION AX023402.1 GI:10183802  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE  
1  
AUTHORS Lipford,G.B., Heeg,K. and Wagner,H.  
TITLE G-motif oligonucleotides and uses thereof  
JOURNAL Patent: WO 0014217-A 17 16-MAR-2000;  
LIPFORD GRAYSON B (DE) ; HEEG KLAUS (DE) ; WAGNER HERMANN (DE) ;





Query Match 74.4%; Score 13.4; DB 6; Length 17;  
Best Local Similarity 93.3%; Pred. No. 4e+05;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAGGGGAGGTGGG 18  
Db 15 GAGGGGAGGAGGG 1

RESULT 10  
AX477615  
LOCUS AX477615 19 bp DNA linear PAT 12-AUG-2002  
DEFINITION Sequence 67 from Patent WO0246433.  
ACCESSION AX477615  
VERSION AX477615.1 GI:22216795  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1  
AUTHORS Saus, J.  
TITLE Tnf-inducible promoters and methods for using  
JOURNAL Patent: WO 0246433-A 67 13-JUN-2002;  
Saus, Juan (ES)  
FEATURES  
source Location/Qualifiers  
1..19  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Primer ON-DHFR-F1"

BASE COUNT 3 a 2 c 11 g 3 t  
ORIGIN

Query Match 74.4%; Score 13.4; DB 6; Length 19;  
Best Local Similarity 93.3%; Pred. No. 3.9e+05;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGGAGGGGAGGTGG 16  
Db 5 TGGAGGAGGAGGTGG 19

RESULT 11  
AX505035  
LOCUS AX505035 19 bp DNA linear PAT 27-SEP-2002  
DEFINITION Sequence 67 from Patent WO0246378.  
ACCESSION AX505035  
VERSION AX505035.1 GI:23386357  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1  
AUTHORS Saus, J.  
TITLE Alternative pol k nucleotide and amino acid sequence and methods for using  
JOURNAL Patent: WO 0246378-A 67 13-JUN-2002;  
Saus, Juan (ES)  
FEATURES  
source Location/Qualifiers  
1..19  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Primer ON-DHFR-F1"

BASE COUNT 3 a 2 c 11 g 3 t  
ORIGIN

Query Match 74.4%; Score 13.4; DB 6; Length 19;  
Best Local Similarity 93.3%; Pred. No. 3.9e+05;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGGAGGGGAGGTGG 16

Db 5 TGGAGGAGGAGGTGG 19

RESULT 12  
I28584  
LOCUS I28584 19 bp DNA linear PAT 06-FEB-1997  
DEFINITION Sequence 37 from patent US 5571937.  
ACCESSION I28584  
VERSION I28584.1 GI:1819360  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Watanabe, K.A., Ren, W.-Y. and Weil, R.  
TITLE Complementary DNA and toxins  
JOURNAL Patent: US 5571937-A 37 05-NOV-1996;  
FEATURES  
source Location/Qualifiers  
1..19  
/organism="unknown"

BASE COUNT 6 a 0 c 12 g 1 t  
ORIGIN

Query Match 74.4%; Score 13.4; DB 6; Length 19;  
Best Local Similarity 93.3%; Pred. No. 3.9e+05;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGGGAGGTGGG 17  
Db 5 GGAGGAGGAGGTGGG 19

RESULT 13  
I58746  
LOCUS I58746 19 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 37 from patent US 5652350.  
ACCESSION I58746  
VERSION I58746.1 GI:2477984  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Watanabe, K.A., Ren, W.-Y. and Weil, R.  
TITLE Complementary DNA and toxins  
JOURNAL Patent: US 5652350-A 37 29-JUL-1997;  
FEATURES  
source Location/Qualifiers  
1..19  
/organism="unknown"

BASE COUNT 6 a 0 c 12 g 1 t  
ORIGIN

Query Match 74.4%; Score 13.4; DB 6; Length 19;  
Best Local Similarity 93.3%; Pred. No. 3.9e+05;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGGGAGGTGGG 17  
Db 5 GGAGGAGGAGGTGGG 19

RESULT 14  
AR297674/c  
LOCUS AR297674 20 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 9409 from patent US 6537751.  
ACCESSION AR297674  
VERSION AR297674.1 GI:31684958  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)

AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.  
TITLE Biallelic markers for use in constructing a high density  
disequilibrium map of the human genome  
JOURNAL Patent: US 6537751-A 9409 25-MAR-2003;  
FEATURES Location/Qualifiers

source 1..20  
BASE COUNT 4 a 11 c 0 g 5 t  
ORIGIN /organism="unknown"

Query Match 74.4%; Score 13.4; DB 6; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.8e+05;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGAGGTG 15  
Db 17 TTGGAGGGGGAGATG 3

RESULT 15  
AX662935  
LOCUS AX662935 20 bp. DNA linear PAT 22-MAR-2003  
DEFINITION Sequence 22 from Patent WO02066681.  
ACCESSION AX662935  
VERSION AX662935.1 GI:29163516  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Poole,J., Roninson,I.B. and Chang,B.D.  
TITLE Reagents and methods for identifying and modulating expression of  
genes regulated by cdk inhibitors  
JOURNAL Patent: WO 02066681-A 22 29-AUG-2002;  
THE BOARD OF TRUSTEES OF THE UNIVERSITY OF ILLINOIS (US)  
FEATURES Location/Qualifiers  
source 1..20  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/note="Antisense PCR primer for CC3 promoter (spec Table  
IIIA)"

BASE COUNT 4 a 0 c 12 g 4 t  
ORIGIN

Query Match 72.2%; Score 13; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.5e+05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AGGGGAGGTGGG 17  
Db 1 AGGGGAGGTGGG 13

Search completed: October 27, 2003, 11:09:27  
Job time : 377.114 secs